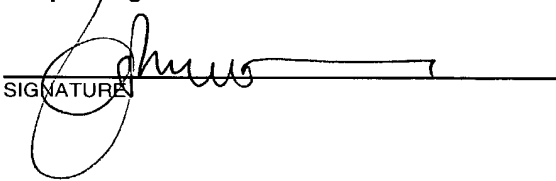


416 Rec'd PCT/PTO 12 JUN 2000

U.S. APPLICATION NO. (If known, see 37 C.F.R. 1.55) 09/4581286		INTERNATIONAL APPLICATION NO. PCT/AU98/01023		ATTORNEY'S DOCKET NUMBER 47-138							
17. <input checked="" type="checkbox"/> The following fees are submitted:				CALCULATIONS PTO USE ONLY							
BASIC NATIONAL FEE (37 C.F.R. 1.492(a)(1)-(5)): -- Neither international preliminary examination fee (37 C.F.R. 1.482) nor international search fee (37 C.F.R. 1.445(a)(2)) paid to USPTO and International Search Report not prepared by the EPO or JPO\$970.00 -- International preliminary examination fee (37 C.F.R. 1.482) not paid to USPTO but International Search Report prepared by the EPO or JPO\$840.00 -- International preliminary examination fee (37 C.F.R. 1.482) not paid to USPTO but international search fee (37 C.F.R. 1.445(a)(2)) paid to USPTO\$690.00 -- International preliminary examination fee paid to USPTO (37 C.F.R. 1.482) but all claims did not satisfy provisions of PCT Article 33(1)-(4)\$670.00 -- International preliminary examination fee paid to USPTO (37 C.F.R. 1.482) and all claims satisfied provisions of PCT Article 33(1)-(4)\$96.00 <div style="text-align: right;">ENTER APPROPRIATE BASIC FEE AMOUNT =</div>				<table border="1" style="width:100%; border-collapse: collapse;"> <tr> <td style="width:10%; text-align: right;">\$</td> <td style="width:60%; text-align: center;">970.00</td> <td style="width:30%;"></td> </tr> <tr> <td style="text-align: right;">\$</td> <td style="text-align: center;">0.00</td> <td></td> </tr> </table>		\$	970.00		\$	0.00	
\$	970.00										
\$	0.00										
Surcharge of \$130.00 for furnishing the oath or declaration later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 C.F.R. 1.492(e)).											
CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE								
Total Claims	34	-20 =	14	X	\$18.00						
Independent Claims	3	-3 =	0	X	\$78.00						
MULTIPLE DEPENDENT CLAIMS(S) (if applicable)				\$260.00	\$ 0.00						
TOTAL OF ABOVE CALCULATIONS =				\$	1222.00						
Reduction by 1/2 for filing by small entity, if applicable. A Small Entity Statement must also be filed (Note 37 C.F.R. 1.9, 1.27, 1.28).					0.00						
SUBTOTAL =				\$	1222.00						
Processing fee of \$130.00, for furnishing the English Translation later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 C.F.R. 1.492(f)).				+	0.00						
TOTAL NATIONAL FEE =				\$	1222.00						
Fee for recording the enclosed assignment (37 C.F.R. 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 C.F.R. 3.28, 3.31). \$40.00 per property				+	\$ 0.00						
Fee for Petition to Revive Unintentionally Abandoned Application (\$1210.00 - Small Entity = \$605.00)				\$	0.00						
TOTAL FEES ENCLOSED =				\$	1222.00						
				Amount to be:							
				refunded	\$						
				Charged	\$						
a. <input checked="" type="checkbox"/> A check in the amount of \$1222.00 to cover the above fees is enclosed. b. <input type="checkbox"/> Please charge my Deposit Account No. 14-1140 in the amount of \$_____ to cover the above fees. A duplicate copy of this form is enclosed. c. <input checked="" type="checkbox"/> The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. 14-1140. A duplicate copy of this form is enclosed. d. <input type="checkbox"/> The entire content of the foreign application(s), referred to in this application is/are hereby incorporated by reference in this application. NOTE: Where an appropriate time limit under 37 C.F.R. 1.494 or 1.495 has not been met, a petition to revive (37 C.F.R. 1.137(a) or (b)) must be filed and granted to restore the application to pending status.											
SEND ALL CORRESPONDENCE TO: NIXON & VANDERHYE P.C. 1100 North Glebe Road, 8 th Floor Arlington, Virginia 22201 Telephone: (703) 816-4000											
				 SIGNATURE							
				Leonard C. Mitchard NAME							
29,009		June 12, 2000									
REGISTRATION NUMBER		Date									

09/581286

416 Rec'd PCT/PTO 1 2 JUN 2000

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Patent Application of

ROSS et al

Atty. Ref.: 47-138

Serial No. Unassigned

Group:

Filed: June 12, 2000

Examiner:

For: P. GINGIVALIS POLYPEPTIDES AND
NUCLEOTIDES

* * * * *

June 12, 2000

Assistant Commissioner for Patents
Washington, DC 20231

PRELIMINARY AMENDMENT

Sir:

Please amend the above application as follows:

IN THE CLAIMS

Claim 11, lines 2 and 3, delete "any one of claims 1 to 10" and replace by --
claim 1--.

Claim 13, line 2, delete "or claim 12".

Claim 16, line 3, delete "any one of claims 1 to 10" and replace by --claim
1--.

Claim 17, lines 2 and 3, delete "claimed in claim 11 or claim 12" and
replace by --defined above--.

Claim 18, line 1 delete "or claim 17".

Claim 19, lines 2 and 3 delete "any one of claims 16 or 18" and replace by -
-claim 16--.

Claim 22, line 3, delete "or claim 12".

Claim 24, line 2, delete "or claim 23".

Claim 27, lines 1 and 2, delete "any one of claims 1 to 10" and replace by --
claim 1--.

Claim 30, lines 1 and 2, delete "any one of claims 27 to 29" and replace by
--claim 27--.

Claim 34, line 4, delete "or claim 33"

[illegible]

The above amendments have been made to place the application in a more traditional format.

NIXON & VANDERHYE P.C.

Leonard C. Mitchard
Reg. No. 29,009

- 3 -

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

09/581286

In re Patent Application of

ROSS et al

Serial No. Unassigned

Filed: June 12, 2000

For: P. GINGIVALIS POLYPEPTIDES AND NUCLEOTIDES

416 Rec'd PCT/PTO 12 JUN 2000

Atty. Ref.: 47-138

Group:

Examiner:

* * * * *

June 12, 2000

Assistant Commissioner for Patents
Washington, DC 20231

Sir:

SUBMISSION OF SEQUENCE LISTING

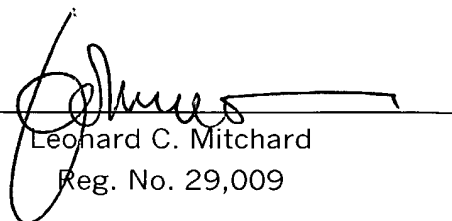
Attached is a printed sequence listing for this application and a copy of the computer readable CD-ROM disk in the attached envelope.

In accordance with 37 C.F.R. 1.821-1.825, I hereby state that the content of the paper and computer-readable copies of the sequence listing submitted in accordance with 37 C.F.R. 1.821(c) and (e), respectively, are the same. I hereby state that the submission, filed in accordance with 37 C.F.R. 1.821(g), does not introduce new matter.

Respectfully submitted,

NIXON & VANDERHYE P.C.

By: _____


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2 / PRTS

09/581286

416 Rec'd PCT/PTO 1 2 JUN 2000

WO 99/29870

PCT/AU98/01023

1

***Porphyromonas gingivalis* polypeptides and nucleotides**

FIELD OF THE INVENTION

5 The present invention relates to *P. gingivalis* nucleotide sequences, *P. gingivalis* polypeptides and probes for detection of *P. gingivalis*. The *P. gingivalis* polypeptides and nucleotides can be used in compositions for use in raising an immune response in a subject against *P. gingivalis* and treating or preventing or reducing the severity of the condition known as
10 periodontitis.

BACKGROUND OF THE INVENTION

15 Periodontal diseases are bacterial-associated inflammatory diseases of the supporting tissues of the teeth and range from the relatively mild form of gingivitis, the non-specific, reversible inflammation of gingival tissue to the more aggressive forms of periodontitis which are characterised by the destruction of the tooth's supporting structures. Periodontitis is associated with a subgingival infection of a consortium of specific Gram-negative
20 bacteria that leads to the destruction of the periodontium and is a major public health problem. One bacterium that has attracted considerable interest is *P. gingivalis* as the recovery of this microorganism from adult periodontitis lesions can be up to 50% of the subgingival anaerobically cultivable flora, whereas *P. gingivalis* is rarely recovered, and then in low
25 numbers, from healthy sites. A proportional increase in the level of *P. gingivalis* in subgingival plaque has been associated with an increased severity of periodontitis and eradication of the microorganism from the cultivable subgingival microbial population is accompanied by resolution of the disease. The progression of periodontitis lesions in non-human primates
30 has been demonstrated with the subgingival implantation of *P. gingivalis*. These findings in both animals and humans suggest a major role for *P. gingivalis* in the development of adult periodontitis.

35 *P. gingivalis* is a black-pigmented, anaerobic, asaccharolytic, proteolytic Gram-negative rod that obtains energy from the metabolism of specific amino acids. The microorganism has an absolute growth requirement for iron, preferentially in the form of haeme or its Fe(III)

oxidation product haemin and when grown under conditions of excess haemin is highly virulent in experimental animals. A number of virulence factors have been implicated in the pathogenicity of *P. gingivalis* including the capsule, adhesins, cytotoxins and extracellular hydrolytic enzymes.

5 In order to develop an efficacious and safe vaccine to prevent, eliminate or reduce *P. gingivalis* colonisation it is necessary to identify and produce antigens that are involved in virulence that have utility as immunogens possibly through the generation of specific antibodies. Whilst it is possible to attempt to isolate antigens directly from cultures of *P. gingivalis*
10 this is often difficult. For example as mentioned above, *P. gingivalis* is a strict anaerobe and can be difficult to isolate and grow. It is also known that, for a number of organisms, when cultured *in vitro* that many virulence genes are down regulated and the encoded proteins are no longer expressed. If conventional chemistry techniques were applied to purify vaccine candidates
15 potentially important (protective) molecules may not be identified. With DNA sequencing, as the gene is present (but not transcribed) even when the organism is grown *in vitro* it can be identified, cloned and produced as a recombinant DNA protein. Similarly, a protective antigen or therapeutic target may be transiently expressed by the organism *in vitro* or produced in
20 low levels making the identification of these molecules extremely difficult by conventional methods.

With serological identification of therapeutic targets one is limited to those responses which are detectable using standard methods such as Western Blotting or ELISA. The limitation here is the both the level of
25 response that is generated by the animal or human and determining whether this response is protective, damaging or irrelevant. No such limitation is present with a sequencing approach to the identification of potential therapeutic or prophylactic targets.

It is also well known that *P. gingivalis* produces a range of broadly
30 active proteases (University of Melbourne International Patent Application No PCT /AU 96/00673, US Patent Nos 5,475,097 and 5,523,390), which make the identification of intact proteins difficult because of their degradation by these proteases.

SUMMARY OF THE INVENTION

The present inventors have attempted to isolate *P. gingivalis* nucleotide sequences which can be used for recombinant production of *P. gingivalis* polypeptides and to develop nucleotide probes specific for *P. gingivalis*. The DNA sequences listed below have been selected from a large number of *P. gingivalis* sequences according to their indicative potential as vaccine candidates. This intuitive step involved comparison of the deduced protein sequence from the *P. gingivalis* DNA sequences to the known protein sequence databases. Some of the characteristics used to select useful vaccine candidates include; the expected cellular location, such as outer membrane proteins or secreted proteins, particular functional activities of similar proteins such as those with an enzymatic or proteolytic activity, proteins involved in essential metabolic pathways that when inactivated or blocked may be deleterious or lethal to the organism, proteins that might be expected to play a role in the pathogenesis of the organism eg. red cell lysis, cell agglutination or cell receptors and proteins which are paralogues to proteins with proven vaccine efficacy.

In a first aspect the present invention consists an isolated antigenic *Porphyromonas gingivalis* polypeptide, the polypeptide comprising;
an amino acid sequence selected from the group consisting of SEQ. ID. NO. 265 to SEQ. ID. NO. 528, SEQ. ID. NO. 531 and SEQ. ID. NO. 532; or
an amino acid sequence at least 85%, preferably at least 95%, identical to an amino acid sequence selected from the group consisting of SEQ. ID. NO. 265 to SEQ. ID. NO. 528, SEQ. ID. NO. 531 and SEQ. ID. NO. 532; or
at least 40 amino acids having a contiguous sequence of at least 40 amino acids identical to a contiguous amino acid sequence selected from the group consisting of SEQ. ID. NO. 265 to SEQ. ID. NO. 528, SEQ. ID. NO. 531 and SEQ. ID. NO. 532.

In an embodiment of the present invention the polypeptide comprises;
an amino acid sequence selected from the group consisting of SEQ. ID. NO. 386 to SEQ. ID. NO. 528 and SEQ. ID. NO. 532; or

an amino acid sequence at least 85%, preferably at least 95%, identical to an amino acid sequence selected from the group consisting of SEQ. ID. NO. 386 to SEQ. ID. NO. 528 and SEQ. ID. NO. 532; or

- 5 at least 40 amino acids having a contiguous sequence of at least 40 amino acids identical to a contiguous amino acid sequence selected from the group consisting of SEQ. ID. NO. 386 to SEQ. ID. NO. 528 and SEQ. ID. NO. 532.

- 10 As used herein % identity for polypeptides is to be calculated using the alignment algorithm of Needleman and Munsch (9) using a standard protein scoring matrix (Blosum 50).

- In a preferred embodiment of the present invention the polypeptide comprises an amino acid sequence selected from the group consisting of
- 15 SEQ. ID. NO. 386, SEQ. ID. NO. 424, SEQ. ID. NO. 425, SEQ. ID. NO. 434, SEQ. ID. NO. 447, SEQ. ID. NO. 458, SEQ. ID. NO. 475, SEQ. ID. NO. 498, SEQ. ID. NO. 499, SEQ. ID. NO. 500, SEQ. ID. NO. 501, SEQ. ID. NO. 387, SEQ. ID. NO. 400, SEQ. ID. NO. 411, SEQ. ID. NO. 419, SEQ. ID. NO. 420, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID. NO. 433, SEQ. ID. NO. 437, SEQ. ID. NO. 438, SEQ. ID. NO. 443, SEQ. ID. NO. 444, SEQ. ID. NO. 448,
- 20 SEQ. ID. NO. 449, SEQ. ID. NO. 452, SEQ. ID. NO. 455, SEQ. ID. NO. 457, SEQ. ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 462, SEQ. ID. NO. 463, SEQ. ID. NO. 467, SEQ. ID. NO. 468, SEQ. ID. NO. 469, SEQ. ID. NO. 482, SEQ. ID. NO. 484, SEQ. ID. NO. 485, SEQ. ID. NO. 494, SEQ. ID. NO. 508, SEQ. ID. NO. 509, SEQ. ID. NO. 510, SEQ. ID. NO. 520, SEQ. ID. NO. 521,
- 25 SEQ. ID. NO. 522, SEQ. ID. NO. 525, SEQ. ID. NO. 526, SEQ. ID. NO. 528, SEQ. ID. NO. 389, SEQ. ID. NO. 390 and SEQ. ID. NO. 391.

- In another preferred embodiment of the present invention the polypeptide comprises an amino acid sequence selected from the group consisting of residue 422 to residue 531 of SEQ. ID. NO. 303, residue 534 to
- 30 residue 582 of SEQ. ID. NO. 303, residue 127 to residue 232 of SEQ. ID. NO. 301, residue 240 to residue 259 of SEQ. ID. NO. 301, residue 139 to residue 156 of SEQ. ID. NO. 295, residue 160 to residue 178 of SEQ. ID. NO. 295, residue 180 to residue 207 of SEQ. ID. NO. 295, residue 221 to residue 257 of SEQ. ID. NO. 295, residue 259 to residue 323 of SEQ. ID. NO. 295, residue
- 35 885 to residue 985 of SEQ. ID. NO. 299, residue 147 to residue 259 of SEQ. ID. NO. 363, residue 140 to residue 252 of SEQ. ID. NO. 344, residue 247 to

residue 356 of SEQ. ID. NO. 353, residue 359 to residue 391 of SEQ. ID. NO. 353, residue 120 to residue 254 of SEQ. ID. NO. 300, residue 287 to residue 311 of SEQ. ID. NO. 286, residue 313 to residue 352 of SEQ. ID. NO. 288, residue 354 to residue 401 of SEQ. ID. NO. 286, residue 208 to residue 252 of
5 SEQ. ID. NO. 287, residue 259 to residue 373 of SEQ. ID. NO. 287, residue 5 to residue 120 of SEQ. ID. NO. 293, residue 123 to residue 139 of SEQ. ID. NO. 293, residue 233 to residue 339 of SEQ. ID. NO. 265, residue 67 to residue 228 of SEQ. ID. NO. 278, residue 130 to residue 172 of SEQ. ID. NO. 274, residue 174 to residue 238 of SEQ. ID. NO. 274, residue 99 to residue
10 112 of SEQ. ID. NO. 274, residue 114 to residue 128 of SEQ. ID. NO. 274, residue 26 to residue 69 of SEQ. ID. NO. 285, residue 71 to residue 128 of SEQ. ID. NO. 285, residue 130 to residue 146 of SEQ. ID. NO. 285, residue 620 to residue 636 of SEQ. ID. NO. 327, residue 638 to residue 775 of SEQ. ID. NO. 327, residue 397 to residue 505 of SEQ. ID. NO. 301, residue 528 to
15 residue 545 of SEQ. ID. NO. 301, residue 556 to residue 612 of SEQ. ID. NO. 301, residue 614 to residue 631 of SEQ. ID. NO. 301, residue 633 to residue 650 of SEQ. ID. NO. 301, residue 553 to residue 687 of SEQ. ID. NO. 299, residue 305 to residue 447 of SEQ. ID. NO. 289, residue 1 to residue 52 of SEQ. ID. NO. 364, residue 65 to residue 74 of SEQ. ID. NO. 364, residue 486
20 to residue 604 of SEQ. ID. NO. 275, residue 158 to residue 267 of SEQ. ID. NO. 272, residue 270 to residue 282 of SEQ. ID. NO. 272, residue 163 to residue 237 of SEQ. ID. NO. 273, residue 240 to residue 251 of SEQ. ID. NO. 273, residue 213 to residue 344 of SEQ. ID. NO. 282, residue 183 to residue 324 of SEQ. ID. NO. 292, residue 327 to residue 341 of SEQ. ID. NO. 292,
25 residue 352 to residue 372 of SEQ. ID. NO. 292, residue 141 to residue 166 of SEQ. ID. NO. 271, residue 168 to residue 232 of SEQ. ID. NO. 271, residue 1 to residue 13 of SEQ. ID. NO. 302, residue 15 to residue 28 of SEQ. ID. NO. 302, residue 30 to residue 72 of SEQ. ID. NO. 302, residue 476 to residue 529 of SEQ. ID. NO. 277, residue 41 to residue 146 of SEQ. ID. NO. 299, residue
30 149 to residue 162 of SEQ. ID. NO. 299, residue 166 to residue 177 of SEQ. ID. NO. 299, residue 192 to residue 203 of SEQ. ID. NO. 299, residue 71 to residue 343 of SEQ. ID. NO. 290, residue 346 to residue 363 of SEQ. ID. NO. 290, residue 36 to residue 240 of SEQ. ID. NO. 331, residue 242 to residue 270 of SEQ. ID. NO. 331, residue 1 to residue 192 of SEQ. ID. NO. 375,
35 residue 286 to residue 290 of SEQ. ID. NO. 375, residue 23 to residue 216 of SEQ. ID. NO. 279, residue 220 to residue 270 of SEQ. ID. NO. 279, residue

285 to residue 386 of SEQ. ID. NO. 279, residue 84 to residue 234 of SEQ. ID. NO. 297, residue 248 to residue 259 of SEQ. ID. NO. 297, residue 261 to residue 269 of SEQ. ID. NO. 297, residue 275 to residue 402 of SEQ. ID. NO. 294, residue 1 to residue 171 of SEQ. ID. NO. 298, residue 403 to residue 417
5 of SEQ. ID. NO. 307, residue 420 to residue 453 of SEQ. ID. NO. 307, residue 456 to residue 464 of SEQ. ID. NO. 307, residue 468 to residue 690 of SEQ. ID. NO. 307, residue 1 to residue 285 of SEQ. ID. NO. 304, residue 287 to residue 315 of SEQ. ID. NO. 304, residue 318 to residue 336 of SEQ. ID. NO. 304, residue 255 to residue 269 of SEQ. ID. NO. 342, residue 271 to residue
10 337 of SEQ. ID. NO. 342, residue 347 to residue 467 of SEQ. ID. NO. 281, residue 116 to residue 136 of SEQ. ID. NO. 375, residue 138 to residue 357 of SEQ. ID. NO. 375, residue 133 to residue 423 of SEQ. ID. NO. 364, residue 141 to residue 299 of SEQ. ID. NO. 305, residue 202 to residue 365 of SEQ. ID. NO. 296, residue 134 to residue 426 of SEQ. ID. NO. 288, residue 1 to
15 residue 218 of SEQ. ID. NO. 276, residue 1 to residue 246 of SEQ. ID. NO. 280, residue 444 to residue 608 of SEQ. ID. NO. 364, residue 10 to residue 686 of SEQ. ID. NO. 283, residue 1 to residue 148 of SEQ. ID. NO. 296, residue 1 to residue 191 of SEQ. ID. NO. 287, residue 193 to residue 204 of SEQ. ID. NO. 287, residue 209 to residue 373 of SEQ. ID. NO. 287, residue
20 211 to residue 470 of SEQ. ID. NO. 284, residue 472 to residue 482 of SEQ. ID. NO. 284, residue 133 to residue 144 of SEQ. ID. NO. 281, residue 146 to residue 336 of SEQ. ID. NO. 281, residue 1 to residue 264 of SEQ. ID. NO. 303, residue 265 to residue 295 of SEQ. ID. NO. 303, residue 297 to residue 326 of SEQ. ID. NO. 303, residue 328 to residue 338 of SEQ. ID. NO. 303,
25 residue 247 to residue 356 of SEQ. ID. NO. 353, residue 358 to residue 391 of SEQ. ID. NO. 353, residue 257 to residue 288 of SEQ. ID. NO. 298, residue 290 to residue 385 of SEQ. ID. NO. 298, residue 245 to residue 256 of SEQ. ID. NO. 298, residue 422 to residue 802 of SEQ. ID. NO. 303, residue 803 to residue 814 of SEQ. ID. NO. 303, residue 139 to residue 156 of SEQ. ID. NO.
30 295, residue 160 to residue 340 of SEQ. ID. NO. 295, residue 145 to residue 361 of SEQ. ID. NO. 282, residue 363 to residue 387 of SEQ. ID. NO. 282, residue 398 to residue 471 of SEQ. ID. NO. 282, residue 573 to residue 679 of SEQ. ID. NO. 320, residue 27 to residue 168 of SEQ. ID. NO. 291, residue 170 to residue 183 of SEQ. ID. NO. 291, residue 185 to residue 415 of SEQ. ID.
35 NO. 291, residue 1 to residue 301 of SEQ. ID. NO. 364, residue 114 to residue 702 of SEQ. ID. NO. 337, residue 377 to residue 412 of SEQ. ID. NO. 321,

residue 413 to residue 772 of SEQ. ID. NO. 321, residue 14 to residue 454 of
SEQ. ID. NO. 265, residue 129 to residue 614 of SEQ. ID. NO. 268, residue 1
to residue 930 of SEQ. ID. NO. 300, residue 932 to residue 1046 of SEQ. ID.
NO. 300, residue 1 to residue 301 of SEQ. ID. NO. 364, residue 1 to residue
5 42 of SEQ. ID. NO. 381, residue 44 to residue 973 of SEQ. ID. NO. 381,
residue 1 to residue 93 of SEQ. ID. NO. 358, residue 95 to residue 179 of SEQ.
ID. NO. 358, residue 181 to residue 227 of SEQ. ID. NO. 358, residue 114 to
residue 702 of SEQ. ID. NO. 337, residue 1 to residue 659 of SEQ. ID. NO.
355, residue 661 to residue 907 of SEQ. ID. NO. 355, residue 1 to residue 131
10 of SEQ. ID. NO. 370, residue 133 to residue 601 of SEQ. ID. NO. 370, residue
1 to residue 813 of SEQ. ID. NO. 344, residue 377 to residue 412 of SEQ. ID.
NO. 321, residue 413 to residue 772 of SEQ. ID. NO. 321, and residue 189 to
residue 614 of SEQ. ID. NO. 364.

In a second aspect the present invention consists in a n isolated
15 antigenic *Porphyromonas gingivalis* polypeptide, the polypeptide comprising
an amino acid sequence selected from the group consisting of SEQ. ID. NO.
386 to SEQ. ID. NO. 528 and SEQ. ID. NO. 532 less the leader sequence set
out in Table 3.

In a third aspect the present invention consists in an isolated DNA
20 molecule, the DNA molecule comprising a nucleotide sequence which
encodes the polypeptide of the first aspect the present invention or a
sequence which hybridises thereto under stringent conditions.

It is preferred that the isolated DNA molecule comprises a nucleotide
sequence selected from the group consisting of SEQ. ID. NO. 1 to SEQ. ID.
25 NO. 264, SEQ. ID. NO. 529 and SEQ. ID. NO. 530.

In a fourth aspect the present invention consists in a recombinant
expression vector comprising the DNA molecule of the second aspect of the
present invention operably linked to a transcription regulatory element.

The present invention also provides a cell comprising this
30 recombinant expression vector.

In a further aspect the present invention consists in a method for
producing a *P. gingivalis* polypeptide comprising culturing the cell under
conditions that permit expression of the polypeptide.

In yet a further aspect the present invention provides a composition
35 for use in raising an immune response directed against *P. gingivalis* in a
subject, the composition comprising an effective amount of at least one

polypeptide of the first aspect of the present invention, or at least one DNA molecule of the second aspect of the present invention, or both, and a pharmaceutically acceptable carrier. It is preferred that the pharmaceutically acceptable carrier is an adjuvant. In other aspects the present invention

5 provides methods of treating *P. gingivalis* infection in subject comprising the administration of the composition to the subject such that treatment of *P. gingivalis* infection occurs. The treatment may be prophylactic or therapeutic.

In yet another aspect the present invention provides an antibody

10 raised against a polypeptide of the first aspect the invention. The antibody may be polyclonal or monoclonal. The present invention also provides compositions including these antibodies. It is preferred that these compositions are adapted for oral use and may be, for example, dentrifices, mouthwashes, etc.

15 In a still further aspect the present invention provides a nucleotide probe comprising at least 18 nucleotides and having a contiguous sequence of at least 18 nucleotides identical to a contiguous nucleotide sequence selected from the group consisting of SEQ. ID. NO. 1 to SEQ. ID. NO. 121, SEQ. ID. NO. 529, and sequences complementary thereto. It is preferred that

20 the probe further comprises a detectable label.

The present invention also provides a method for detecting the presence of *P. gingivalis* nucleic acid in a sample comprising:

- (a) contacting a sample with the nucleotide probe under conditions in which a hybrid can form between the probe and a *P. gingivalis*
- 25 nucleic acid in the sample; and
- (b) detecting the hybrid formed in step (a), wherein detection of a hybrid indicates the presence of a *P. gingivalis* nucleic acid in the sample.

30 DETAILED DESCRIPTION

Definitions

A purified or isolated polypeptide or a substantially pure preparation of a polypeptide are used interchangeably herein and, as used herein, mean a

35 polypeptide that has been separated from other proteins, lipids, and nucleic acids with which it naturally occurs. Preferably, the polypeptide is also

As used herein, a "coding sequence" is a nucleic acid which is transcribed into messenger RNA and/or translated into a polypeptide when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a translation start codon at the five prime terminus and a translation stop code at the three prime terminus. A

coding sequence can include but is not limited to messenger RNA synthetic DNA, and recombinant nucleic acid sequences.

A "complement" of a nucleic acid as used herein refers to an anti-parallel or antisense sequence that participates in Watson-Crick base-pairing with the original sequence.

A "gene product" is a protein or structural RNA which is specifically encoded by a gene.

As used herein, the term "probe" refers to a nucleic acid, peptide or other chemical entity which specifically binds to a molecule of interest. Probes are often associated with or capable of associating with a label. A label is a chemical moiety capable of detection. Typical labels comprise dyes, radioisotopes, luminescent and chemiluminescent moieties, fluorophores, enzymes, precipitating agents, amplification sequences, and the like. Similarly, a nucleic acid, peptide or other chemical entity which specifically binds to a molecule of interest and immobilizes such molecule is referred herein as a "capture ligand". Capture ligands are typically associated with or capable of associating with a support such as nitro-cellulose, glass, nylon membranes, beads, particles and the like. The specificity of hybridization is dependent on conditions such as the base pair composition of the nucleotides, and the temperature and salt concentration of the reaction. These conditions are readily discernible to one of ordinary skill in the art using routine experimentation.

Homologous refers to the sequence similarity or sequence identity between two polypeptides or between two nucleic acid molecules. When a position in both of the two compared sequences is occupied by the same base or amino acid monomer subunit, e.g., if a position in each of two DNA molecules is occupied by adenine, then the molecules are homologous at that position. The percent of homology between two sequences is a function of the number of matching or homologous positions shared by the two sequences divided by the number of positions compared x 100.

The terms peptides, proteins, and polypeptides are used interchangeably herein.

An "immunogenic component" as used herein is a moiety, such as an *P. gingivalis* polypeptide, analog or fragment thereof, that is capable of eliciting a humoral and/or cellular immune response in a host animal.

An "antigenic component" as used herein is a moiety, such as *P. gingivalis* polypeptide, analog or fragment thereof, that is capable of binding to a specific antibody with sufficiently high affinity to form a detectable antigen-antibody complex.

5 As used herein, the term "cell-specific promoter" means a DNA sequence that serves as a promoter, i.e., regulates expression of a selected DNA sequence operably linked to the promoter, and which effects expression of the selected DNA sequence in specific cells of a tissue. The term also covers so-called "leaky" promoters, which regulate expression of a selected
10 DNA primarily in one tissue, but cause expression in other tissues as well.

As used herein, the term "control sequence" refers to a nucleic acid having a base sequence which is recognized by the host organism to effect the expression of encoded sequences to which they are ligated. The nature of such control sequences differs depending upon the host organism; in
15 prokaryotes, such control sequences generally include a promoter, ribosomal binding site, terminators, and in some cases operators; in eukaryotes, generally such control sequences include promoters, terminators and in some instances, enhancers. The term control sequence is intended to include at a minimum, all components whose presence is necessary for expression, and
20 may also include additional components whose presence is advantageous, for example, leader sequences.

As used herein, the term "operably linked" refers to sequences joined or ligated to function in their intended manner. For example, a control sequence is operably linked to coding sequence by ligation in such a way
25 that expression of the coding sequence is achieved under conditions compatible with the control sequence and host cell.

A "sample" as used herein refers to a biological sample, such as, for example, tissue or fluid isolated from an individual (including without limitation plasma, serum, cerebrospinal fluid, lymph, tears, saliva and tissue
30 sections) or from *in vitro* cell culture constituents, as well as samples from the environment.

The practice of the invention will employ, unless otherwise indicated, conventional techniques of chemistry, molecular biology, microbiology, recombinant DNA, and immunology well known to those
35 skilled in the art. Such techniques are described and explained throughout the literature in sources such as, J. Perbal, A Practical Guide to Molecular

- Cloning, John Wiley and Sons (1984), J. Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbour Laboratory Press (1989), T.A. Brown (editor), Essential Molecular Biology: A Practical Approach, Volumes 1 and 2, IRL Press (1991), D.M. Glover and B.D. Hames (editors), DNA
- 5 Cloning: A Practical Approach, Volumes 1-4, IRL Press (1995 and 1996), and F.M. Ausubel et al. (Editors), Current Protocols in Molecular Biology, Greene Pub. Associates and Wiley-Interscience (1988, including all updates until present). The disclosure of these texts are incorporated herein by reference.

10 Pharmaceutically Acceptable Carriers

- The antibodies, polypeptides and DNA of the present invention can be included in compositions which include a carrier or diluent. These compositions include pharmaceutical compositions where the carrier or
- 15 diluent will be pharmaceutically acceptable. Pharmaceutically acceptable carriers or diluents include those used in compositions suitable for oral, rectal, nasal, topical (including buccal and sublingual), vaginal, parenteral (including subcutaneous, intramuscular, intravenous, intradermal, intrathecal and epidural) administration. They are non-toxic to recipients at
- 20 the dosages and concentrations employed. Representative examples of pharmaceutically acceptable carriers or diluents include, but are not limited to; water, isotonic solutions which are preferably buffered at a physiological pH (such as phosphate-buffered saline or Tris-buffered saline) and can also contain one or more of, mannitol, lactose, trehalose, dextrose, glycerol,
- 25 ethanol or polypeptides (such as human serum albumin). The compositions may conveniently be presented in unit dosage form and may be prepared by any of the methods well known in the art of pharmacy.

- As will be well understood by those skilled in the art alterations may
- 30 be made to the amino acid sequences set out in the Sequence Listings. These alterations may be deletions, insertions, or substitutions of amino acid residues. The altered polypeptides can be either naturally occurring (that is to say, purified or isolated from a natural source) or synthetic (for example, by performing site-directed metagenesis on the encoding DNA). It is
- 35 intended that such altered polypeptides which have at least 85%, preferably at least 95% identity with the sequences set out in the Sequence Listing are

within the scope of the present invention. Antibodies raised against these altered polypeptides will also bind to the polypeptides having one of the sequences set out in the Sequence Listings. The level of % identity is to be calculated as set out above.

- 5 Protein sequences are homologous if they are related by divergence from a common ancestor. Consequently, a species homologue of the protein will be the equivalent protein which occurs naturally in another species. Within any one species a homologue may exist as numerous allelic variants, and these will be considered homologues of the protein. Allelic variants and
10 species homologues can be obtained by following standard techniques known to those skilled in the art.

An allelic variant will be a variant that is naturally occurring within an individual organism.

15 Mutants, Variants and Homology - Nucleic Acids

- Mutant polynucleotides will possess one or more mutations which are deletions, insertions, or substitutions of nucleotide residues. Mutants can be either naturally occurring (that is to say, isolated from a natural source) or synthetic (for example, by performing site-directed metagenesis on
20 the DNA). It is thus apparent that polynucleotides of the invention can be either naturally occurring or recombinant (that is to say prepared using recombinant DNA techniques).

An allelic variant will be a variant that is naturally occurring within an individual organism.

- 25 Nucleotide sequences are homologous if they are related by divergence from a common ancestor. Consequently, a species homologue of the polynucleotide will be the equivalent polynucleotide which occurs naturally in another species. Within any one species a homologue may exist as numerous allelic variants, and these will be considered homologues of the
30 polynucleotide. Allelic variants and species homologues can be obtained by following standard techniques known to those skilled in the art.

Antibody Production

- 35 Antibodies, either polyclonal or monoclonal, which are specific for a polypeptide of the present invention can be produced by a person skilled in the art using standard techniques such as, but not limited to, those described

by Harlow *et al.* Antibodies: A Laboratory Manual, Cold Springs Harbor Laboratory Press (1988), and D. Catty (editor), Antibodies: A Practical Approach, IRL Press (1988).

Various procedures known in the art may be used for the production of polyclonal antibodies to epitopes of a protein. For the production of polyclonal antibodies, a number of host animals are acceptable for the generation of antibodies by immunization with one or more injections of a polypeptide preparation, including but not limited to rabbits, mice, rats, etc. Various adjuvants may be used to increase the immunological response in the host animal, depending on the host species, including but not limited to Freund's (complete and incomplete), mineral gels such as aluminium hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, oil emulsions, keyhole limpet hemocyanins, dinitrophenol, and potentially useful human adjuvants such as BCG (bacille Calmette-Guerin) and *Corynebacterium parvum*.

A monoclonal antibody to an epitope of a protein may be prepared by using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include but are not limited to the hybridoma technique originally described by Kohler and Milstein (1975, *Nature* 256, 493-497), and the more recent human B-cell hybridoma technique (Kesber *et al.* 1983, *Immunology Today* 4:72) and EBV-hybridoma technique (Cole *et al.* 1985, *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc. pp. 77-96). In addition, techniques developed for the production of "chimeric antibodies" by splicing the genes from antibody molecule of appropriate antigen specificity together with genes from a human antibody molecule of appropriate biological activity may be used (Morrison *et al.* 1984, *Proc. Natl. Acad. Sci.*, 81:6851-6855; Neuberger *et al.* 1984 *Nature* 312:604-608; Takeda *et al.* 1985 *Nature* 31:452-454). Alternatively, techniques described for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce 4-specific single chain antibodies.

Recombinant human or humanized versions of monoclonal antibodies are a preferred embodiment for human therapeutic applications. Humanized antibodies may be prepared according to procedures in the literature (e.g. Jones *et al.* 1986, *Nature* 321:522-25; Reichman *et al.* 1988 *Nature* 332:323-27; Verhoeven *et al.* 1988, *Science* 239:1534-36). The

recently described "gene conversion metagenesis" strategy for the production of humanized monoclonal antibody may also be employed in the production of humanized antibodies (Carter et al. 1992 Proc. Natl. Acad. Sci. U.S.A. 89:4285-89). Alternatively, techniques for generating the recombinant phase library of random combinations of heavy and light regions may be used to prepare recombinant antibodies (e.g. Huse et al. 1989 Science 246:1275-81).

Antibody fragments which contain the idiotype of the molecule such as $F(ab1)$ and $F(ab2)$ may be generated by known techniques. For example, such fragments include but are not limited to: the $F(ab)$ E2 fragment which can be produced by pepsin digestion of the intact antibody molecule; the Fab' fragments which can be generated by reducing the disulfide bridges of the $F(ab')_2$ fragment, and the two Fab fragments which can be generated by treating the antibody molecule with papain and a reducing agent. Alternatively, Fab expression libraries may be constructed (Huse et al. 1989, Science 246:1275-1281) to allow rapid and easy identification of monoclonal Fab fragment with the desired specificity to a protein.

Adjuvants

"Adjuvant" means a composition comprised of one or more substances that enhances the immunogenicity and efficacy of a vaccine composition. Non-limiting examples of suitable adjuvants include squalane and squalene (or other oils of animal origin); block copolymers; detergents such as Tween®-80; Quil® A, mineral oils such as Drakeol or Marcol, vegetable oils such as peanut oil; *Corynebacterium*-derived adjuvants such as *Corynebacterium parvum*; *Propionibacterium*-derived adjuvants such as *Propionibacterium acne*; *Mycobacterium bovis* (Bacillus Calmetic and Guerin or BCG); interleukins such as interleukin 2 and interleukin-12; monokines such as interleukin 1; tumour necrosis factor; interferons such as gamma interferon; combinations such as saponin-aluminium hydroxide or Quil-A aluminium hydroxide; liposomes; ISCOM adjuvant; mycobacterial cell wall extract; synthetic glycopeptides such as muramyl dipeptides or other derivatives; Avridine; Lipid A; dextran sulfate; DEAE-Dextran or DHAE-Dextran with aluminium phosphate; carboxypolymethylene such as Carbopol® EMA; acrylic copolymer emulsions such as Neocryl A640 (e.g. U.S.

Pat. No. 5,047,238); vaccinia or animal poxvirus proteins; sub-viral particle adjuvants such as cholera toxin, or mixtures thereof.

As used herein, stringent conditions are those that (1) employ low ionic strength and high temperature for washing, for example, 0.015 M NaCl/0.0015 M sodium citrate/0.1% NaDodSO₄ at 50°C; (2) employ during hybridisation a denaturing agent such as formamide, for example, 50% (vol/vol) formamide with 0.1% bovine serum albumin, 0.1% Ficoll, 0.1% polyvinylpyrrolidone, 50 mM sodium phosphate buffer at pH 6.5 with 750 mM NaCl, 75 mM sodium citrate at 42°C; or (3) employ 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS and 10% dextran sulfate at 42°C in 0.2 x SSC and 0.1% SDS

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As will be understood the present invention includes within its scope DNA vaccination. Further information regarding DNA vaccination may be found in Donnelly et al, Journal of Immunological Methods 176(1994) 145-152, the disclosure of which is incorporated herein by reference.

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Throughout this specification the word "comprise", or variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated element or integer or group of elements or integers but not the exclusion of any other element or integer, or group of elements or integers.

25 Preparation of the *P. gingivalis* library for sequencing.

To determine the DNA sequence of *P. gingivalis* genomic DNA was isolated from *P. gingivalis* strain W50 (ATCC 53978) essentially by the method described by Mamur J. (J. Mol. Biol. 3, 208-218, 1961). Cloning of DNA fragments was performed essentially as described by Fleischmann *et al.*, (Science; 269, 496-512, 1995)(2). Briefly, purified genomic DNA from *P. gingivalis* was nebulized to fragment the DNA and was treated with Bal31 nuclease to create blunt ends then run twice through preparative 1% agarose gels. DNA fragments of 1.6-2.0 kb were excised from the gel and the DNA recovered. This DNA was then ligated to the vector pUC18 (*Sma*I digested and dephosphorylated; Pharmacia) and electrophoresed through a 1%

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preparative agarose gel. The fragment comprising linear vector plus one insert was excised, purified and this process repeated to reduce any vector without insert contamination. The recovered vector plus insert DNA was blunt-ended with T4 DNA polymerase, then a final ligation to produce circular DNA was performed. Aliquots of Epicurian Coli Electroporation-Competent Cells (Stratagene) were transformed with the ligated DNA and plated out on SOB agar antibiotic diffusion plates containing X-gal and incubated at 37°C overnight. Colonies with inserts appeared white and those without inserts (vector alone) appeared blue. Plates were stored at 4°C until the white clones were picked and expanded for the extraction of plasmid DNA for sequencing.

DNA sequencing

Plasmid DNA was prepared by picking bacterial colonies into 1.5ml of LB, TB or SOB broth supplemented with 50-100ug/ml Ampicillin in 96 deep well plates. Plasmid DNA was isolated using the QIAprep Spin or QIAprep 96 Turbo miniprep kits (QIAGEN GmbH, Germany). DNA was eluted into a 96 well gridded array and stored at -20C.

Sequencing reactions were performed using ABI PRISM Dye Terminator and ABI PRISM BIGDye Terminator Cycle Sequencing Ready Reaction kits with AmpliTaq DNA polymerase FS (PE Applied Biosystems, Foster City, CA) using the M13 Universal forward and reverse sequencing primers. Sequence reactions were conducted on either a Perkin-Elmer GeneAmp 9700 (PE Applied Biosystems) or Hybaid PCR Express (Hybaid, UK) thermal cyclers. Sequencing reactions were analysed on ABI PRISM 377 DNA sequencers (PE Applied Biosystems).

The sequences obtained are set out below. The relationship between these sequences is set out in Table 1. The initiation codon was calculated using a combination of sequence homology alignment (FASTA), signal sequence prediction (PSORT, SignalP) or ORF prediction (GeneMark).

Table 1: Reference table indicating the relationships of each sequence ID to the selected proteins.

Protein name	DNA sequence of complete ORF	Amino acid sequence of complete ORF	DNA sequence of protein	Amino acid sequence of protein
PG1	1	265	122	386
PG10	2	266	123	387
PG100	3	267	124	388
PG101	4	268		
PG102	5	269	125, 126	389, 390
PG104	6	270	127	391
PG105	7	271	128	392
PG106	8	272	129	393
PG107	9	273	130, 131, 132	394, 395, 396
PG108	10	274	133	397
PG109	11	275	134, 135	398, 399
PG11	12	276	136	400
PG110	13	277	137	401
PG111	14	278		
PG112	15	279	138, 139	402, 403
PG113	16	280	140	404
PG114	17	281	141	405
PG115	18	282	142	406
PG116	19	283	143	407
PG117	20	284	144	408
PG118	21	285	145	409
PG119	22	286	146	410
PG12	23	287	147	411
PG120	24	288	148	412

Protein name	DNA sequence of complete ORF	Amino acid sequence of complete ORF	DNA sequence of protein	Amino acid sequence of protein
PG121	25	289	149	413
PG122	26	290	150	414
PG123	27	291	151	415
PG124	28	292	152	416
PG125	29	293	153	417
PG126	30	294	154	418
PG13	31	295	155	419
PG14	32	296	156	420
PG15	33	297	157	421
PG16	34	298	158	422
PG18	35	299	159	423
PG2	36	300	160, 161	424, 425
PG21	37	301	162	426
PG22	38	302	163	427
PG23	39	303	164	428
PG24	40	304	165	429
PG25	41	305	166	430
PG27	42	306	167	431
PG28	43	307	168	432
PG29	44	308	169	433
PG3	45	309	170	434
PG30	46	310	171	435
PG31	47	311	172	436
PG32	48	312	173	437
PG33	49	313	174	438
PG34	50	314	175, 176	439, 440
PG35	51	315	177	441
PG36	52	316	178	442
PG37	53	317	179, 180	443, 444
PG38	54	318	181	445

Protein name	DNA sequence of complete ORF	Amino acid sequence of complete ORF	DNA sequence of protein	Amino acid sequence of protein
PG39	55	319	182	446
PG4	56	320	183	447
PG40	57	321	184	448
PG41	58	322	185	449
PG42	59	323	186	450
PG43	60	324	187	451
PG44	61	325	188	452
PG45	62	326	189	453
PG46	63	327	190	454
PG47	64	328	191	455
PG48	65	329	192	456
PG49	66	330	193	457
PG5	67	331	194	458
PG50	68	332	195	459
PG51	69	333	196	460
PG52	70	334	197	461
PG53	71	335	198	462
PG54	72	336	199	463
PG55	73	337	200	464
PG56	74	338	201, 202	465, 466
PG57	75	339	203, 204, 205	467, 468, 469
PG58	76	340	206, 207	470, 471
PG59	77	341	208, 209, 210	472, 473, 474
PG6	78	342	211	475
PG60	79	343	212	476
PG61	80	344	213	477
PG62	81	345	214	478
PG63	82	346	215	479
PG64	83	347	216	480
PG65	84	348	217	481

Protein name	DNA sequence of complete ORF	Amino acid sequence of complete ORF	DNA sequence of protein	Amino acid sequence of protein
PG66	85	349	218	482
PG67	86	350	219	483
PG68	87	351	220, 221	484, 485
PG69	88	352	222	486
PG7	89	353	223	487
PG70	90	354	224	488
PG71	91	355	225	489
PG72	92	356	226	490
PG73	93	357	227	491
PG74	94	358	228	492
PG75	95	359	229	493
PG76	96	360	230	494
PG77	97	361	231	495
PG78	98	362	232	496
PG79	99	363	233	497
PG8	100	364	234, 235, 236, 237	498, 499, 500, 501
PG80	101	365	238	502
PG81	102	366	102	366
PG82	103	367	239	503
PG83	104	368	240	504
PG84	105	369	241, 242	505, 506
PG85	106	370	243	507
PG86	107	371	244, 245	508, 509
PG87	108	372	246	510
PG88	109	373	247, 248, 249	511, 512, 513
PG89	110	374	250	514
PG9	111	375	251, 252, 253	515, 516, 517
PG90	112	376	254, 255	518, 519
PG91	113	377	256	520

Protein name	DNA sequence of complete ORF	Amino acid sequence of complete ORF	DNA sequence of protein	Amino acid sequence of protein
PG92	114	378	257	521
PG93	115	379	258	522
PG94	116	380	259	523
PG95	117	381	260	524
PG96	118	382	261	525
PG97	119	383	262	526
PG98	120	384	263	527
PG99	121	385	264	528
PG127	529	531	530	532

DNA sequence analysis

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DNA files in FASTA format were converted to GCG format files and imported into a database. The DNA files were translated into amino acid files using the program Flip obtained from ANGIS(Australian Genomic Information Service, University of Sydney, Australia). A series of

10 bioinformatic analyses were performed on the proteins in order to select potential vaccine candidates. The programs used were FASTA homology searching (1), PSORT (2,3), SignalP (4), TopPred (5), and GeneMark (6). The proteins and their bioinformatic results were stored in the custom written database for search and retrieval of proteins with the desired characteristics

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The FASTA homology results for these proteins were then examined for any alignment with a protein suggesting surface location or vaccine efficacy. All proteins were searched for homology against a non-redundant bacterial protein database compiled by ANGIS using the FASTA algorithm. The settings used for the FASTA searches were Ktup = 2, gap creation

20 penalty = -12, gap extension penalty = -2, width for deriving alignment in opt = 16 and the Blosum 50 scoring matrix. Individual FASTA search results were examined for significant homology by statistical probability and amino acid alignments. The results are set out in Table 2.

Protein files were then trimmed to the first, second, third, fourth and fifth methionine residues using a protein trimming program (ANGIS). The trimmed proteins were then subjected to PSORT analysis for the detection of signal sequences and the prediction of cell location. Proteins exhibiting a PSORT probability of outer membrane >0.8 were considered to indicate surface localisation. A second signal sequence detection program SignalP was also performed and, in certain instances, this program detected signals not identified with PSORT. All proteins identified by other methods were also analysed by PSORT and SignalP. Previously, the C-terminal amino acid of bacterial outer membrane proteins has been shown to be important for the assembly of the protein on the outer membrane (7). A typical structure definition for outer membrane proteins has been determined as the presence of a signal sequence at the N-terminus and a tyrosine or phenylalanine at the C-terminus. A number of the selected proteins exhibit this characteristic structure. The program TopPred was used to determine the presence and number of membrane spanning domains (MSDs) and the presence of such sequences indicates a preference to be attached to membranes such as the outer membrane. The results of PSORT, SignalP and TopPred analyses with the C-terminal amino acids of the selected proteins are set out in Table 3.

The 70 amino acids from the C-terminus of a number of *P. gingivalis* outer membrane proteins share 50-100% protein sequence identity. These proteins included RGP1, RGP2, KGP, HagA, HagC, HagD, prtH and prtT. This conserved motif may be involved in the attachment or sorting of proteins to the outer membrane. The protein data set was searched using FASTA homology as described above and a number of novel proteins were identified which demonstrate similar motifs at their C-termini. The results are listed in Table 4

The TonBIII box is a 30 amino acid motif present within TonB outer membrane receptors in a wide variety of bacteria. The TonBIII box of *P. gingivalis* (8) was used to search the protein data set for homology by FASTA as described above. Those proteins demonstrating significant homology are listed in Table 5.

Table 2: FASTA protein homology results of complete ORFs against a non-redundant protein database.

Protein name	Homology description	Genbank accession number	Length of homolog	Length of <i>P. gingivalis</i> protein	FASTA homology results		
					Identity %	Overlap	E value
PG1	48kD outer membrane protein, <i>Actinobacillus pleuropneumoniae</i>	U24402	449aa	451aa	32	454aa	1.40E-42
PG2	Outer membrane protein (susC), <i>Bacteroides thetaiotaomicron</i>	U49338	1038aa	1017aa, 1014aa	28	1099aa	4.60E-32
PG3	Outer membrane porin F adhesin, <i>Pseudomonas fluorescens</i>	U19743	317aa	223aa	35	187aa	1.10E-10
PG4	Outer membrane protein A, <i>Escherichia fergusonii</i>	M63352	243aa	672aa	48	88aa	4.10E-10
PG5	Adhesin protein (AdcA), <i>Streptococcus pneumoniae</i>	Z71552	423aa	315aa	25	279aa	9.40E-15
PG6	Hemolysin A (phvA), <i>Prevotella melaninogenica</i>	U27587	332aa	324aa	60	306aa	3.00E-74
PG7	Hemolysin (tlvC), <i>Serpulina hyodysenteriae</i>	X73141	268aa	404aa	33	268aa	1.40E-24
PG8	Heme uptake protein A, <i>Bacteriodes fragilis</i>	X97122	431aa	598aa, 550aa, 458aa, 426aa	79	417aa	6.70E-121
PG9	Internalin A (inlA), <i>Lysteria monocytogenes</i>	M67471	744aa	1266aa, 1232aa, 1174aa	38	340aa	7.30E-23

Protein name	Homology description	Genbank accession number	Length of homolog	Length of <i>P. gingivalis</i> protein	FASTA homology results		
					Identity %	Overlap	E value
PG10	Macrophage infectivity potentiator (MIP), <i>Legionella oakridgensis</i> .	U92214	234aa	195aa	50	201aa	4.70E-31
PG11	Haemagglutinin (phg), <i>Prevotella Intermedia</i>	AF017417	309aa	313aa	44	309aa	3.80E-44
PG12	Outer membrane lipoprotein, <i>Haemophilus influenzae</i>	M88502	274aa	271aa	36	254aa	9.80E-27
PG13	Ferric receptor (cfrA), <i>Campylobacter coli</i>	U80812	696aa	757aa	24	625aa	1.20E-18
PG14	38kD antigen, <i>Helicobacter pylori</i>	U88610	329aa	331aa	37	326aa	1.10E-35
PG15	Outer membrane protein, <i>Erwinia amylovora</i>	X77921	377aa	287aa	30	253aa	5.40E-08
PG16	C-terminal protease, <i>Bartonella bacilliformis</i>	L37094	434aa	589aa	36	357aa	3.00E-35
PG18	Protein-export membrane protein (secD), <i>Helicobacter pylori</i>	AEO0652	503aa	981aa	32	611aa	1.10E-36
PG21	Surface antigen gene, <i>Methanosarcina mazei</i>	X84710	783aa	821aa	37	331aa	6.20E-33
PG22	Alpha-hemolysin gene, <i>Aeromonas hydrophila</i>	L36482	85aa	106aa	57	87aa	2.60E-14
PG23	clpA/clpB protease, <i>Bacillus subtilis</i>	D26185	810aa	859aa	45	855aa	7.10E-122
PG24	Putative hemolysin, <i>Streptococcus mutans</i>	AF051356	445aa	417aa	29	432aa	1.80E-29

Protein name	Homology description	Genbank accession number	Length of homolog	Length of <i>P. gingivalis</i> protein	FASTA homology results		
					Identity %	Overlap	E value
PG25	Cysteine protease, <i>Porphyromonas gingivalis</i>	U54691	1723aa	293aa	42	142aa	1.10E-12
PG27	TonB linked adhesin, <i>Porphyromonas gingivalis</i>	Y07818	1097aa	312aa	45	360aa	3.20E-41
PG28	Cysteine protease / hemagglutinin, <i>Porphyromonas gingivalis</i>	S75942	886aa	843aa	35	838aa	7.00E-90
PG30	Putative NlpD lipoprotein, <i>Aquifex aeolicus</i>	AE000754	187aa	337aa	42	142aa	1.80E-12
PG31	Hemolysin (HlyC), <i>Serpulina hvodysenteriae</i>	X73141	141aa	151aa	31	123aa	1.80E-07
PG32	Major outer membrane protein (oprF), <i>Pseudomonas aeruginosa</i>	M94078	350aa	391aa	26	382aa	3.40E-07
PG33	Major outer membrane protein (oprF), <i>Pseudomonas fluorescens</i>	L21200	317aa	385aa	32	163aa	2.30E-06
PG34	Putative membrane protein, <i>Rhodobacter capsulatus</i>	Q07396	193aa	190aa	46	190aa	2.20E-38
PG35	Colicin 1 receptor, <i>Escherichia coli</i>	J04229	863aa	833aa	25	590aa	2.40E-10
PG36	Outer membrane antigen (oma87), <i>Pasteurella multocida</i>	U60439	789aa	891aa	21	894aa	3.70E-10
PG37	Cationic outer membrane protein (ompH), <i>Yersinia enterocolitica</i>	M34854	164aa	174aa, 170aa	27	168aa	4.30E-07

Protein name	Homology description	Genbank accession number	Length of homolog	Length of <i>gingivalis</i> protein	FASTA homology results		
					Identity %	Overlap	E value
PG38	Cationic outer membrane protein (ompH), <i>Yersinia enterocolitica</i>	M34854	164aa	163aa	23	180aa	5.90E-05
PG39	Outer membrane protein (susC) <i>Bacteroides thetaiotaomicron</i>	L49338	1038aa	827aa	24	347aa	1.50E-06
PG40	Heme receptor (Hut A), <i>Vibrio cholera</i>	Q56844	693aa	772aa	23	722aa	4.90E-09
PG41	Outer membrane protein (tolC) <i>Escherichia coli</i>	X54049	495aa	462aa	22	436aa	4.60E-09
PG42	Neuraminidase, <i>Micromonospora viridifaciens</i>	D01045	847aa	492aa	32	375aa	2.10E-22
PG43	Immunoreactive outer membrane protein (omp28), <i>Brucella melitensis</i>	U30815	250aa	245aa	24	178aa	0.0015
PG44	Macrophage infectivity potentiator, <i>Legionella israelensis</i>	U92208	242aa	275aa	35	218aa	9.10E-18
PG45	Outer membrane protein, <i>Neisseria meningitidis</i>	AF021245	787aa	775aa	21	699aa	0.0034
PG46	Outer membrane protein 85, <i>Neisseria gonorrhoeae</i>	U01959	792aa	774aa	31	117aa	0.00098
PG47	Outer membrane protein (susC) <i>Bacteroides thetaiotaomicron</i>	L49338	1038aa	867aa	20	962aa	1.00E-03

Protein name	Homology description	Genbank accession number	Length of homolog	Length of <i>P. gingivalis</i> protein	FASTA homology results		
					Identity %	Overlap	E value
PG48	Immunoglobulin binding surface protein (sir22), <i>Streptococcus pyogenes</i>	X75750	365aa	431aa	25	269aa	5.20E-05
PG49	Fimbriin (orf2), <i>Porphyromonas gingivalis</i>	D42067	453aa	333aa	23	298aa	0.062
PG50	Outer membrane protein (susC) <i>Bacteroides thetaiotaomicron</i>	L49338	1038aa	948aa	26	579aa	1.80E-11
PG51	PGaA antigen, <i>Porphyromonas gingivalis</i>	X95938	202aa	202aa	54	126aa	1.20E-25
PG52	Alkaline protease secretion apparatus (aprF) <i>Pseudomonas aeruginosa</i>	X84558	481aa	455aa	21	427aa	3.50E-08
PG53	Protein export protein (tolC), <i>Salmonella enteritidis</i>	U25178	491aa	444aa	23	436aa	6.20E-11
PG54	Protease I, <i>Achromobacter lyticus</i>	J5128	853aa	940aa	24	695aa	1.50E-22
PG55	Fimbriin (orf3), <i>Porphyromonas gingivalis</i>	D42067	670aa	670aa	43	888aa	4.90E-108
PG56	Cysteine protease <i>Porphyromonas gingivalis</i>	U88468	364aa	1282aa, 1274aa	25	212aa	0.00012
PG57	Cysteine protease, <i>Porphyromonas gingivalis</i>	U88468	1358aa	924aa, 922aa, 921aa	31	742aa	1.40E-23
PG60	Outer membrane protein 11, <i>Helicobacter pylori</i>	AEO00562	186aa	547aa	25	183aa	2.20E+00
PG61	Ferric pseudobactin M114 receptor protein (pbuA), <i>Pseudomonas sp.</i>	X73412	826aa	749aa	22	585aa	1.00E-05

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Protein name	Homology description	Genbank accession number	Length of homolog	Length of <i>P. gingivalis</i> protein	FASTA homology results		
					Identity %	Overlap	E value
PG89	NADH-ubiquinone oxidoreductase, <i>Helicobacter pylori</i>	AE000631	512aa	259aa	24	186aa	3.90E-01
PG91	Neuraminidase (nanH), <i>Bacteroides fragilis</i>	D28493	544aa	540aa	24	251aa	1.60E-00
PG92	Hypothetical protein, <i>Mycobacterium tuberculosis</i>	AL021942	877aa	771aa	29	770aa	8.00E-30
PG93	Cytoadherence protein P1, <i>Mycoplasma pneumoniae</i>	X07191	219aa	778aa	41	63aa	6.90E-01
PG94	Arginyl endopeptidase, <i>Porphyromonas gingivalis</i>	D28470	991aa	1157aa	24	328aa	7.80E-08
PG95	Sensor protein (EVGS), <i>Escherichia coli</i>	D14008	1197aa	961aa	28	511aa	2.80E-17
PG105	Plasma cell membrane glycoprotein, Human	P22413	873aa	449aa	34	404aa	5.80E-33
PG106	Hypothetical secreted protein, <i>Helicobacter pylori</i>	O24951	242aa	248aa	30	252aa	7.80E-22
PG107	Cell division ATP binding protein, <i>Mycobacterium leprae</i>	O32883	228aa	246aa, 241aa, 232aa	46	193aa	1.20E-26
PG108	ABC transporter, <i>Archaeoglobus fulgidis</i>	O29244	228aa	218aa	51	218aa	3.80E-41
PG109	Proteinase IV, <i>Escherichia coli</i>	F64936	618aa	595aa, 589aa	38	597aa	1.10E-57
PG110	Preprotein translocase, <i>Staphylococcus aureus</i>	O06446	843aa	523aa	43	521aa	8.00E-71
PG111	ABC transporter, <i>Synechocystis</i> sp.	P73758	574aa	> 720aa	40	579aa	1.70E-73
PG112	Glycosyl transferase, <i>Erwinia amylovora</i>	Q48834	351aa	375aa, 362aa	31	383aa	1.60E-32

Protein name	Homology description	Genbank accession number	Length of homolog	Length of <i>P. gingivalis</i> protein	FASTA homology results		
					Identity %	Overlap	E value
PG113	Heat shock protein (dnaK), <i>Treponema pallidum</i>	AE001203	835aa	640aa	62	644aa	9.10E-138
PG114	Dihydrolipamide dehydrogenase, <i>Clostridium magnum</i>	Q59299	578aa	449aa	37	450aa	3.80E-54
PG115	Zinc protease, <i>Escherichia coli</i>	P31828	931aa	941aa	27	890aa	8.60E-57
PG116	Heat shock protein (HSPG), <i>Escherichia coli</i>	P10413	624aa	684aa	32	627aa	4.60E-48
PG117	Transcriptional regulator, <i>Aquifex aeolicus</i>	O66591	506aa	464aa	39	389aa	2.40E-49
PG118	ABC transporter, <i>Bacillus subtilis</i>	H70019	281aa	250aa	59	251aa	1.50E-60
PG119	ATP-dependent protease, <i>Aquifex aeolicus</i>	O66827	444aa	461aa	46	458aa	1.60E-77
PG120	Nitrogen assimilation regulatory protein, <i>Bradyrhizobium</i> sp.	P10576	480aa	457aa	49	242aa	3.80E-45
PG121	Cobalamin synthesis protein, <i>Bacillus megaterium</i>	E1331323	387aa	602aa	36	324aa	9.20E-37
PG122	Outer membrane integrity (tolA), <i>Haemophilus influenzae</i>	P71397	819aa	443aa	37	441aa	1.90E-54
PG123	Fimbriin, <i>Porphyromonas gingivalis</i>	D1034032	490aa	479aa	32	480aa	7.30E-48
PG124	Heat shock protein (dnaJ), <i>Leptospira interrogans</i>	AF007813	369aa	383aa	46	358aa	2.30E-57

Protein name	Homology description	Genbank accession number	Length of homolog	Length of <i>P. gingivalis</i> protein	FASTA homology results		
					Identity %	Overlap	E value
PG125	Cobalamin biosynthesis protein(CBIK), <i>Salmonella typhimurium</i>	Q06592	264aa	293aa	37	259aa	3.70E-26
PG126	ABC-type permease, <i>Pseudomonas aeruginosa</i>	O88878	328aa	356aa	33	333aa	1.30E-30
PG127	Endonuclease excision repair protein (uvrB), <i>Pseudomonas aeruginosa</i>	X83486	670aa	678aa	56	675aa	1.10E-134

32

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Table 3: Results of PSORT, SignalP and TopPred analysis of the proteins. The signal present column indicates the presence of a signal sequence detected with either PSORT or SignalP. The terms in parentheses indicates the type of signal sequence as determined by PSORT. The cell location & probability values are generated by PSORT and represent the probability of the protein being in the cell compartments outer membrane (OM), inner membrane (IM), periplasmic space (PC) or cytoplasm (C). The number of transmembrane domains (TMDs) was determined by TopPred and does not include uncleavable signal sequences.

Protein name	Protein seqID number	Protein Length	Signal Present	Methionine in ORF	SignalP cleavage site	PSORT cleavage site	Cell Location & probability				C-terminal Amino Acid	Number of TMD's
							OM	IM	PS	C		
PC1	386	451aa	Y	1	24	34	0	0	0	0.22	N	0
PC2	424	1017aa	Y	1	20	20	0.94	0	0.33	0	F	3
PG2	425	1014aa	Y	2	17	17	0.94	0	0.29	0	F	3
PG3	434	223aa	Y (lipoprotein)	1	-	18	0.79	0.78	0	0	K	3
PG4	447	872aa	Y (lipoprotein)	1	22	22	0.79	0.7	0	0	R	0
PG5	458	315aa	Y	1	40	35	0	0.25	0	0	R	0
PG6	475	324aa	N	1	-	-	0	0	0	0.2	S	1
PG7	487	404aa	N	1	7	-	0	0.42	0	0	E	3
PG8	498	598aa	N	1	-	-	0	0	0	0.22	N	0
PC8	499	550aa	N	2	-	-	0	0	0	0.25	N	0

Protein name	Protein seqID number	Protein Length	Signal Present	Methionine in ORF	SignalP cleavage site	PSORT cleavage site	Cell Location & probability				C-terminal Amino Acid	Number of TMD's
							OM	IM	PS	C		
PG8	500	458aa	N	3	-	-	0	0	0	0.34	N	0
PG8	501	426aa	N	4	-	-	0	0	0	0.24	N	0
PG9	515	1260aa	N	1	7	-	0	0	0	0.22	E	1
PG9	516	1232aa	N	2	-	-	0	0	0	0.39	E	1
PG9	517	1174aa	N	3	-	-	0	0	0	0.47	E	1
PG10	387	185aa	N	1	-	-	0	0	0	0.11	K	0
PG11	400	313aa	Y	1	22	28	0.24	0	0.93	0	R	1
PG12	411	271aa	Y (lipoprotein)	3	27	29	0.79	0.7	0	0	R	0
PG13	419	757aa	Y	1	23	25	0.94	0	0.29	0	N	0
PG14	420	331aa	Y (uncleavable)	1	35	26	0	0.58	0	0	K	1
PG15	421	267aa	Y	2	24	18	0	0.11	0	0	K	1
PG16	422	569aa	Y (lipoprotein)	1	24	18	0.79	0.7	0	0	G	0
PG18	423	361aa	Y	1	30	-	0	0.58	0	0	K	11
PG21	426	821aa	Y	2	24	27	0.34	0	0.37	0	G	1
PG22	427	108aa	Y (uncleavable)	1	41	41	0	0.20	0	0	P	0
PG23	428	359aa	N	1	-	-	0	0.12	0	0	A	1

Protein name	Protein seqID number	Protein Length	Signal Present	Methionine in ORF	SignalP cleavage site	PSORT cleavage site	Cell Location & probability				C-terminal Amino Acid	Number of TMD's
							OM	IM	PS	C		
PG24	429	417aa	Y	1	19	19	0	0.44	0	0	N	3
PG25	430	293aa	Y	1	27	28	0.2	0	0.82	0	R	0
PG27	431	312aa	N	1	-	-	0	0	0	0.28	Q	1
PG28	432	843aa	Y	1	21	21	0.93	0	0.24	0	H	1
PG29	433	290aa	Y	1	18	16	0.28	0	0.94	0	K	1
PG30	435	337aa	Y	1	21	21	0.24	0	0.4	0	K	0
PG31	438	151aa	N	1	-	-	0	0	0	0.3	T	0
PG32	437	391aa	Y	1	20	20	0.62	0	0.13	0	K	0
PG33	438	365aa	Y	1	26	26	0.81	0	0.31	0	E	1
PG34	439	190aa	Y	1	-	13	0	0.5	0	0	A	5
PG34	440	186aa	Y (uncleavable)	2	-	47	0	0.5	0	0	A	4
PG35	441	833aa	Y	1	22	22	0.94	0	0.37	0	F	1
PG36	442	891aa	Y (uncleavable)	1	-	40	0	0.31	0	0	F	2
PG37	443	174aa	Y (uncleavable)	1	28	24	0	0.35	0	0	K	0

Protein name	Protein seqID number	Protein Length	Signal Present	Methionine in ORF	SignalP cleavage site	PSORT cleavage site	Cell Location & probability				C-terminal Amino Acid	Number of TMD's
							OM	IM	PS	C		
PG37	444	170aa	Y (uncleavable)	2	24	20	0	0.35	0	0	K	0
PG38	445	183aa	Y	1	18	18	0.21	0	0.93	0	K	1
PG39	446	827aa	Y	1	36	36	0.93	0	0.25	0	P	3
PG40	448	772aa	Y	2	19	19	0.94	0	0.32	0	F	4
PG41	449	462aa	Y	2	27	27	0.25	0	0.54	0	Q	2
PG42	450	492aa	Y	5	30	-	0	0	0.00	0.13	Q	2
PG43	451	245aa	Y (uncleavable)	2	28	22	0	0.38	0	0	K	1
PG44	452	276aa	Y	1	19	24	0.15	0	0.89	0	K	0
PG45	453	775aa	Y (lipoprotein)	1	19	23	0.79	0.7	0	0	P	4
PG46	454	774aa	Y	1	27	27	0.73	0	0.22	0	P	2
PG47	455	867aa	Y	1	24	24	0.94	0	0.38	0	P	2
PG48	456	431aa	Y	1	24	24	0	0.1	0	0	R	1
PG49	457	333aa	Y (uncleavable)	1	24	18	0	0.12	0	0	I	0
PG50	459	948aa	Y	1	21	21	0.94	0	0.34	0	F	3
PG51	460	202aa	Y	1	28	25	0.2	0	0.61	0	S	0
PG52	461	455aa	Y (uncleavable)	1	23	21	0	0.18	0	0	P	1

Protein name	Protein seqID number	Protein Length	Signal Present	Methionine in ORF	SignalP cleavage site	PSORT cleavage site	Cell Location & probability				C-terminal Amino Acid	Number of TMD's
							OM	IM	PS	C		
PG53	462	444aa	Y	1	14	17	0.38	0	0.22	0	D	2
PG54	463	940aa	Y	1	27	20	0.88	0	0.25	0	Q	5
PG55	464	670aa	Y (lipoprotein)	1	23	23	0.79	0.7	0	0	K	2
PG56	465	1282aa	Y (uncleavable)	1	-	21	0	0.04	0	0	K	4
PG56	466	1274aa	N	2	-	-	0	0	0	0.27	K	5
PG57	467	925aa	Y	1	28	24	0.53	0	0.2	0	P	3
PG57	468	922aa	Y	2	25	21	0.53	0	0.2	0	P	3
PG57	469	921aa	Y	3	24	20	0.53	0	0.2	0	P	3
PG58	470	593aa	Y	1	24	24	0.82	0	0.19	0	F	1
PG58	471	589aa	Y	2	20	20	0.82	0	0.19	0	F	1
PG59	472	348aa	Y	1	37	-	0	0.18	0	0	P	1
PG59	473	345aa	Y	2	38	56	0.92	0	0.15	0	F	1
PG59	474	330aa	Y	3	21	41	0.92	0	0.25	0	P	1
PG80	476	547aa	Y	1	28	28	0.93	0	0.25	0	F	0
PG81	477	749aa	Y	2	21	21	0.94	0	0.29	0	F	3
PG82	478	494aa	Y	1	21	21	0.93	0	0.24	0	P	2

Protein name	Protein seqID number	Protein Length	Signal Present	Methionine in ORF	SignalP cleavage site	PSORT cleavage site	Cell Location & probability				C-terminal Amino Acid	Number of TMD's
							OM	IM	PS	C		
PG63	479	294aa	Y	1	20	20	0.93	0	0.24	0	P	1
PG64	480	204aa	Y	1	20	20	0.83	0	0.19	0	P	1
PG65	481	243aa	Y	1	18	18	0.93	0	0.25	0	F	1
PG66	482	206aa	Y	1	21	21	0.94	0	0.3	0	F	1
PG67	483	950aa	Y	1	28	36	0.93	0	0.27	0	Y	4
PG68	484	1226aa	Y	1	25	25	0.91	0	0.31	0	Y	0
PG68	485	1225aa	Y	2	24	24	0.91	0	0.31	0	Y	0
PG68	486	425aa	Y	1	29	29	0.93	0	0.21	0	P	1
PG70	488	260aa	Y	1	18	24	0.93	0	0.24	0	P	0
PG71	489	334aa	Y	2	20	20	0.94	0	0.31	0	N	2
PG72	490	399aa	Y	1	27	27	0.94	0	0.32	0	H	2
PG73	491	382aa	Y	2	20	20	0.94	0	0.3	0	L	1
PG74	492	222aa	Y	1	24	24	0.94	0	0.32	0	L	0
PG75	493	391aa	Y	1	26	26	0.94	0	0.3	0	H	1
PG76	494	446aa	Y	1	21	22	0.94	0	0.32	0	V	3
PG77	495	308aa	Y	2	28	28	0.94	0	0.38	0	K	0

Protein name	Protein seqID number	Protein Length	Signal Present	Methionine in ORF	SignalP cleavage site	PSORT cleavage site	Cell Location & probability				C-terminal Amino Acid	Number of TMD's
							OM	IM	PS	C		
PG78	496	314aa	Y	1	23	23	0.94	0	0.29	0	D	0
PG79	497	285aa	Y	1	-	32	0.93	0	0.26	0	G	2
PG80	502	240aa	Y	1	19	19	0.93	0	0.22	0	N	2
PG81	366	>235aa	Y	1	28	20	0.93	0	0.21	0	Q	1
PG82	503	434aa	Y	1	30	24	0.93	0	0.2	0	N	3
PG83	504	828aa	Y	1	23	57	0.93	0	0.21	0	S	1
PG84	505	400aa	Y	1	25	25	0.93	0	0.25	0	N	1
PG84	506	398aa	Y	2	23	23	0.93	0	0.25	0	N	1
PG85	507	381aa	Y	1	20	20	0.93	0	0.46	0	L	2
PG86	508	239aa	Y	1	44	-	0	0	0	0.12	H	0
PG88	509	211aa	Y	2	16	46	0.91	0	0.03	0	H	0
PG87	510	781aa	Y	1	26	47	0.89	0	0.21	0	N	2
PG88	511	271aa	Y	2	28	19	0.89	0	0.25	0	P	0
PG88	512	270aa	Y	3	27	18	0.89	0	0.25	0	P	0
PG88	513	267aa	Y	4	24	15	0.89	0	0.23	0	P	0
PG89	514	258aa	Y	2	23	25	0.88	0	0.35	0	N	1

Protein name	Protein seqID number	Protein Length	Signal Present	Methionine in ORF	SignalP cleavage site	PSORT cleavage site	Cell Location & probability				C-terminal Amino Acid	Number of TMD's
							OM	IM	PS	C		
PG90	518	229aa	Y	1	22	21	0.85	0	0.44	0	K	0
PG90	519	228aa	Y	2	21	20	0.85	0	0.44	0	K	0
PG91	520	540aa	Y	1	25	25	0.85	0	0.30	0	E	0
PG92	521	771aa	Y	2	19	19	0.85	0	0.3	0	R	3
PG93	522	778aa	Y	1	25	25	0.85	0	0.37	0	R	4
PG94	523	1157aa	Y	1	23	28	0.8	0	0.25	0	Q	5
PG95	524	981aa	Y (lipoprotein)	1	-	19	0.79	0.87	0	0	V	1
PG96	525	583aa	Y	1	23	23	0.40	0	0.33	0	K	0
PG97	526	437aa	Y	1	23	23	0.32	0	0.65	0	Q	0
PG98	527	318aa	Y (lipoprotein)	1	19	19	0.79	0.7	0	0	L	1
PG99	528	461aa	Y (uncleavable)	1	22	20	0	0	0.3	0	R	0
PG100	388	278aa	Y	1	20	18	0.28	0	0.54	0	I	0
PG101	288	>157aa	N (ORF incomplete)								R	1
PG102	389	582aa	Y	1	29	29	0.19	0	0.4	0	S	3
PG102	390	558aa	Y	2	25	25	0.26	0	0.46	0	S	3
PG104	391	391aa	Y	1	17	17	0.62	0	0.22		R	0

Protein name	Protein seqID number	Protein Length	Signal Present	Methionine in ORF	SignalP cleavage site	PSORT cleavage site	Cell Location & probability				C-terminal Amino Acid	Number of TMD's
							OM	IM	PS	C		
PG105	392	449aa	Y	1	22	19	0.31	0	0.91	0	P	3
PG106	393	246aa	Y	2	41	48	0	0	0	0.02	L	0
PG107	394	246aa	N	1	-	-	0	0	0	0.32	D	1
PG107	395	241aa	N	2	-	-	0	0	0	0.3	D	1
PG107	396	232aa	N	3	-	-	0	0	0	0.21	D	1
PG108	397	219aa	N	1	-	-	0	0	0	0.19	R	1
PG109	398	595aa	Y	1	35	37	0.26	0	0.93	0	Y	3
PG109	399	589aa	Y	2	29	31	0.27	0	0.93	0	Y	3
PG110	401	>523aa	N	1	-	-	0	0	0	0.38	Incomplete	0
PG111	278	>720aa	N (ORF incomplete)	-	-	-	-	-	-	-	G	1
PG112	402	375aa	Y	1	-	43	0	0.12	0	0	N	1
PG112	403	362aa	Y	2	-	30	0	0	0.12	0	N	1
PG113	404	640aa	N	1	-	-	0	0	0	0.25	K	1
PG114	405	449aa	N	1	-	-	0	0.12	0	0	G	4
PG115	406	941aa	Y	1	23	22	0.13	0	0.92	0	Q	2
PG116	407	984aa	N	1	-	-	0	0.12	0	0	L	2

WO 99/29870

PCT/AU98/01023

42

Protein name	Protein seqID number	Protein Length	Signal Present	Methionine in ORF	SignalP cleavage site	PSORT cleavage site	Cell Location & probability				C-terminal Amino Acid	Number of TMD's
							OM	IM	PS	C		
PG117	408	464aa	N	1	-	-	0	0.19	0	0	L	1
PG118	409	250aa	N	1	-	-	0	0	0	0.27	E	1
PG119	410	401aa	N	1	-	-	0	0.28	0	0	E	2
PG120	412	457aa	N	1	-	-	0	0	0	0.21	E	0
PG121	413	602aa	N	1	-	-	0	0	0	0.31	E	3
PG122	414	443aa	N	1	-	-	0	0	0	0.14	Q	4
PG123	415	478aa	Y	2	22	22	0.28	0	0.94	0	K	0
PG124	416	383aa	N	1	-	-	0	0	0	0.29	D	2
PG125	417	293aa	Y	1	23	15	0.18	0	0.93	0	R	1
PG126	418	356aa	N	1	-	-	0	0.52	0	0	D	9
PG127	532	678aa	N	1	-	-	0	0	0	0.28	A	2

Table 4: Percentage identity and percentage similarity of various proteins with the 70 amino acids from the C-terminal of the *P. gingivalis* arginine protease 1 (RGP1), arginine protease 2 (RGP2), and the cysteine protease/hemagglutinin (prtT).

5

Protein name	Percent identity			Percent similarity		
	RGP1	RGP2	prtT	RGP1	RGP2	prtT
PG21	17	29	21	40	57	49
PG25	43	41	9	64	73	14
PG27	41	33	7	73	74	11
PG28	21	26	34	49	57	74
PG54	19	13	16	40	43	33
PG57	11	14	19	20	24	34
PG91	31	21	39	57	53	74
PG96	0	13	20	0	24	43
PG97	10	26	33	14	47	61
PG98	16	20	0	47	54	0
PG99	19	0	26	41	0	54
PG100	20	21	24	39	57	41
PG101	11	16	27	17	39	60
PG102	27	20	31	50	61	61
PG104	16	23	26	46	44	49

Table 5: Percentage identity and percentage similarity of various proteins with the TonBIII box of *P. gingivalis*.

Protein name	Percent identity	Percent similarity
PG2	46	71
PG13	57	93
PG35	50	96
PG47	39	71
PG50	54	93

Cloning, expression and purification of recombinant *P. gingivalis* genes.

PG1

- 5 Oligonucleotides to the 5' and 3' regions of the deduced protein were used to amplify the gene of interest from a preparation of *P. gingivalis* W50 genomic DNA using the TaqPlus Precision PCR System (Stratagene) and a PTC-100 (MJ Research) thermal cycler or similar device. The 5' oligonucleotide primer sequence was GCGCCATATGCTGGCCGAACCGGCC, the 3' oligonucleotide primer sequence was GCGCCTCGAGTCAATTCATTTCCTTATAGAG. The PCR fragment was purified, digested with Nde I, Xho I restriction enzymes (Promega) and ligated into the corresponding sites of the plasmid pProEx-1 (Gibco-BRL) and transformed into *E. coli* ER1793 cells (a gift from Elizabeth Raleigh, New England Biolabs). A resulting clone expressing the correct insert was selected and induced with or without 0.1mM IPTG (Promega) for expression of the recombinant protein. Expression of the recombinant protein was determined by SDS-PAGE analysis and Western Blot using the one of the rabbit antisera described above or an anti-hexahistidine antibody (Clontech) that detects the hexahistidine tag that was fused to the *P. gingivalis* recombinant protein. PG1 was purified by disruption of the *E. coli* cells by sonication in binding buffer (Novagen) and solubilisation by the addition of sarkosyl (N-Lauroyl sarcosine) to a 1% final concentration. There after the preparation was diluted to 0.1% sarkosyl in binding buffer, bound to a Nickel-nitrilotriacetic acid column (Ni-NTA; Qiagen), after washing bound proteins were eluted with 1M imidazole in elution buffer (Novagen) according to the Qiagen recommendations with 0.1% sarkosyl added to all buffers. Following purification samples were dialysed against 500mM NaCl, 20mM Tris, 0.1% sarkosyl at pH7.4 to remove the imidazole, concentrated as required and stored at 4°C until used. Purity and antigenicity were assessed by SDS-PAGE and Western blot using selected antisera (from those described above) and the protein concentration was determined by the BCA assay (Pierce).
- 10
- 15
- 20
- 25
- 30

PG2

The methods used for PG2 were essentially the same as for PG1 with the following exceptions. The 5' oligonucleotide primer sequence was CGCGGTATACATGAAAAGAATGACGC, the 3' oligonucleotide primer
 5 sequence was CGCGAGATCTGAAAGACAACCTGAATACC and the PCR product was cloned into pGex-stop RBS(IV) (Patent application WO9619496, JC Cox, SE Edwards, I Frazer and EA Webb. Variants of human papilloma virus antigens) using the BstZ 171 and Bgl II restriction sites. 2% sarkosyl was used to solubilise PG2 and 8M urea was added to the solubilisation buffer
 10 and to all other buffers. Urea was removed from the purified protein by sequential dialysis (4M then 2M then 1M then 0.5M then 0M urea all in 50mM Tris, 500mM NaCl, 0.1% sarkosyl, pH7.4). Purified protein was stored at 4°C until required.

15 PG3

The methods used for PG3 were essentially the same as for PG1 with the following exceptions. The 5' oligonucleotide primer sequence was GCGCGTATACATGAAGAAATCAAGTGTAG, the 3' oligonucleotide primer
 20 sequence was GCGCAGATCTCTTCAGCGTACCTTGCTGTG and DNA was amplified with Pfu DNA polymerase (Stratagene). The PCR product was cloned directly into pCR-Blunt and transformed into *E. coli* Top10F'(InVitrogen) before subcloning into the expression plasmid pGex-stop RBS(IV) using the Bst Z171 and Bgl II restriction sites and transformed into *E. coli* BL21DE3 (Pharmacia Biotech). The following modifications were
 25 made to the purification of PG3 from the PG1 method. Cells expressing the recombinant protein were disrupted by sonication in binding buffer and the insoluble inclusion bodies concentrated by centrifugation. Inclusion bodies were then solubilised in 6M urea (Sigma) in binding buffer and eluted with 6M urea added to the elution buffer. In some instances 6M guanidine
 30 hydrochloride (Sigma) was used instead of urea for these steps. Urea (or guanidine hydrochloride when it was substituted) was removed from the purified protein by sequential dialysis against reducing levels of urea (3M then 1.5M then 0.5M then 0M urea all in 50mM Tris, 500mM NaCl, 8% glycerol, pH7.4). Purified protein was stored frozen at -80°C until required.
 35 Protein concentration was determined by the Coomassie Plus protein assay (Pierce).

PG4

The methods used for PG4 were essentially the same as for PG3 with the following exceptions. The 5' oligonucleotide primer sequence was CTTCTGTATACTTACAGCGGACATCATAAAATC, the 3' oligonucleotide
5 primer sequence was TTCCAGGAGGGTACCACGCAACTCTTCTTCGAT and DNA was amplified with the Tth XL PCR kit (Perkin Elmer). The PCR product was cloned into the expression plasmid pGex-stop RBS(IV) using the Bst Z171 and Kpn I restriction sites and transformed into *E. coli* ER1793.

10 PG5

The methods used for PG5 were essentially the same as for PG3 with the following exceptions. The 5' oligonucleotide primer sequence was TTGCAACATATGATCAGAACGATACTTTCA, the 3' oligonucleotide primer
15 sequence was AGCAATCTCGAGCGGTTTCATGAGCCAAAGC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24 (Novagen) using the Nde I and Xho I restriction sites and transformed into *E. coli* BL21 (Pharmacia Biotech). Removal of urea was not proceeded past 1M urea as the protein was insoluble at lower
20 concentrations of urea. Purified protein was stored at 4°C until required.

20 PG6

The methods used for PG6 were essentially the same as for PG3 with the following exceptions. The 5' oligonucleotide primer sequence was TAAACATATGTGCCTCGAACCCATAATTGCTCCG, the 3' oligonucleotide
25 primer sequence was CGTCCGCGGAAGCTTTGATCGGCCATTGCTACT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Nde I and Hind III restriction sites and transformed into *E. coli* BL21.

30 PG8

The methods used for PG8 were essentially the same as for PG3 with the following exceptions. The 5' oligonucleotide primer sequence was CGCGGTATACATGGAGTTCAAGATTGTG, the 3' oligonucleotide primer
35 sequence was CGCGAGATCTGTTTTCTGAAAGCTTTTC and DNA was amplified with the TaqPlus Precision PCR System. The PCR product was

cloned into the expression plasmid pProEx-1 using the Nde I and Xho I restriction sites and transformed into *E. coli* ER1793.

PG8A

5 PG8A is a shortened version of PG8 and has the first 173 amino acids removed. The methods used for PG8A were essentially the same as for PG3 with the following exceptions. The 5' oligonucleotide primer sequence was CGCGGTATACATGGAAAACCTTAAAGAAC, the 3' oligonucleotide primer sequence was CGCGAGATCTGTTTTCTGAAAGCTTTTC and DNA was
10 amplified with the TaqPlus Precision PCR System. The PCR product was cloned into the expression plasmid pGex-stop RBS(IV) using the Bst Z171 and Bgl II restriction sites and transformed into *E. coli* ER1793. Prior to dialysis of the purified protein EDTA (Sigma) was added to a final concentration of 10mM.

15

PG10

The methods used for PG10 were essentially the same as for PG3 with the following exceptions. The 5' oligonucleotide primer sequence was CGCGGATATCATGGATAAAGTGAGCTATGC, the 3' oligonucleotide primer
20 sequence was CGCGAGATCTTTTGTTGATACTCAATAATTC and DNA was amplified with the TaqPlus Precision PCR System. The PCR product was digested with Eco RV and Bgl II and ligated into the expression plasmid pGex-stop RBS(IV) using the Bst Z171 and Bgl II restriction sites and transformed into *E. coli* ER1793.

25

PG11

The methods used for PG11 were essentially the same as for PG1 with the following exceptions. The 5' oligonucleotide primer sequence was GCGCGTATACATGAGAGCAAACATTTGGCAGATACTTTCCG, the 3'
30 oligonucleotide primer sequence was GCGCAGATCTGCGCAAGCGCAGTATATCGCC and DNA was amplified with Tli DNA polymerase (Promega). The PCR product was cloned into pCR-Blunt and transformed into *E. coli* Top10F' before subcloning into the expression plasmid pGex-stop RBS(IV) using the Bst Z171 and Bgl II restriction sites and
35 transformed into *E. coli* ER1793. PG11 was purified by solubilisation of *E. coli* cells with 2% sarkosyl in binding buffer (Qiagen) which was diluted to

0.1% sarkosyl in binding buffer, bound to a Nickel-nitrilotriacetic acid column (Ni-NTA; Qiagen), after washing bound proteins were eluted with 1M imidazole (0.7% CHAPS (Sigma) in elution buffer; Qiagen) according to the Qiagen recommendations. Following purification samples were dialysed
5 against 500mM NaCl, 20mM Tris, 0.7% CHAPS, 20% glycerol (Sigma) at pH7.4 to remove the imidazole, concentrated as required and stored at 4°C until used.

PG12

10 The methods used for PG12 were essentially the same as for PG1 with the following exceptions. The 5' oligonucleotide primer sequence was GCGCGTATACATGAATAGCAGACATCTGACAATCACAATCATTGCCGG, the 3' oligonucleotide primer sequence was
15 GCGCAGATCTGCTGTTCTGTGAGTGCAGTTGTTTAAGTG and DNA was amplified with Tli DNA polymerase. The PCR product was cloned into pCR-Blunt and transformed into *E. coli* Top10F' cells before subcloning into the expression plasmid pGex-stop RBS(IV) using the Bst Z171 and Bgl II restriction sites and transformed into *E. coli* BL21. Purification of the recombinant protein was essentially the same as PG11 except 0.5% DHPC
20 (1,2-Diheptanoyl-*sn*-glycero-3-phosphocholine; Avanti) in 50mM Tris, 50mM NaCl, pH8.0 was used to solubilise the inclusion bodies instead of sarkosyl and the DHPC was diluted to 0.1% before addition to the Ni-NTA and 0.1% DHPC was added to all buffers.

25 PG13

The methods used for PG13 were essentially the same as for PG3 with the following exceptions. The 5' oligonucleotide primer sequence was GCGCCATATGCGGACAAAACTATCTTTTTTGCG, the 3' oligonucleotide primer sequence was
30 GCGCCTCGAGGTTGTTGAATCGAATCGCTATTTGAGC and DNA was amplified with Tli DNA polymerase. The PCR product was cloned the expression plasmid pET24b using the Nde I and Xho I restriction sites and transformed into *E. coli* BL21. Purification of the recombinant protein was essentially the same as PG3 using 6M urea and 1% NOG (n-octyl glucoside;
35 Sigma) was added to the dialysis buffer. Removal of urea was not proceeded

past 2M urea as the protein was insoluble at lower concentrations of urea. Purified protein was stored at 4°C until required.

PG14

- 5 The methods used for PG12 were essentially the same as for PG1 with the following exceptions. The 5' oligonucleotide primer sequence was GCGCGGCGCCATGACGGACAACAAACAACGTAATATCG, the 3' oligonucleotide primer sequence was GCGCCTCGAGTTACTTGCGTATGATCACGGACATACCC and DNA was
10 amplified with Tli DNA polymerase. The PCR product was cloned the expression plasmid pProEx-1 using the Ehe I and Xho I restriction sites and transformed into *E. coli* BL21. Purification of the recombinant protein was essentially the same as PG12.

15 PG15

- The methods used for PG15 were essentially the same as for PG3 with the following exceptions. The 5' oligonucleotide primer sequence was CAAAAGTATACTAATAAATATCATTTCTCAA, the 3' oligonucleotide primer sequence was GCTTATGGTACCTTTGGTCTTATCTATTAT and DNA was
20 amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pGex-stop RBS(IV) using the Bst Z171 and Kpn I restriction sites and transformed into *E. coli* ER1793.

PG22

- 25 The methods used for PG22 were essentially the same as for PG1 with the following exceptions. The 5' oligonucleotide primer sequence was CCCCGGATCCGATGCGACTGATCAAGGC, the 3' oligonucleotide primer sequence was CCCCTCGAGCGGAACGGGGTCATAGCC and DNA was
30 amplified with the TaqPlus Precision PCR System. The PCR product was cloned into the expression plasmid pET24b using the Bam HI and Xho I restriction sites and transformed into *E. coli* BL21DE3. Once PG22 was purified dialysis was performed in the same manner as for PG1 but in the presence of 1M imidazole.

PG24

The methods used for PG24 were essentially the same as for PG3 with the following exceptions. The 5' oligonucleotide primer sequence was CGCGGTATACATGAATTACCTGTACATAC, the 3' oligonucleotide primer
5 sequence was CGCGGGATCCGTTTCGATTGGTCGTCGATGG and DNA was amplified with the TaqPlus Precision PCR System. The PCR product was digested with Bst Z171 and Bam HI and ligated into the expression plasmid pGex-stop RBS(IV) using the Bst Z171 and Bgl II restriction sites and transformed into *E. coli* ER1793. Due to the low level of expression of PG24
10 purification was not proceeded with except on small scale.

PG24A

A modified version of PG24 was also cloned and expressed. PG24A is the same as PG24 with the predicted N-terminal sequence removed. The
15 methods used for PG24A were essentially the same as for PG3 with the following exceptions. The 5' oligonucleotide primer sequence was CGCGCATATGGAGATTGCTTTCCTTCTCG, the 3' oligonucleotide primer sequence was CGCGCTCGAGTTAGTTCGATTGGTCGTCG and DNA was amplified with the TaqPlus Precision PCR System. The PCR product was
20 cloned into the expression plasmid pProEx-1 using the Nde I and Xho I restriction sites and transformed into *E. coli* ER1793. Purification of the recombinant protein was essentially the same as PG3 except 8M urea was used to solubilise the inclusion bodies and in the buffers used for the Ni-NTA column purification. Urea was removed by sequential dialysis (4M then 2M,
25 then 1M then 0.5M then 0M urea all in 50mM Tris, 500mM NaCl, 8% glycerol, pH7.4). Purified protein was stored frozen at -80°C until required.

PG29

The methods used for PG29 were essentially the same as for PG3 with
30 the following exceptions. The 5' oligonucleotide primer sequence was GCGCGATATCGCTAGCATGAAAAAGCTATTTCTC, the 3' oligonucleotide primer sequence was GCGCAGATCTCTCGAGTTTGCCATCGGATTGCGGATTG and DNA was amplified with Pfu DNA polymerase being used. The PCR product was
35 cloned into pCR-Blunt (InVitrogen) and transformed into *E. coli* Top10F' before subcloning into the expression plasmid pGex-stop RBS(IV)

using the EcoR V and Bgl II restriction sites and transformed into *E. coli* BL21. 6M urea was used throughout the purification process.

PG30

- 5 The methods used for PG30 were essentially the same as for PG3 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was TACGGAATTCGTGACCCCGTCAGAAATGTGCGC, the 3' oligonucleotide primer sequence was
- 10 CTATGCGGCCGCTTTGATCCTCAAGGCTTTGCCCGG and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates of PG30. 10ml cultures of
- 15 recombinant *E. coli* were grown to an OD of 2.0 (A_{600nm}) in terrific broth and the cells were induced with 0.5mM IPTG and samples taken for analysis at 4 hours post induction. Purification was not done for these studies.

PG31

- 20 The methods used for PG31 were essentially the same as for PG30 with the following exceptions. The 5' oligonucleotide primer sequence was CGGGGAATTCGCAAAAATCAATTTCTATGCTGAA, the 3' oligonucleotide primer sequence was CTATGCGGCCGCTGTATGCAATAGGGAAAGCTCCGA and DNA was amplified with the Tth XL PCR kit. The PCR product was
- 25 cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG32

- 30 The methods used for PG32 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was CGCAGAATTCCAGGAGAATACTGTACCGGCAACG, the 3'
- 35 oligonucleotide primer sequence was CTATGCGGCCGCTTGGAGCGAACGATTACAACAC and DNA was

amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done
5 for these studies.

PG33

The methods used for PG33 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was
10 removed from the recombinant protein.

The 5' oligonucleotide primer sequence was TGCAGAATTCCAAGAAGCTACTACACAGAACAAA, the 3' oligonucleotide primer sequence was CTATGCGGCCGCTTCCGCTGCAGTCATTACTACAA and DNA was amplified with the Tth XL PCR kit. The PCR product was
15 cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

20 PG35

The methods used for PG35 were essentially the same as for PG30 with the following exceptions. The 5' oligonucleotide primer sequence was GCGCGAATTCATGAAACAATAACATTATCAGC, the 3' oligonucleotide primer sequence was GCGTGCGGCCGCGAAATTGATCTTTGTACCGACGA
25 and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

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PG36

The methods used for PG36 were essentially the same as for PG30 with the following exceptions. The 5' oligonucleotide primer sequence was AAAGGAATTCTACAAAAAGATTATTGCCGTAGCA, the 3' oligonucleotide
35 primer sequence was CTATGCGGCCGCGAACTCCTGTCCGAGCACAAAGT and DNA was amplified with the Tth XL PCR kit. The PCR product was

cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

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PG37

The methods used for PG37 were essentially the same as for PG30 with the following exceptions. The 5' oligonucleotide primer sequence was TGGCGAATTCAAACGGTTTTTGTATTTTGATCGGC, the 3' oligonucleotide
10 primer sequence was CTATGCGGCCCGCCTTGCTAAAGCCCATCTTGCTCAG and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates.
15 Purification was not done for these studies.

PG38

The methods used for PG38 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was
20 removed from the recombinant protein. The 5' oligonucleotide primer sequence was CCTCGAATTCCAAAAGGTGGCAGTGGTAAACACT, the 3' oligonucleotide primer sequence was CTATGCGGCCCGCCTTGATTCCGAGTTTCGCTTTTAC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the
25 expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG39

The methods used for PG39 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer
30 sequence was AGCTGGATCCCAAGGCGTCAGGGTATCGGGCTAT, the 3' oligonucleotide primer sequence was
35 CTATGCGGCCCGCAATTTCGACGAGGAGACGCAGGT and DNA was

amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Bam HI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done
5 for these studies.

PG40

The methods used for PG40 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer
10 sequence was GGCTGAATTCAAGACGGACAACGTCCCGACAGAT, the 3' oligonucleotide primer sequence was CTATGCGGCCGCGAAGTTGACCATAACCTTACCCA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the
15 expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

20 PG41

The methods used for PG41 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GACTGAATTCCAAAACGCCTCCGAAACGACGGTA, the 3'
25 oligonucleotide primer sequence was CTATGCGGCCGCTTGTTTCGGGAATCCCCATGCCGTT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity
30 studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG42

The methods used for PG42 were essentially the same as for PG30 with the following exceptions. The 5' oligonucleotide primer sequence was GTTTGAATTCGCAAATAATACTCTTTTGCGGAAG, the 3' oligonucleotide

primer sequence was

GAGTGCGGCCGCTTTGCCGGACATCGAAGAGATCGTC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG43

The methods used for PG43 were essentially the same as for PG30 with the following exceptions. The 5' oligonucleotide primer sequence was GCGCGAATTCAAAAAAGAAAAACTTTGCATTGCG, the 3' oligonucleotide primer sequence was CTATGCGGCCGCTTCAAAGCGAAAGAAGCCTTAAC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG44

The methods used for PG44 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was AGCCGAATTCTGTAAGAAAAATGCTGACACTACC, the 3' oligonucleotide primer sequence was CTATGCGGCCGCTTTTCCCGGGCTTGATCCCGAT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG45

The methods used for PG45 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer

sequence was GACAGGATCCTGCTCCACCACAAAGAATCTGCCG, the 3' oligonucleotide primer sequence was CTATGCGGCCGCGAAGGGATAGCCGACAGCCAAAT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Bam HI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

10 PG46

The methods used for PG46 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was CTCGGAATTCCGTTATGTGCCGGACGGTAGCAGA, the 3' oligonucleotide primer sequence was CTATGCGGCCGCGAACGGATAGCCTACTGCAATGT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG47

The methods used for PG47 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was CGCCGAATTCCAAACAGTGGTGACCGGTAAGGTGATCGATTTCAGAA, the 3' oligonucleotide primer sequence was CTATGCGGCCGCGAAGTTTACACGAATACCGGTAGACCAAGTGCGGCC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

The methods used for PG50 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GCTGGGATCCGCGACAGACACTGAGTTCAAGTAC, the 3' oligonucleotide primer sequence was CTATGCGGCCGCGAACTTCACTACCAAGCCCATGT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Bam HI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity

studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG51

- 5 The methods used for PG51 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was TCTTGAATTCGCGCAAAGTCTTTTCAGCACCGAA, the 3' oligonucleotide primer sequence was
- 10 CTATGCGGCCGCACTTTTTCGTGGGATCACTCTCTT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done
- 15 for these studies.

PG52

- The methods used for PG52 were essentially the same as for PG30 with the following exceptions. The 5' oligonucleotide primer sequence was
- 20 AGAAGAATTCAAACGGACAATCCTCCTGACGGCA, the 3' oligonucleotide primer sequence was CTATGCGGCCGCGAAGTCTTTGCCCTGATAGAAATC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies
- 25 and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG53

- The methods used for PG53 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GGCTGAATTCGCGAATCCCCTTACGGGCCAATCG, the 3' oligonucleotide primer sequence was
- 30 CTATGCGGCCGCGTCCGAAAGGCAGCCGTAATAGG and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and
- 35

transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

5 PG54

The methods used for PG54 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was CGCTGAATTCCAGATTTTCGTTCCGAGGGGAACCC, the 3' oligonucleotide primer sequence was CTATGCGGCCGCTGCTTCACGATCTTTTGGCTCA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG55

The methods used for PG55 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was CGAGGGATCCGAGCTCTCTATTTGCGATGGCGAG, the 3' oligonucleotide primer sequence was GAGTGC GGCCGCTCTTACCTGACTTCTTGTCACGAAT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Bam HI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

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PG56

The methods used for PG56 were essentially the same as for PG30 with the following exceptions. The 5' oligonucleotide primer sequence was AAATGGATCCCGAAAAATTTTGAGCTTTTGGATG, the 3' oligonucleotide primer sequence was CTATGCGGCCGCTTTGATTCGTAATTTTCCGTATC and DNA was amplified with the Tth XL PCR kit. The PCR product was

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cloned into the expression plasmid pET24a using the Bam HI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

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PG57

The methods used for PG57 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer
10 sequence was TGCTGGATCCCAAGAGATCTCAGGCATGAATGCA, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTCGGCCTCTTTATCTCTACCTTTTC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Bam HI and Not I restriction sites and
15 transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG58

The methods used for PG58 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer
20 sequence was CCGTGAATTCCAAACCCACGAAATACAGAAACC, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTGAAAGTCCAGCTAAAACCGGCGAA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and
25 transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.
30

PG59

The methods used for PG59 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer
35 sequence was TGCTGAATTCCAACAAGAGAAGCAGGTGTTTCAT, the 3'

The methods used for PG61 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was AGCAGAATTCCCCGTCTCCAACAGCGAGATAGAT, the 3' oligonucleotide primer sequence was GAGTCCGCCGCTGAAATCGATTGTCAGACTACCCAG and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG62

The methods used for PG62 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer
5 sequence was TGCTGAATTCCAGCGGTTTCCGATGGTGCAGGGA, the 3' oligonucleotide primer sequence was
GAGTGCGGCCGCTGAAAGTGAAATCCGACACGCAGCTG and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and
10 transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG63

15 The methods used for PG63 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GGCAGAATTCCAAGAAGCAAACACTGCATCTGAC, the 3' oligonucleotide primer sequence was
20 GAGTGCGGCCGCTGAAAGTGACGCAACACCCACGCC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done
25 for these studies.

PG64

The methods used for PG64 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer
30 sequence was TGCTGAATTCCAGAGTCGTCCTGCTCTTAGACTG, the 3' oligonucleotide primer sequence was
GAGTGCGGCCGCTGAAGCGAACACCGAGACCCACAAA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and
35 transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity

studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG65

- 5 The methods used for PG65 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GGCCGGATCCATCGGACAAAGCCGCCCGGCACTT, the 3' oligonucleotide primer sequence was
- 10 GAGTGCGGCCGCTAAAGCGGTAACCTATGCCCACGAA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Bam HI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done
- 15 for these studies.

PG66

- The methods used for PG66 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was
- 20 removed from the recombinant protein. The 5' oligonucleotide primer sequence was GTTTGAATTCCAAGACGTTATCAGACCATGGTCA, the 3' oligonucleotide primer sequence was
- GAGTGCGGCCGCTAAAATGAGTGGAGAGCGTGCCCAT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the
- 25 expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

30 PG67

- The methods used for PG67 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GAACGAGCTCGCGGAACGTCCTATGGCCGGAGCA, the 3'
- 35 oligonucleotide primer sequence was
- GAGTGCGGCCGCTATACCAAGTATTTCGTGATGGGACG and DNA was

amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Sac I and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG68

The methods used for PG68 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GCTTGCGGCCGCCCTTATGAAAGATTTGCAGAT, the 3' oligonucleotide primer sequence was GGTGCTCGAGTATACTCAACAAGCACCTTATGCAC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Not I and Xho I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG69

The methods used for PG69 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was TGCTGAATTCCAGGAAGGGGAGGGGAGTGCCCGA, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTGAAGCTGTAGCGGGCTTTGAACCA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG70

The methods used for PG70 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer

sequence was CGGTGGATCCTCGCAAATGCTCTTCTCAGAGAAT, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTAAACGAAATATCGATACCAACATC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Bam HI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

10 PG71

The methods used for PG71 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was TGCTGAATTCCAGAACAATACCCTCGATGTACAC, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTATTGCCGGTAGGATTTCTTGTCC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG72

The methods used for PG72 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was TGCTGAATTCCGAGAGCGACTGGAGACGGACAGC, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTATGATTGCCTTTCAGAAAAGCTAT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed TGCTGAATTCCGAGAGCGACTGGAGACGGACAGC into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG73

The methods used for PG73 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer
 5 sequence was CCGTGAATTCCAACAGACAGGACCGGCCGAACGC, the 3' oligonucleotide primer sequence was
 GAGTGCGGCCGCTTAAGAAAGGTATCTGATAGATCAG and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and
 10 transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG74

15 The methods used for PG74 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was TGCTGAATTCCAAGAAAATAATACAGAAAAGTCA, the 3' oligonucleotide primer sequence was
 20 GAGTGCGGCCGCTGAGGTTTAATCCTATGCCAATACT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done
 25 for these studies.

PG75

The methods used for PG75 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer
 30 sequence was GGCGGGATCCGCTCAGGAGCAACTGAATGTGGTA, the 3' oligonucleotide primer sequence was
 GAGTGCGGCCGCTGTGGAACAAATTGCGCAATCCATC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Bam HI and Not I restriction sites and
 35 transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity

PG76

5 The methods used for PG76 were essentially the same as for PG30
with the following exceptions. The predicted N-terminal signal sequence was
removed from the recombinant protein. The 5' oligonucleotide primer
sequence was AGCAGAATTCGGAACGCACAGAGCTTTTGGGAA, the 3'
oligonucleotide primer sequence was
10 GAGTGCGGCCGCTTACCTGCACCTTATGACTGAATAC and DNA was
amplified with the Tth XL PCR kit. The PCR product was cloned into the
expression plasmid pET24a using the Eco RI and Not I restriction sites and
transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity
studies were carried out on whole *E. coli* lysates. Purification was not done
15 for these studies.

PG77

The methods used for PG77 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was TGCTGAATTCCAAGAGAAAAAGGATAGTCTCTCT, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTCTTCITATCGCCATAGAATACAGG and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

30 PG78

The methods used for PG78 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GGCAGAATTCCAGGATTCTTCCCACGGTAGCAAT, the 3' oligonucleotide primer sequence was GAGTGC GGCCGCTATCATGATAGTAAAGACTGGTTCT and DNA was

amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done
5 for these studies.

PG79

The methods used for PG79 were essentially the same as for PG30 with the following exceptions. The 5' oligonucleotide primer sequence was
10 TGCTGAATTTCGTAGTGACGCTGCTCGTAATTGTC, the 3' oligonucleotide primer sequence was
GAGTGCGGCCGCTGCCGTCCTGCCTTTCTGCCTGACG and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and
15 transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG80

The methods used for PG80 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GGCCGAATTCCAAAACGTGCAGTTGCACTACGAT, the 3' oligonucleotide primer sequence was
25 GAGTGCGGCCGCTGTTGAAAGTCCATTTGACCGCAAG and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done
30 for these studies.

PG81

The methods used for PG81 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was
35 removed from the recombinant protein. The 5' oligonucleotide primer sequence was GTTGAATTCCAGGATTTTCTCTATGAAATAGGA, the 3'

The methods used for PG84 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was TGCTGGATCCCAGAATGATGACATCTTCGAAGAT, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTATTGCGTCCCCGGCCACTACGTCC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Bam HI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG85

The methods used for PG85 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer
5 sequence was CCGTGAATTTCGTACCAACGGACAGCACGGAATCG, the 3' oligonucleotide primer sequence was
GAGTGCGGCCGCTCAGATTGGTGCTATAAGAAAGGTA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and
10 transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG86

15 The methods used for PG86 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was TGCTGGATCCCAAACGCATGATCATCTCATCGAA, the 3' oligonucleotide primer sequence was
20 GAGTGCGGCCGCTGTGGTTCAGGCCGTGGCAAATCT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Bam HI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done
25 for these studies.

PG87

The methods used for PG87 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer
30 sequence was GGCGGAATTCCAGAGCTATGTGGACTACGTTCGAT, the 3' oligonucleotide primer sequence was
GAGTGCGGCCGCTATTACTGTGATTAGCGCGACGCTG and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and
35 transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity

The methods used for PG90 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GGCAGAATTCCAAACAACGACGAACAGTAGCCGG, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTTTTTTGTGTGATACTGTTTGGGC and DNA was

amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done
5 for these studies.

PG91

The methods used for PG91 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was
10 removed from the recombinant protein. The 5' oligonucleotide primer sequence was TGCTGAATTCCAGACGATGGGAGGAGATGATGTC, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTTCCACGATGAGCTTCTCTACGAA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the
15 expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

20 PG92

The methods used for PG92 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GGCCGAATTGCGCGATGCACAAAGCTCTGTCTCT, the 3'
25 oligonucleotide primer sequence was GAGTGCGGCCGCTTCGAGGACGATTGCTTAGTTCGTA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity
30 studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG93

The methods used for PG93 were essentially the same as for PG30
35 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer

30 GAGTGGCGCCGCTAACTGTCTCCTTGTGCTCCCCGG and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Sac I and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG96

The methods used for PG96 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer
 5 sequence was TGCTGAGCTCCAAACGCAAATGCAAGCAGACCGA, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTTTTGAGAATTTTCATTGTCTCACG and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Sac I and Not I restriction sites and
 10 transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG97

15 The methods used for PG97 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GCGGGATCCAGTTTGTTCCGGCTCCCACCACA, the 3' oligonucleotide primer sequence was
 20 GAGTGCGGCCGCTCTGTTTGATGAGCTTAGTGGTATA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Bam HI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done
 25 for these studies.

PG98

The methods used for PG98 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer
 30 sequence was AGCAGAATTCCAAGAAAGAGTCGATGAAAAAGTA, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTTAGCTGTGTAACATTAAGTTTTTTATTGAT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into
 35 the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and

immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG99

- 5 The methods used for PG99 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was TGCTGAATTCAAGGACAATTCTTCTTACAAACCT, the 3' oligonucleotide primer sequence was
- 10 GAGTGCGGCCGCTTCGAATCACGACTTTTCTCACAAA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done
- 15 for these studies.

PG100

- The methods used for PG100 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GGCAGAAATCCAGTCTTTGAGCACAATCAAAGTA, the 3' oligonucleotide primer sequence was
- 20 GAGTGCGGCCGCTGATAGCCAGCTTGATGCTCTTAGC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done
- 25 for these studies.

30 PG101

- The methods used for PG101 were essentially the same as for PG30 with the following exceptions. The 5' oligonucleotide primer sequence was TGCTGAATTCAAAGGCAAGGGCGATCTGGTCCGG, the 3' oligonucleotide primer sequence was
- 35 GAGTGCGGCCGCTTCTCTTCTCGAACTTGCCCGAGTA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the

35 Various antisera were raised for detecting the expression and refolding of the recombinant *P. gingivalis* proteins. A whole cell antisera was raised by injecting New Zealand White rabbits with 3 doses of sonicated

P. gingivalis (strain W50) containing approximately 2mg of protein. The first dose was given in Freund's complete adjuvant (FCA) and the second and third doses were given in Freund's incomplete adjuvant (IFA) at 3 week intervals. Doses (1ml) were given intramuscularly into the hind legs and rabbits bled 7 days after the last dose, the blood clotted and serum removed and stored at -20°C until required. A second rabbit antiserum was produced in a similar manner but using a sarkosyl insoluble fraction (each dose was 0.69mg of protein) derived from *P. gingivalis* W50 according to the method of Doidg and Trust T. *et al* 1994 as the immunogen. A third rabbit antiserum was produced in a similar manner to the first only the sarkosyl soluble fraction (1mg of protein per dose) derived from *P. gingivalis* W50 cells according to the method of Doidg P. and Trust TJ. (1994 Infect Immun 62:4526-33) was used as the immunogen.

A "protected rat serum" pool was also used in these studies and was obtained from rats immunised with formalin killed whole *P. gingivalis* cells in FIA (strain ATCC 33277; 2 doses of 2×10^9 cells, 3 weeks apart). Rats were then challenged 2 weeks after their last dose with live *P. gingivalis* cells (strain 33277) given orally as previously described (Klaussen B. *et al.* 1991, Oral Microbiol Immunol 6:193-201) and the serum obtained from these rats 6 weeks after the final challenge inoculation at the time of sacrifice.

Human sera were obtained from adult patients undergoing treatment or assessment for periodontitis at an outpatient clinic. These patients had at least 6 teeth with 6mm attachment loss and had *P. gingivalis* present in their sub-gingival plaque as detected using a *P. gingivalis* specific DNA probe. Sera was pooled from these patients and compared to a pool of sera from periodontally healthy patients.

Immunization and Murine Lesion Model Protocols

The mouse abscess model was used to assess the efficacy of immunising mice with recombinant *P. gingivalis* proteins in protecting mice from formation of a subcutaneous abscess. This model has been used by others as a predictor of potential vaccines against periodontal disease (Bird PS, *et al.* 1995 J. Periodontol. 66:351-362. BALB/c mice 6-8 weeks old were immunised by subcutaneously injecting them with 0.1 ml containing either 10 or 20µg of recombinant *P. gingivalis* protein, 20µg of *E. coli* lysate protein,

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Immunoscreening

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onto Hybond-C Extra nitrocellulose membranes (Amersham) by transblotting and the membranes were then blocked for 2h at room temperature (RT) in 5% skim milk in 20mM Tris, 0.5M NaCl, 0.05% Tween-20, pH 7.5 (TTBS).

Immunoscreening was performed separately with the rabbit
5 anti-*P. gingivalis* whole cell serum, the rat protective serum, a pool of human periodontal patients serum, and in many cases an anti-T7-Tag antibody HRP conjugate (Novagen). Prior to use, the rabbit, rat and human sera were diluted 1/5000, 1/1000 and 1/500 respectively in 5% skim milk in TTBS and absorbed with 100µl (for the rabbit serum) or 250µl (for the rat and human
10 sera) *E. coli* extract (20mg/ml; Promega) for 6h at RT.

Membranes were incubated overnight at RT with the absorbed antisera, or for 1 hr at RT with 1/5000 diluted anti-T7-Tag conjugate. Following 3x10min washes with TTBS, HRP-conjugated anti-rabbit (Silenus),
anti-mouse (Silenus) or anti-human (KPL) antibody, diluted 1/5000 in 5%
15 skim milk in TTBS, was added for 1h at RT. Membranes were washed as before, prior to addition of TMB membrane peroxidase substrate (KPL) for detection of immunoreactive proteins. Results of reactivity for the recombinant *P. gingivalis* proteins is shown in Table 7.

In addition some of the sera (pooled sera diluted 1/1000) from the
20 mice immunised with *P. gingivalis* recombinant proteins (prior to challenge) were analysed for their reactivity against Western blots of whole native W50 *P. gingivalis* proteins using similar techniques as those outlined above. PG2, PG8A, PG29 and PG3 all showed bands at a similar molecular weight to that of the recombinant PG protein in the native W50 blot. This indicates that PG
25 proteins are expressed in the W50 strain and that the recombinant proteins have at least some identical immunogenicity to the native proteins.

m-RNA analysis

30 Hot Phenol RNA Extraction

P. gingivalis W50 cells (150ml culture) were grown anaerobically to mid log phase (OD A_{600} =0.18) mixed with 50% glycerol and stored at -70°C until RNA extraction. Cells were pelleted by centrifugation at 6000g, and
35 resuspended in 8ml ASE (20mM NaOAc, 0.5% SDS, 1mM EDTA). An equal volume of 20mM NaOAc(pH 4.5)-saturated phenol was added and mixed by

shaking for 30 seconds, incubated at 65°C for 5 minutes, followed by a further 5 second shaking and repeated incubation. After cooling, 2ml chloroform was added and mixed by shaking for 5 seconds, and the mixture spun at 10000g for 10 minutes at 4°C. The top aqueous phase was transferred and re-extracted by repeating the phenol and chloroform steps. The aqueous phase was transferred again and 100U RNase inhibitor (RNasin; Promega) were added. RNA was precipitated with 3 volumes 100% ethanol at -20°C overnight. The RNA precipitate was recovered by centrifugation at 10000g at 4°C for 15 minutes, then washed with 100% ethanol, dried and resuspended in 600µl sterile, deionised, dH₂O with 1µl of fresh RNase inhibitor. RNA was aliquoted and stored at -70°C. The RNA concentration was determined spectrophotometrically. A formaldehyde RNA gel confirmed RNA integrity (Sambrook J. et al. 1989, Molecular Cloning. A laboratory manual. Cold Spring Laboratory Press, New York. 2nd Edition).

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RT-PCR

The isolated RNA was used as a template for Reverse Transcription (RT) to produce cDNA. Varying RNA concentrations were used for the RT as each RNA transcript was potentially present at different levels. Subsequent amplification of the cDNA was performed using Polymerase Chain Reaction (PCR). RT-PCR was performed using GeneAmp® RNA PCR Kit (Perkin Elmer) according to the manufacturer's protocol with the following exception to the PCR; 35 cycles were performed as follows: Melt phase 95°C for 30 seconds, Anneal phase varied between 50-60°C for 30 seconds, Extension phase 72°C for 1 minute. Amplification was performed in a PTC-100 Programable Thermal Controller (MJ Research Inc.). As a control to demonstrate that the amplified product did not arise from contaminating DNA, Reverse Transcriptase (RTase) was omitted from a parallel tube. The PCR products were examined against DNA markers (GIBCO 1kB ladder) on a 1% agarose gel stained with ethidium bromide.

RT-PCR results are shown in Table 6 using the oligonucleotide primers as used in "Cloning, expression and purification of recombinant *P. gingivalis* genes" section described above, except for the following changes. For PG1 the 3' reverse primer used was

PG #	RNA μg	Annealing temp. °C	RT-PCR	PCR (-RT)	Approx. fragment size bp	Expected fragment size bp
1	0.15	55	+	-	1300	1362
2	1.0	50	+	-	3200	3051
3	0.15	60	+	-	720	690
4	2.9	55	-	-	N.D.	2000
5	0.02	50	+	-	1000	947
6	1.0	55	+	-	1000	972
8A	0.15	50	+	-	1200	1278
10	0.15	55	+	-	590	585
11	0.10	60	+	-	960	942
12	0.02	60	+	-	880	831
13	1.0	50	+	-	2150	2274
14	0.15	60	+	-	1050	996

PG #	RNA µg	Annealing temp. °C	RT-PCR	PCR (-RT)	Approx. fragment size bp	Expected fragment size bp
22	1.0	60	-	-	N.D.	228
24	1.0	55	+	+	1150	1194
29	0.15	60	+	-	880	885

5 **Table 7:** Immunoblot results of proteins expressed in *E.coli* against rabbit, rat and human antisera. Deduced MW was calculated from amino acid sequence of the *P. gingivalis* proteins, some of which had their N-terminal signal sequences removed. Apparent MW was determined from SDS-PAGE gels. The N- and C-terminal tags add approximately 2.5 KDa to the deduced MW of the recombinant proteins. The symbols are + positive, - negative, +/- weak positive, ND not done.

10

Protein number	Deduced MW (KDa)	Apparent MW (KDa)	Antisera reactivity			
			T7	Rabbit	Rat	Human
PG1	47.5	63	ND	-	-	-
PG2	112.4	125.7	ND	+	-	-
PG3	22.6	18.3	ND	- ^a	-	-
PG4	75	90.6	ND	-	-	-
PG5	34.9	43.8	ND	-	-	-
PG6	36.7	47.1	ND	-	-	-
PG8	67.5	63.1	ND	- ^b	-	-
PG8A	47.7	90.6	ND	-	-	-
PG10	21.3	25.5	ND	+	-	+
PG11	36.2	42.4	ND	-	-	-
PG12	30.7	30.6	ND	-	-	-
PG13	84.5	101	ND	-	-	-
PG14	36	42.4	ND	-	+	+
PG22	8.6	11.1	ND	-	-	-
PG24A	47	63.1	ND	-	-	-
PG29	31.1	40.9	ND	+	+	+

Protein number	Deduced MW (KDa)	Apparent MW (KDa)	Antisera reactivity			
			T7	Rabbit	Rat	Human
PG30	35.1	46.9	+	-	-	-
PG31	16.7	-	-	-	-	-
PG32	41.2	59.5	+	+	+	-
PG33	39.9	52.7	+	+	+	-
PG35	92.6	116.6	+	-	-	-
PG36	98.9	120.2	-	-	-	-
PG37	18.8	23.1	+	+	-	-
PG38	16.1	22.9	+	-	-	-
PG39	87.9	116.6	+	-	-	-
PG40	76.6	103.1	+	-	-	-
PG41	48.3	81.1	+	-	+	+
PG42	59.3	73.9	+	-	-	-
PG43	27.1	50.3	+	-	-	-
PG44	28.6	32.3	+	-	+	-
PG45	84	100.6	+	-	-	-
PG46	83	97.7	+	-	-	-
PG47	93.7	42.5	+	+	-	+
PG48	45.2	37.9	+	-	-	-
PG49	33.3	64.1	+	-	+	-
PG50	91.9	113.2	+	+	-	-
PG51	19.6	27.2	+	-	-	-
PG52	50.4	64.4	+	+	-	+
PG53	47.4	45.4	+	-	-	+
PG54	101.4	46.7	+	+	-	-
PG55	70.4	68.4	+	-	-	-
PG56	142.3	-	-	-	-	-
PG57	100	134.5	+	+	+	+
PG58	63	82.9	+	-	-	-
PG59	33.3	43.6	+	-	-	-
PG60	55.6	77.8	+	-	-	-
PG61	81.5	107.3	+	-	-	-

WO 99/29870

PCT/AU98/01023

84

Protein number	Deduced MW (KDa)	Apparent MW (KDa)	Antisera reactivity			
			T7	Rabbit	Rat	Human
PG62	51.9	58.4	+	-	-	-
PG63	29.6	43.6	+	-	-	-
PG64	18.5	26.9	+	-	-	-
PG65	25.9	28.8	+	-	-	-
PG66	22.2	25.1	+	+	-	-
PG67	103.7	105	+	-	-	-
PG68	133.3	30.7	+	-	+	+
PG69	44.4	50.8	+	-	-	-
PG70	25.9	30.8	+	-	-	-
PG71	88.9	105.5	+	-	-	-
PG72	40.7	49.8	+	-	-	-
PG73	40.7	29	+/-	-	-	-
PG74	22.2	32.5	+	-	-	-
PG75	40.7	46.7	+	-	-	-
PG76	48.1	55.6	+	-	-	+
PG77	29.6	36.9	+	-	-	-
PG78	33.3	35.4	+	-	-	-
PG79	33.3	-	-	-	-	-
PG80	25.9	20.5	+	-	-	-
PG81	23	25.8	+	-	-	-
PG82	44.8	48.5	+	-	-	-
PG84	41.7	52.4	+	-	-	+/-
PG85	62.7	72.4	+	-	-	-
PG86	21.7	27.4	+	-	-	+/-
PG87	83	91.3	+	-	-	+
PG88	27	40.1	+	-	-	-
PG89	26.2	29.4	+	-	-	-
PG90	23	28.4	+	-	-	-
PG91	57.2	85.7	+	+	+	+
PG92	83.6	110.4	+	-	-	+
PG93	83.4	110.4	+	-	-	+

Protein number	Deduced MW (KDa)	Apparent MW (KDa)	Antisera reactivity			
			T7	Rabbit	Rat	Human
PG96	59.3	70.3	+	+	+	+
PG97	44.4	57.5	+	-	+	+
PG98	33.3	36	+	-	-	-
PG99	40.7	55.6	+	-	+	+
PG100	29.6	10.8	+	-	-	-
PG101	14.8	19.7, 14.1	+	-	-	-
PG102	59.3	70.3	+	-	-	+
PG104	40.7	57.5	+	-	-	+

- a. Positive reaction detected with the rabbit antiserum to sarkosyl insoluble *P. gingivalis* antigen.
- b. Purified protein demonstrated weak positive reaction with the rabbit antiserum to whole *P. gingivalis*.

- 10 It will be appreciated by persons skilled in the art that numerous variations and/or modifications may be made to the invention as shown in the specific embodiments without departing from the spirit or scope of the invention as broadly described. The present embodiments are, therefore, to be considered in all respects as illustrative and not restrictive.

References.

1. Lipman DJ, Pearson WR. 1985. Rapid and sensitive protein similarity searches. *Science* 277:1435-1441.
- 5 2. Horton, P. and Nakai, K. (1996). A probabilistic classification system for predicting the cellular localization sites of proteins. *Intellig. Syst. Mol. Biol.* 4: 109-115.
3. Nakai K, Kanehisa M. 1991. Expert systems for predicting protein localization sites in Gram-negative bacteria. *Proteins: Structure,*
10 *Function, and Genetics* 11:95-110.
4. Nielsen H, Engelbrecht J, Brunak S and von Heijne G. 1997. Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites. *Protein Engineering* 10, 1-6.
5. Claros MG and G von Heijne. (1994). TopPred II: an improved
15 software for membrane protein structure predictions. *Comput. Appl. Biosci.* 10: 685-686.
6. Borodovsky M, Rudd KE, and EV Koonin. (1994). Intrinsic and extrinsic approaches for detecting genes in a bacterial genome. *Nucleic Acids Res.* 22:4756-4767.
- 20 7. Struvye M, Moons M, Tommassen J. 1991. Carboxy-terminal phenylalanine is essential for the correct assembly of a bacterial outer membrane protein *J. Mol. Biol.* 218:141-148.
8. Aduse-Opoku J, Slaney JM, Rangarajan M, Muir J, Young KA, Curtis MA. 1997. The Tla receptor protein of *Porphyromonas gingivalis* W50: a homolog of the RI precursor (PrpRI) is an outer membrane
25 receptor required for growth on low levels of hemin. *J. Bacteriol.* 179:4778-4788.
9. Needleman SB, Munsch CD. 1970. A general method applicable to the search of similarity in the amino acid sequence of two proteins.
30 *J. Molec. Biol.* 48: 443-453.

CLAIMS:-

1. An isolated antigenic *Porphyromonas gingivalis* polypeptide, the polypeptide comprising;
an amino acid sequence selected from the group consisting of SEQ.
5 ID. NO. 265 to SEQ. ID. NO. 528, SEQ. ID. NO. 531 and SEQ. ID. NO. 532; or
an amino acid sequence at least 85%, preferably at least 95%, identical to an amino acid sequence selected from the group consisting of SEQ. ID. NO. 265 to SEQ. ID. NO. 528, SEQ. ID. NO. 531 and SEQ. ID. NO. 532;
10 at least 40 amino acids having a contiguous sequence of at least 40 amino acids identical to a contiguous amino acid sequence selected from the group consisting of SEQ. ID. NO. 265 to SEQ. ID. NO. 528, SEQ. ID. NO. 531 and SEQ. ID. NO. 532.
- 15 2. A polypeptide as claimed in claim 1 in which the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ. ID. NO. 265 to SEQ. ID. NO. 528, SEQ. ID. NO. 531 and SEQ. ID. NO. 532.
- 20 3. A polypeptide as claimed in claim 1 in which the polypeptide comprises an amino acid sequence at least 85%, preferably at least 95%, identical to an amino acid sequence selected from the group consisting of SEQ. ID. NO. 265 to SEQ. ID. NO. 528, SEQ. ID. NO. 531 and SEQ. ID. NO. 532.
- 25 4. A polypeptide as claimed in claim 1 in which the polypeptide comprises at least 40 amino acids having a contiguous sequence of at least 40 amino acids identical to a contiguous amino acid sequence selected from the group consisting of SEQ. ID. NO. 265 to SEQ. ID. NO. 528, SEQ. ID. NO. 531 and SEQ. ID. NO. 532.
- 30 5. A polypeptide as claimed in claim 1 in which the polypeptide comprises;
an amino acid sequence selected from the group consisting of SEQ. ID. NO. 386 to SEQ. ID. NO. 528 and SEQ. ID. NO. 532; or
an amino acid sequence at least 85%, preferably at least 95%, identical to an amino acid sequence selected from the group
35 consisting of SEQ. ID. NO. 386 to SEQ. ID. NO. 528 and SEQ. ID. NO. 532; or

at least 40 amino acids having a contiguous sequence of at least 40 amino acids identical to a contiguous amino acid sequence selected from the group consisting of SEQ. ID. NO. 386 to SEQ. ID. NO. 528 and SEQ. ID. NO. 532.

- 5 6. A polypeptide as claimed in claim 1 in which the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ. ID. NO. 386 to SEQ. ID. NO. 528 and SEQ. ID. NO. 532.
7. A polypeptide as claimed in claim 1 in which the polypeptide comprises an amino acid sequence at least 85%, preferably at least 95%,
10 identical to an amino acid sequence selected from the group consisting of SEQ. ID. NO. 386 to SEQ. ID. NO. 528 and SEQ. ID. NO. 532.
8. A polypeptide as claimed in claim 1 in which the polypeptide comprises at least 40 amino acids having a contiguous sequence of at least 40 amino acids identical to a contiguous amino acid sequence selected from the
15 group consisting of SEQ. ID. NO. 386 to SEQ. ID. NO. 528 and SEQ. ID. NO. 532.
9. A polypeptide as claimed in claim 6 in which the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ. ID. NO. 386, SEQ. ID. NO. 424, SEQ. ID. NO. 425, SEQ. ID. NO. 434,
20 SEQ. ID. NO. 447, SEQ. ID. NO. 458, SEQ. ID. NO. 475, SEQ. ID. NO. 498, SEQ. ID. NO. 499, SEQ. ID. NO. 500, SEQ. ID. NO. 501, SEQ. ID. NO. 387, SEQ. ID. NO. 400, SEQ. ID. NO. 411, SEQ. ID. NO. 419, SEQ. ID. NO. 420, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID. NO. 433, SEQ. ID. NO. 437, SEQ. ID. NO. 438, SEQ. ID. NO. 443, SEQ. ID. NO. 444, SEQ. ID. NO. 448,
25 SEQ. ID. NO. 449, SEQ. ID. NO. 452, SEQ. ID. NO. 455, SEQ. ID. NO. 457, SEQ. ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 462, SEQ. ID. NO. 463, SEQ. ID. NO. 467, SEQ. ID. NO. 468, SEQ. ID. NO. 469, SEQ. ID. NO. 482, SEQ. ID. NO. 484, SEQ. ID. NO. 485, SEQ. ID. NO. 494, SEQ. ID. NO. 508, SEQ. ID. NO. 509, SEQ. ID. NO. 510, SEQ. ID. NO. 520, SEQ. ID. NO. 521,
30 SEQ. ID. NO. 522, SEQ. ID. NO. 525, SEQ. ID. NO. 526, SEQ. ID. NO. 528, SEQ. ID. NO. 389, SEQ. ID. NO. 390 and SEQ. ID. NO. 391.
10. An isolated antigenic *Porphyromonas gingivalis* polypeptide, the polypeptide comprising an amino acid sequence selected from the group consisting of SEQ. ID. NO. 386 to SEQ. ID. NO. 528 and SEQ. ID. NO. 532
35 less the leader sequence set out in Table 3.

23. A composition as claimed in claim 22 in which the pharmaceutically acceptable carrier is an adjuvant.
24. A method of treating a subject for *P. gingivalis* infection comprising administering to the subject a composition as claimed in claim 22 or claim 23
5 such that treatment of *P. gingivalis* infection occurs.
25. A method as claimed in claim 24, wherein the treatment is a prophylactic treatment.
26. A method as claimed in claim 24, wherein the treatment is a therapeutic treatment.
- 10 27. An antibody raised against a polypeptide as claimed in any one of claims 1 to 10.
28. An antibody as claimed in claim 27 in which the antibody is polyclonal.
29. An antibody as claimed in claim 27 in which the antibody is
15 monoclonal.
30. A composition comprising at least one antibody as claimed in any one of claims 27 to 29.
31. A composition as claimed in claim 30 in which the composition adapted for oral use.
- 20 32. A nucleotide probe comprising at least 18 nucleotides and having a contiguous sequence of at least 18 nucleotides identical to a contiguous nucleotide sequence selected from the group consisting of SEQ. ID. NO. 1 to SEQ. ID. NO. 121, SEQ. ID. NO. 529 and sequences complementary thereto.
33. A nucleotide probe as claimed in claim 32 in which the probe further
25 comprises a detectable label.
34. A method for detecting the presence of *P. gingivalis* nucleic acid in a sample comprising:
 - (a) contacting a sample with the nucleotide probe as claimed in claim
30 32 or claim 33 under conditions in which a hybrid can form between the probe and a *P. gingivalis* nucleic acid in the sample; and
 - (b) detecting the hybrid formed in step (a), wherein detection of a hybrid indicates the presence of a *P. gingivalis* nucleic acid in the sample.

09/581286

WO 99/29870

PCT/AU98/01023

1/2

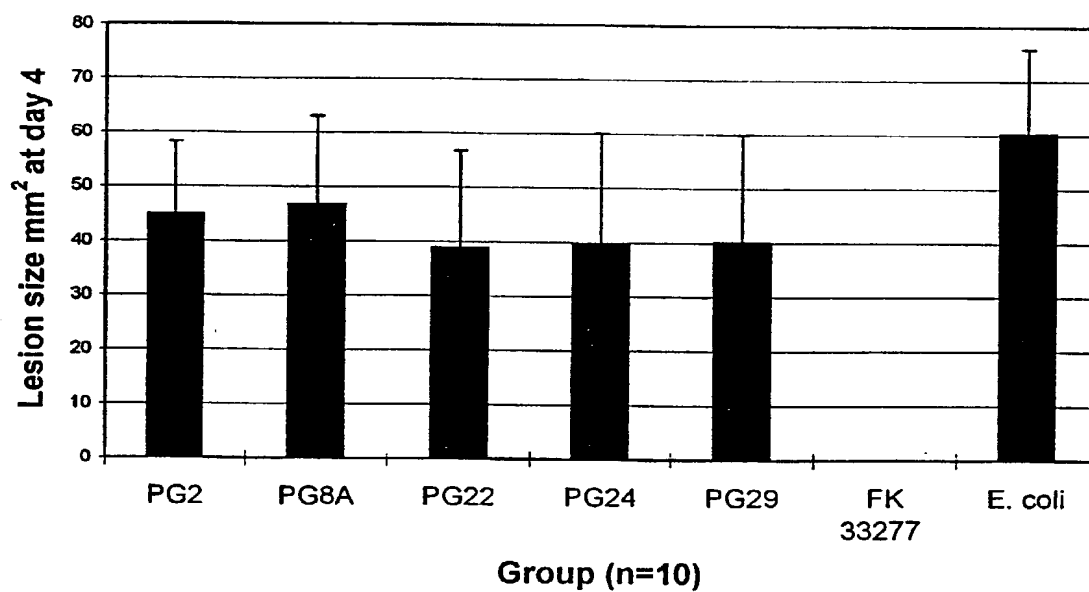


Figure 1

WO 99/29870

PCT/AU98/01023

2/2

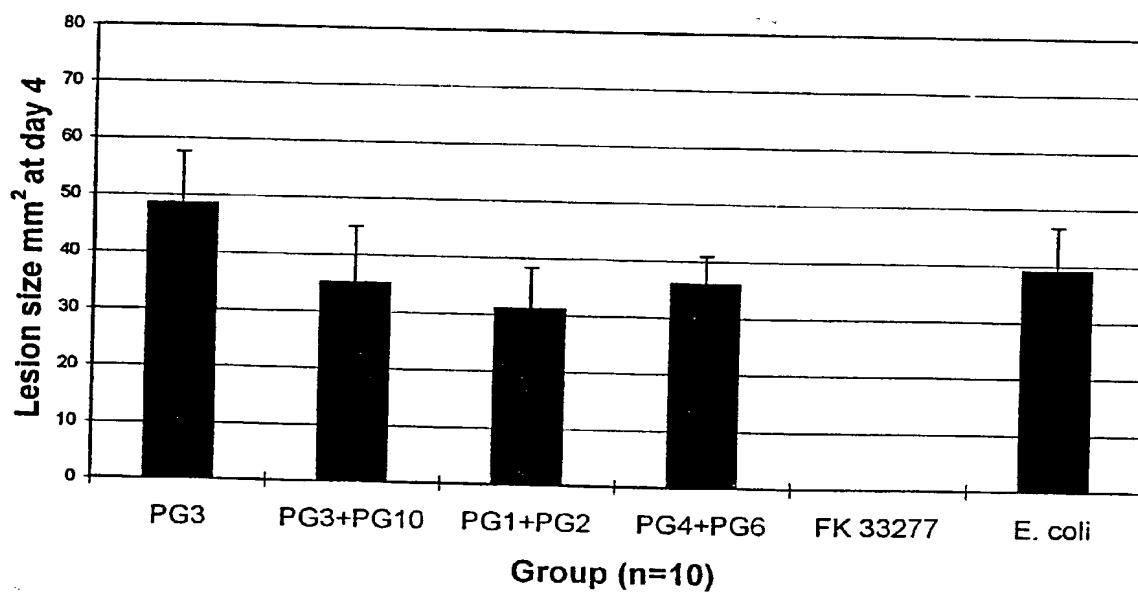


Figure 2

47-138
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Nixon & Vanderhye P.C. (10/99)
(Domestic Non-Assigned/Foreign) Page 1 of 3

RULE 63 (37 C.F.R. 1.63)
INVENTORS DECLARATION FOR PATENT APPLICATION
IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

As a below named inventor, I hereby declare that my residence, post office address and citizenship are as stated below next to my name, and I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

P. GINGIVALIS POLYPEPTIDES AND NUCLEOTIDES

the specification of which (check applicable box(es)):

☐ is attached hereto
☒ was filed on _____ as U.S. Application Serial No. Unassigned (Atty Dkt. No. 47-138)
☒ was filed as PCT international application No. PCT/AU98/01023 on 10 December 1998
and (if applicable to U.S. or PCT application) was amended on _____

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above. I acknowledge the duty to disclose information which is material to the patentability of this application in accordance with 37 C.F.R. 1.56. I hereby claim foreign priority benefits under 35 U.S.C. 119/365 of any foreign application(s) for patent or inventor's certificate listed below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of the application on which priority is claimed or, if no priority is claimed, before the filing date of this application:

Priority Foreign Application(s):

Application Number	Country	Day/Month/Year Filed
PP0839	Australia	10 December 1997

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below.

Application Number	Date/Month/Year Filed
--------------------	-----------------------

I hereby claim the benefit under 35 U.S.C. 120/365 of all prior United States and PCT international applications listed above or below and, insofar as the subject matter of each of the claims of this application is not disclosed in such prior applications in the manner provided by the first paragraph of 35 U.S.C. 112, I acknowledge the duty to disclose material information as defined in 37 C.F.R. 1.56 which occurred between the filing date of the prior applications and the national or PCT international filing date of this application:

Prior U.S./PCT Application(s):

Application Serial No.	Day/Month/Year Filed
PCT/AU98/01023	10 December 1998

Status: patented
pending, abandoned

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon. And on behalf of the owner(s) hereof, I hereby appoint NIXON & VANDERHYE P.C., 1100 North Glebe Rd., 8th Floor, Arlington, VA 22201-4714, telephone number (703) 816-4000 (to whom all communications are to be directed), and the following attorneys thereof (of the same address) individually and collectively owner's/owners' attorneys to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith and with the resulting patent: I also authorize Nixon & Vanderhye to delete any attorney names/numbers no longer with the firm and to act and rely solely on instructions directly communicated from the person, assignee, attorney, firm, or other organization sending instructions to Nixon & Vanderhye on behalf of the owner(s).

1. <input checked="" type="checkbox"/>	Inventor's Signature: <u>[Signature]</u> Date: <u>6 JUN 2000</u>
	Inventor: <u>Bruce</u> <u>C.</u> <u>Ross</u> (first) (MI) (last) Australian (citizenship)
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	(Zip Code) <u>3058</u>
2. <input checked="" type="checkbox"/>	Inventor's Signature: <u>[Signature]</u> Date: <u>6 June 2000</u>
	Inventor: <u>Ian</u> <u>G.</u> <u>Barr</u> (first) (MI) (last) Australia (citizenship)
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	Post Office Address: <u>13; Shakespeare Drive, Templestowe, Victoria, Australia</u>
	(Zip Code) <u>3108</u>

FOR ADDITIONAL INVENTORS, check box ☒ and attach sheet with same information and signature and date for each.

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(2)

47-138
Serial No. Unassigned

Nixon & Vanderhye P.C. (10/99
(Domestic Non-Assigned/Foreign)
Page 2 of 3

RULE 63 (37 C.F.R. 1.63)
INVENTORS DECLARATION FOR PATENT APPLICATION
IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

As a below named inventor, I hereby declare that my residence, post office address and citizenship are as stated below next to my name, and I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

P. GINGIVALIS POLYPEPTIDES AND NUCLEOTIDES

the specification of which (check applicable box(es)):

☐ is attached hereto
☒ was filed on _____ as U.S. Application Serial No. Unassigned (Atty Dkt. No. 47-138)
☒ was filed as PCT International application No. PCT/AU98/01023 on 10 December 1998
and (if applicable to U.S. or PCT application) was amended on _____

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above. I acknowledge the duty to disclose information which is material to the patentability of this application in accordance with 37 C.F.R. 1.56. I hereby claim foreign priority benefits under 35 U.S.C. 119/365 of any foreign application(s) for patent or inventor's certificate listed below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of the application on which priority is claimed or, if no priority is claimed, before the filing date of this application:

Priority Foreign Application(s):

Application Number	Country	Day/Month/Year Filed
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Application Number	Date/Month/Year Filed
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Prior U.S./PCT Application(s):

Application Serial No.	Day/Month/Year Filed	Status: patented pending, abandoned
PCT/AU98/01023	10 December 1998	

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon. And on behalf of the owner(s) hereof, I hereby appoint NIXON & VANDERHYE P.C., 1100 North Glebe Rd., 8th Floor, Arlington, VA 22201-4714, telephone number (703) 816-4000 (to whom all communications are to be directed), and the following attorneys thereof (of the same address) individually and collectively owner's/owners' attorneys to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith and with the resulting patent. I also authorize Nixon & Vanderhye to delete any attorney names/numbers no longer with the firm and to act and rely solely on instructions directly communicated from the person, assignee, attorney, firm, or other organization sending instructions to Nixon & Vanderhye on behalf of the owner(s).

3. ∞	Inventor's Signature: <u>[Signature]</u>	Date: <u>8/6/00</u>
	Inventor: <u>Michelle</u> <u>A.</u> <u>Patterson</u> (first) (MI) (last) Australian (citizenship)	
	Residence: (city) <u>Victoria</u> <u>AUX</u> (state/country) <u>Australia</u>	
	Post Office Address: <u>14 Cotterell Way, Laverton, Victoria, Australia</u> (Zip Code) <u>3021</u>	
4. ∞	Inventor's Signature: <u>[Signature]</u>	Date: <u>20.6.00</u>
	Inventor: <u>Catherine</u> <u>T.</u> <u>Agus</u> (first) (MI) (last) Australian (citizenship)	
	Residence: (city) <u>Victoria</u> <u>AUX</u> (state/country) <u>Australia</u>	
	Post Office Address: <u>250 Elgar Road, Box Hill South, Victoria, Australia</u> (Zip Code) <u>3128</u>	
5. ∞	Inventor's Signature: <u>[Signature]</u>	Date: <u>6.6.00</u>
	Inventor: <u>Linda</u> <u>J.</u> <u>Rothel</u> (first) (MI) (last) Australian (citizenship)	
	Residence: (city) <u>Victoria</u> <u>AUX</u> (state/country) <u>Australia</u>	
	Post Office Address: <u>10 Rothschild Street, Glenhuntly, Victoria, Australia</u> (Zip Code) <u>3128</u>	
6. ∞	Inventor's Signature: <u>[Signature]</u>	Date: <u>6.6.00</u>
	Inventor: <u>Mai</u> <u>B.</u> <u>Margetts</u> (first) (MI) (last) Australian (citizenship)	
	Residence: (city) <u>Victoria</u> <u>AUX</u> (state/country) <u>Australia</u>	
	Post Office Address: <u>92 Bent Street, Monce Ponds, Victoria, Australia</u> (Zip Code) <u>3039</u>	

FOR ADDITIONAL INVENTORS, check box ☒ and attach sheet with same information and signature and data for each.

430944

47-138
Serial No. Unassigned

Nixon & Vanderhye P.C. (10/99
(Domestic Non-Assigned/Foreign)
Page 3 of 3

RULE 63 (37 C.F.R. 1.63)
INVENTORS DECLARATION FOR PATENT APPLICATION
IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

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P. GINGIVALIS POLYPEPTIDES AND NUCLEOTIDES

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☒ was filed on _____ as U.S. Application Serial No. Unassigned (Atty Dkt. No. 47-138)
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and (if applicable to U.S. or PCT application) was amended on _____

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Application Number	Date/Month/Year Filed
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I hereby claim the benefit under 35 U.S.C. 120/365 of all prior United States and PCT international applications listed above or below and, insofar as the subject matter of each of the claims of this application is not disclosed in such prior applications in the manner provided by the first paragraph of 35 U.S.C. 112, I acknowledge the duty to disclose material information as defined in 37 C.F.R. 1.56 which occurred between the filing date of the prior applications and the national or PCT international filing date of this application:

Prior U.S./PCT Application(s): Application Serial No.	Day/Month/Year Filed	Status: patented pending, abandoned
PCT/AU98/01023	10 December 1998	

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon. And on behalf of the owner(s) hereof, I hereby appoint **NIXON & VANDERHYE P.C., 1100 North Glebe Rd., 8th Floor, Arlington, VA 22201-4714, telephone number (703) 816-4000 (to whom all communications are to be directed)**, and the following attorneys thereof (of the same address) individually and collectively owner's/owners' attorneys to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith and with the resulting patent: I also authorize Nixon & Vanderhye to delete any attorney names/numbers no longer with the firm and to act and rely solely on instructions directly communicated from the person, assignee, attorney, firm, or other organization sending instructions to Nixon & Vanderhye on behalf of the owner(s).

7. cc Inventor's Signature: *D. M. Hocking* Date: 6 June 2000
Inventor: Dianna M Hocking Australian
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(Zip Code) 3031

8. cc Inventor's Signature: *Elizabeth A. Webb* Date: 8 June 2000
Inventor: Elizabeth A. Webb Australian
(first) (last) (citizenship)
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Post Office Address: 36 Zigzag Road, Victoria, Australia
(Zip Code) 3422

WO 99/29870

PCT/AU98/01023

1 / 490

(2) INFORMATION FOR SEQ ID NO:1

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1362 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1

25	TTCTGTGTCA TGGCAAAAGT TATAAAAACA AAAAAAGGCC TTGCACTTAA TCTGAAAGGA	60
	AAACCGCTGC CCGAGATGCT GGCCGAACCG GCCCAAAGTC CTACTTACGC GGTCTGTGCC	120
	GACGATTTTG AAGGTGTTAT CCCCAAGGTG ACGGCTCGTC CGGGGATAA GGTGCGTGCC	180
	GGCTCAGCAC TGATGCACCA CAAGGCATAT CCGGAGATGA AGTTTACAAG TCCGGTTAGC	240
	GGCGAAGTGA TCGCGGTGAA TCGCGGTGCC AAGCGCAAGG TGTTGAGCAT CGAGGTGAAA	300
30	CCGGACGGAC TGAACGAATA CGAGTCATTC CCTGTGCGGG ATCCGTCCTGC CCTCTCTGCC	360
	GAACAGATCA AGGAGCTTTT ACTGTGAGGC GGTATGTGGG GTTTTATTAA GCAACGTCCT	420
	TACGACATAG TGGCTACACC GGATATAGCT CCACGCGACA TTTATATTAC TGCCAACTTT	480
	ACTGCACCAT TGGCTCCGGA CTTCGATTTC ATCGTTCGAG GAGAAGAACG CGCCCTGCAG	540
	ACTGCCATCG ATGCCCTGGC CAAACTCAGC ACAGGAAAGG TGTATGTGGG CCTGAAGCCG	600
35	GGTAACGTGG GCGTGCTGAT CAATGCAGAA ATCCTAGAAG TACACGGACC TCATCCGGCA	660
	ACGCTCAAGG CTACCGACCT GATCGTGATC GGACGTTTCC TGCTTACGGG CAAAGCCGAT	720
	TTTACCAGAA TGATTGCCAT GACCGGCTCA CACGCTGCAG CTCACGGATA CGTCCGTATT	780
	ATGCCGGGTT GCAATGTCTT TGCTTCCTTC CCGGCCGAC TGACAATAAA GGAATCTCAC	840
	GAGCGTGTGA TCGATGGCAA TGTGCTGACC GGTAAAGAAG TCTGCGAGAA GGAGCCTTTC	900
40	CTGTGAGCCC GGTGTGACCA GATCAGGTTG ATCCCGGAAG GCGACGATGT GGACGAACTC	960
	TTCCGGTGGG CTGCACCCCG TCTCCATCAG TACAGCATGA GCAGAGCTTA TTTCTCTTGG	1020
	TTGCAGGGGA AAAACAAAGA GTACGTACTC GATCCCCGGA TCAAGGGTGG CGAACGTGCT	1080
	ATCATCATGA GCAACGAGTA TGACCGCGTT TCCCGCATGG ACATCTATCC GGAGTATTTG	1140
	CTCAAGGCTA TTATAGCATT CGACATCGAC AAGATGGAGG ACTTAGGCAT ATATGAAGTG	1200
45	GCTCCGGAGG ACTTTGCCAC TTGCGAATT GTGGATACAT CCAAGATCGA GCTGCAGCGT	1260
	ATCGTTCGCG AGGGCTTGA TATGCTCTAT AAGGAATGA AT	1320
		1362

(2) INFORMATION FOR SEQ ID NO:2

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 603 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2

70	GAACCTAAGCA AGTGTTACAT GGATAAAGTG AGCTATGCTC TGGGATTGAG CATCGGTAAT	60
	AATTTCAAGT CTTCCGGCAT CGACAGCGTC GTTATGGATG ATTTTCATGA AGGTCTGTCT	120
75	GATGTAAGT AAGAAAAAGC CCCTCAGCTC TCGTATGACG AGGCCAAGCG CGAAATAGAG	180
	GCGTATTTCA TGGATTGCA GCAGAAGGCT GTCAACTGA ACAAAGAGGC CGGAGAAGAA	240

WO 99/29870

PCT/AU98/01023

3 / 490

5
GATGTTCTCC AGCATAGGAT GAAAGTGTAT CCCAACCCCTG CCACGACGGA GCTGCATGTG 300
GAAGCCCTGT CCGCATGGGT GGCCGAGCAG GCTGCGGTAT ATGATATGCG TGGTCGTGCG 360
GTATCGGCTC GGACGGTGA TAGCGAGAAG CTGTGCATCG ACATTGCCCTC ACTGCCCGTG 420
GGCGTCTATA TGCTGCGCAT CGGCAGCTAC TCGGCCAAGT TCGAGAAGAG A 471

(2) INFORMATION FOR SEQ ID NO:5

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1686 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
15 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
20 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
(ix) FEATURE:
25 (A) NAME/KEY: misc_feature
(B) LOCATION 1...1686

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5

30 ACAAGAAATG TTCACTCAT AAAAATGCCA AGAATTATGA AATTAAAAAT TGCACTCAGA 60
CTGCTGCTGG CGACTTTTGC CATAGTTTTA TTTAGCCCTC TGGCCAAAGGC CCAGATGGAT 120
ATTGTTGGAG ACGATGTATT GATCGAGACG ATGTCCACCC TATCAGGATA TTCAGAGGAT 180
TTTTATTACA AGATGGCTGT GGCAGACAAT GGATGGATCT ATGTGATGT' GGATTTCTCT 240
CGTATTTTAT TTGATGATGT CAGGCTGTAT CGTTCCAAAG ACGGTGGTGC TACTTACCAA 300
AAGTTAGGGT CTTTGGGGTC TTTGGTGCTT TATGACTTCG ATGTCTCGCA TTGCGATTTT 360
ATTGTAACGG GAAAGGATGA AGATGATATC AATGTTTGA CAGTCATGAC AGCATTCCGAA 420
TATGTAGGTG GTACTATTGG CAATGGCGTT TTGCTGATGC ATGCCCATGA TGCAGATATC 480
AATAATACAG AGTGTGTGTA CAAGAAGGAT TTCCCTAATA ATAGACTGAT GGGGTAGGCC 540
ATCGCCTCCA ACTACCGTGC GCCCTCTCCT TACGGTTTGG GGGGCGATCC TTTTGCTCTC 600
GCTGTCCGGC TTAGTGGCTC CGGAAGCGAT CACAGCTTCT TGGACTATAT TTTTCTGTTA 660
GATGTGGGAG TACACTTTGA GCAAAAGCGT ATTTACACAA GACCCCAAAA ACTGACTATC 720
AATAGAGTAG ACCTTTCATT AGGCAGTACA TCTCCTTCTC TTGGATTAA TACTTGGCCA 780
CTAATGGGAG TCGTATTGTA AATGAATAAG AACCTTGATG GCTTCGACAT TGGTTTCATT 840
TCCAACCTTG TGGACTATGA TCCCGCTAT CCGTGGTCTG AACCGATAAT AATAGAAGAA 900
GACTGTGGAT GGACTGATT TAATCCTTTG GGAGCACTAA GTATAGAGAT CCAATGATG 960
TTGGATGACA ATTCCGATAA TACCGTGGGT GGAGAAGCGT CCCATAACTT CCTGATCACT 1020
TACCCGGGCC ATTACGTATA TCCGAAGCAA TCTTTCATT ATTCTCCCGG ACATACACCG 1080
ACAAAGAAAG ATCTGGTCTT TAAACACTGT ATAGGTATTC CGGCTTTGGC ATACGATAAG 1140
GAAGGCGATC GTTATCTGAC TACTTTTCAA GATCACAATC TAATGAGATA CAGATGGATC 1200
50 AAATACGATG ACATTAACTC TTTTATGGT TGGAGTTCCG CATATGTATA TGCAAAAGAA 1260
GCTAAAGATA AAAAGAGGCG CCGTCCGCAA GTAGCACTCA ATCCTACCAA TGGAAAGGCT 1320
TGTGGGTAT GGCATACTCG CAAGAGCCCA TATGATGAAA CCAAAACCACA TCCTACTCCT 1380
GTAATTATTA AACATTTTCT ATGTTCCGAT ACGGAGTGGG TACATGCTCT GGACGTGGGG 1440
GACGTATTGC AGAAGGAGGG TAGCATGAAG CTCTACCCCA ATCCTGCCAA AGAATATGTT 1500
55 CTGATCAACC TACCCAAAGA AGGGGGGCAC GAGGCAGTCG TATACGACAT GCAGGGCCGA 1560
ATCGTGGAGA AAGTTTCATT TTCAGGGAAA GAATATAAGC TGAATGTGCA GTATCTGTCC 1620
AAAGGTACGT ACATGCTGAA AGTTGTAGCG GATACGGAGT ATTTCTGGGA AAAAATCATT 1680
GTAGAG 1686

(2) INFORMATION FOR SEQ ID NO:6

65 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1173 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
70 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: UNKNOWN
75 (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6

CAAATGAAAC GATTACTCCC CTTTCTCCTT TTAGCAGGAC TCGTAGCCGT AGGAAACGTG 60
TCTGCTCAST CAGCCCCAAT CCTCAAGTG GATGTACACA CTCGCATCGC AAGAAATGCC 120
CGTTATCGAC TGGACAAGAT CAGTGTCCTG GATTCTCGTC AGATATTCGA TTACTTCTAT 180
AAAGAAGAAA CGATACCCAC TAAATACAA ACGACCACAG GAGGTGCAAT TACAAGCATC 240
GATTGCTTT TCTATGAAGA CGACAGGTTG GTTCAGGTGC GCTATTTTGA CAATAACCTT 300
GAATTAAAC AAGCGGAGAA GTATGTATAC GACGGTTCTA AGCTGGTCTT TCGAGAAATT 360
CGCAAGTCGC CGACAGACGA AAGCGCAATA AAGAAAGTTA GCTATCACTA TCTCTGTGGC 420
AGCGATATGC CTTTGGACAT TAGCACAGAG ATGAGCGATG GCTATTTTGA AAGCCATACG 480
CTTAACATATC TGAATGGAJA GATTGCCGGA ATAGATATCA TGACTCAACA GAACCCATCG 540
GCCGAATTGA TCGAAACGGG TAGAATGGTA TATGAGTTTG ATGCCAATAA TGATGCTGTA 600
CTGCTTCGTG ACAGTGATAT TCTTCTCTT CAAAACAAGT GGGTAGAAAT GTTACTCAC 660
CGTTATACAT ACGACAATAA GCATATTTGT ATTCGTTGGG AACAGACGA ATTCGGCACC 720
CTCACCCCTG CCAACAACCT CGAATACGAC ACCACTATCC CTCTGTCTGC TGTATTGTTT 780
CCCACGCAAG AGGAGTTCTT CCGTCTCTT CTTCCTCAAT TTATGAAGCA TATGCGTACG 840
AAGCAAAAGT ATTCAATAA CTCCGGAGAA GGCTTGTGAG AGGTATGCGA TTACAACATC 900
TTCTATACCG ATATGCAAGG TAATGCACTG ACCGATGTTG CCGTGAACGA ATCGATCAAG 960
ATTATCTCTC GTCTGCGCAC GGATTTCTG CGTATAGAAC GTTCGCACT GCTTCGCTT 1020
TCGCTATTGC ACATGAACGG GAAGCTCATC AGAGCTACCG AATTGACAGG CGATTGGGCC 1080
ATTATCGGAG TTGCATCTCT TCGAGAGGCG ACTTACATCG CAGAAATAAC TGCTGCAAAAC 1140
AGCAAAACCA TACGTGCAAA AGTATCGCTC AGA 1173

(2) INFORMATION FOR SEQ ID NO:7

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1284 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1284

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7

AAGAGGAATC CCTTACCTTT GACGGCATCA AATCGAAAGA TTTTATAAAA AATGAGACAG 60
CATTTATCTC TATTTCTTTT TATCTTGTTT CTGCTTCTTG CCTTCTCTTA TGTGCGTTGC 120
AGAACAGTCC GACAAACACC TAAGCAGTCC GAACGGTACG TCGTAGTCTT GTCTTTGGAC 180
GGCTTCCGAC CGGACTATAC CGATCGGGCA CGTACACCGG CGTTGGATCG GATGGCACAG 240
GAGGGATTGA GCGGGTCTGT CCAACCATGC TTCCCTCTCG TTACATTTCC CAATCATTAC 300
AGCATGGCTA CGGGGCTTTA CCCCATCAT CACGGTATCG TAGCCAATGA GTTTGTGGAT 360
TCGCTACTGG GCATCTTTCG TATATCCGAC CGAAAGCCG TGGAGACCCC CGGATTTTGG 420
GGCGGCGGAG CGGTTTGGAA TACGGCCGCA CGCCAAGGCA TCCGTACCGG TGTCTACTTT 480
TGGGTAGGAT CCGAAACGGC TGTGAACGGA AATCGGCGGT GCGGGTGGAA AAAATTCTCC 540
TCCACCGTTC CGTTTCGTGA CCGTGCCGAC TCCGTCATCG CGTGGCTUGG ACTGCCCGAA 600
AAGGAGCGAC CGCGCTTGCT CATGTGGTAC ATCGAGGAGC CGGATATGAT CGGACACAGC 660
CAAACGCCCG AAAGCCCGCT GACACTGGCA ATGCTAGAGC GGTGGACAG TGTGCTCGGC 720
TATTTCCGCA AGCGSTTGA CTCTCTGCCC ATAGCCGAC AGACCGACTT CATCATAGTA 780
TCCGATCAGC GTATGGCCAC GTACGAAAT GAGAAATGT TCAATCTGTG GCATATCTG 840
CCTGCCGACA GTTTCCTCTA CATGGCCACC GGGGCCCTCA CCCACTTGTG CCLGAAGCCC 900
TCCTATACCG AGCGAGCCTA TGAGATCCTG CGGGCCATTC CACATATATC GGTTTACGCG 960
AAGGGGGAGG TGCCCAAGCG TTTCGCGTGT GGCACCAATC CTGTTTGGG CGAAGTGGTC 1020
GTGATTCGCG ACATAGGCTC CACCGTCITT TTCGCAATAA ATGAAGACGT TCGTCCGGGA 1080
CGGGCACATG GCTATGACAA CCAAGCACCG GAAATGCGGG CTTTACTCCG GGCTGTCCGA 1140
CCCGATTTCG GTCCGGGCGA TAGGGTGGAA AACCTGCCGA ATATCCCAT CTATCCGCTC 1200
ATATGCAAGC TGTGGGTAT AGAGCCTGCA CCCAACGATG CGGACGAAAC GTTGTGAAC 1260
GGCCTGATCC GAGACAAACG ACCA 1284

WO 99/29870

PCT/AU98/01023

5 / 490

(2) INFORMATION FOR SEQ ID NO:8

5 (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 846 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

10 (11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

15 (1v) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

20 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...846

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8

CTTCCCGTG	GAGTTTTC	CCTGATGTAT	GGCCGAAGAG	SAAGCATTCTG	TGCCTCTTCA	60
GGGCATAGGG	ACAAAATTTT	TAAGAATACA	ATTATCAGAT	TTATCACAAT	GAAAGTAGGT	120
TTGTTTCATCC	CCTGTTATGT	CAATGCAGTG	TATCCGGGAG	TGGGTATCGC	CACGTACAAA	180
CTGCTGAAGA	GTTTGGACAT	AGATGTCGAC	TACCCGATGG	ATCAGACATG	TTGCGGCCAG	240
CCTATGCECA	ATGCCGGATT	CGAACAGAAA	GCTCAAAAGC	TGGCTTTGCG	ATTCTGAAGAG	300
CTGTTGAGT	CGTATGATGT	AGTCGTAGGG	CCATCGGCCA	GTTGCGTTGC	TTTCGTGAAA	360
GAAACTATG	ATCATATCCT	CAGACCGACA	GGACATGTCT	GCAAGTCGGC	AGCCAAGGTT	420
CGGGATATAT	GCGAGTTCTT	GCACGATGAC	CTGAAGATCA	CCAGCCCTCC	CTCCCGATTCT	480
GCCCATAAGG	TGAGCCTGCA	CAACAGTTGC	CACGGTGTGC	GCGAAGTCCA	TCTGTCCACC	540
CCCACTGAAG	TGCACCGACC	GTACCACAAC	AAGGTGCGCC	GGCTATTGGA	GATGGTGACG	600
GGCATAGAGG	TATTCGAGCC	GAAGCGAATA	GACGAATGCT	GCGGTTTCGG	CGGTATGTAC	660
TGGGTGGAGG	AGCCGGAGGT	ATCCACCTGT	ATGGGGCATG	ACAAGGTGCT	GGATCACATA	720
TCCACAGGTG	CGGAGTACAT	CACAGGGCCG	GACAGCTCGT	GCCTCATGCA	TATGCAGGGA	780
GTGATAGACA	GAGAGAAATT	GCCGATCAAG	ACAATTCATG	CAGTAGAAAT	TTTAGCAGCA	840
AACTTA						846

(2) INFORMATION FOR SEQ ID NO:9

45 (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 753 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

50 (11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

55 (1v) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

60 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...753

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9

CCCTGAAAA	AACGAATGGA	TATTGTAAGT	ATGGCCGATA	AAGCTCTTGT	ACTGGAGATG	60
AGAGATCTGA	CGCTCTGTCA	GGAGGAAAAC	GTCAITTTTC	AAAATTTGAA	TCTGACCCTT	120
TCCGCCGGAG	ACTTCGTCTA	TCTGATAGGC	TCAGTGGGAT	CGGGGAAGAG	CACCTTGCTG	180
AAGGCTTTGT	ATGCTGAGGT	GCCTATCTCT	GCCGTTTATG	CCCGCGTGAT	AGATTATGAT	240
CTGGCAAAGT	TGAAACGGAA	GCAGTTGCC	TATCTGCCCA	GGAATTTGGG	CATTGTGTTT	300
CAGGATTTCC	AGTTGCTGAA	CGGACGTACT	GTTGCGGAGA	ATTGGAATT	CGTTTTCGCA	360
GCTACGGACT	GGAAAAACCG	AGCCGATCGC	GAGCAGCGTA	TCCAGGAGGT	TTTGACCCGT	420
GTGGGAATGT	CTCGGAAGGC	TTATAAGAGA	CCGCACCAAC	TGTCCGGAGG	GGAGCAACAA	480
CGTGTGGGTA	TAGCCAGAGC	TTTGCTGGCG	AAGCCTGCGT	TGATCCTGGC	CGACGAACCC	540
ACAGGCAACC	TCGATTCCGT	GACCGGATTG	CAGATCGCTT	CTCTGCTCTA	CGAAATCAGT	600

WO 99/29870

PCT/AU98/01023

6 / 490

AAGCAGGGCA CTGCAGTACT TATGAGCAGC CACAACAGCA GCCTGCTGTC GCATCTGCCG 660
GCACGGACAT TGGCCGTTTC TAAGAATGGC GATGCCTCCT CTTTGGTTCGA GCTGAGTGCA 720
GATGCTGTTT CAAGAAAAAA TACGGAAATA GAT 753

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(2) INFORMATION FOR SEQ ID NO:10

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 714 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10

30 ACCAGGCAAT GTCCGGCTTG TCGCTCTTCC TTTCACCTCA TAAAAACAAG TAAAACAATG 60
ATTGAAATCA GCAACCTCAC CAAGGTTTTT AGAACAGAG AAATAGAGAC GGTAGCCCTC 120
GATGGCGTAT CGCTCAAAGT GGACAAAGGC GAATTTATCG CCATTAATGGG GCCTTCGGGA 180
TGCCTTAAGT CCACTCTGCT CAATATCCTC GGCCCTTCTCG ACAATCCCAC TTCCGGTATC 240
TACAAGCTCG ATGGGGCAGA AGTGGGCAAC CTCGGGGAAA AAGACAGGAC TGCCGTCCGT 300
AAGGGCAATA TCGGCTTCGT ATTCCAGAGC TTCAACCTCA TCGAAGAGAT GACGGTAAGC 360
35 GAGAAGCTGG AGTTGCCGCT CGTCTATCTG GGTGTGAAG CCTCCGAGCG GAAAGAGCGA 420
GTGGAGGAGG CACTGGCGAA GATGAGCATC AGCCACCGGG CCGGCCACTT CCCCATCAG 480
CTCTCCGGAG GACAACAGCA GCGCGTGGCT ATCGCCCGTG CCGTGGTGGC CAATCCGAAG 540
CTCATCTCG CCGATGAACC CACGGGTAAC CTCGACTCCA AAAACGGAGC CGATGTCATG 600
40 GAAGTCTCA GAGGTCTCAA TCGCGAAGGT GCAACCATCG TCATGGTGAC GCACTCCGAG 660
CACGATGCAC GTAGTGCCCG CCGCATCATC AATCTGTTCG ACGGTAAGAT TCGC 714

(2) INFORMATION FOR SEQ ID NO:11

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1812 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...1812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11

65 AGCACAGAAA CAAATAGCAA ATCTGAAATG AAAGAATTTT TCAAAATGTT TTTCCGCTCG 60
ATCCTCGGGG TTATAACGGC AGGAATCATC TTGTTCTGTA TCTTTCTATT TATCTTTTTC 120
GGCATCGTAG CCGGTATTGC CTCCAAGGCA ACGGGAGGAA CCATTCCGAA GATCGAAGCA 180
70 AACTCCATCC TACATATANA CAATTCTTCT TTCCCTGAGA TCGTATCCGC CAATCCCTGG 240
AGCATGCTCA CAGGCAAGA CGAGTCCGTA TCGCTCTCAC AGGCAGTCGA AGCCATCGGC 300
CAAGCCAAAA ATAATCCCAA CATAACCGGT ATCTTCTCAG ATCTGGACAA CCTTCCGTC 360
GGTATGGCAT CGGCAGAGGA ATTGCGTCGC GCGTTGCAGG ATTTCAAGAT GTCGGGCAAG 420
TTGCTGCTAT CCTATGCCGA CAGATACACC CAAAAGGGTT ACTACCTCTC CAGTATTGCA 480
75 GACAACTCT ACCTCAATCC GAAAGGAATG TTGGGGCTTA TCGGGATTGC GACCCAAACA 540
ATGTTCTACA AAGATGCCCT CGACAAATTC GGCGTGAAGA TGGAGATCTT CAAGGTAGGC 600

WO 99/29870

PCT/AU98/01023

7 / 490

5 ACCTCAAGG CAGCCGTAGA GCCATTTCATG CTCAACAGGA TGAGCGATGC CAATCGCGAA 660
 CAAATCAGCA CATACATAAA CGGGCTTTGG GACAAGATCA CATCCGATAT TGCAGAGTCG 720
 CGCAAGACGG CAATGGATTC CGTGAAAATG TTTGCCGACA AAGGCGAAAT GTTCGGTCTT 780
 GCGGAGAAAG CGGTGGAGAT GAAGCTCGTG GATGAGCTGG CTTACCGTAC CGATGTGGAG 840
 AAAGAACTCA AAVAGATGTC CCAAGCGGGA GAGAAAGATG AACTTCGGTT CGTATCGCTT 900
 TCTCAGGTTT TGGCCAATGG CCCGATGAAC AAAACGAAAG GCAGTCGGAT CGCGTTCTC 960
 TTTGCCGAAG GTGAAATAAC GGAAGAAATA ATAAAGAAAG CGTTCGACAC TGCAGGTAGC 1020
 TCCATCACAC AAGAACTCGC CAAAGAAATC AAGGCAGCAG CCGATGACGA TGATATCAAA 1080
 GCGGTAGTAC TTCGTGTCAA TTCTCCGGGA GGTAGTGCTT TCACTTCCGA ACAGATATGG 1140
 10 AAGCAGGTAG CCGATCTCAA GGCCTAAAG CCTATCGTGG TCTCCATGGG CGAGGTAGCA 1200
 GCCTCGGGCG GATACTACAT AGCCTGCGCA GCCAACAGTA TCGTGGCAGA GCATACGACT 1260
 CTGACCGGCT CCACTCGGCAT ATTCGGCATG TTCCCGAACT TCGCGGGCGT AGCCAAGAAG 1320
 ATAGGAGTGA ATATGGAGCT CGTACAGACA TCCAGTATG CAGACTTGGG CAACACCTTC 1380
 GCTCCGATCA CGGTGGAAGA TCGTGCCCTC ATCCAACGCT ACATAGAGCA GGGCTACGAC 1440
 15 CTCTTCTTCA CTCGCGTATC GGAAGGCCGC AACCACACCA AGGCACAGAT CGACAGCATC 1500
 GCTCAAGGCG GTGTATGGCT CGGCGACAAA GCTCTTGCC TCGGTTTGGT GGATGAGCTT 1560
 GGAGTTTGG ACACAGCTAT CAAACGGGCC GCGAAGCTGG CTCAGCTCGG TGGCAACTAC 1620
 AGCATAGAGT ATGGCAAGAC CAAGCGCAAC TTCTTCGAAG AGTTGCTCTC CTCATCAGCA 1680
 GCGGATATGA AGTCTGCCAT CTTGAGTACC ATTCTCTCCG ATCCGGAAAT AGAAGTTCTG 1740
 20 CGCGAATCC GCTCCATGCC GCGCCGCTCT TCGGGCATAC AGGCACGTCT CCCCTATTAC 1800
 TTCATGCCGT AC 1812

25 (2) INFORMATION FOR SEQ ID NO:12
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 972 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
 (ii) MOLECULE TYPE: DNA (genomic)
 35 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 40 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...972

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12
 CTACGTTGT TTTGTTGCAA CTATTTCAA CAGATGAGAG CAAACATTG GCAGATACTT 60
 TCCGTTTCGG TTCTCTTTT CTTCGGGACA GCGATCGGAC AGGCTCAGAG TCGAAACCGT 120
 ACATACGAGG CTTATGTGAA ACAGTACGCC GACGAAGCTA TCCGACAGAT GAGCCGCTAC 180
 50 AATATACCGG CAAGCATCAC CATAGCACAG GCTTTGGTGG AGACAGGAGC CGGAGCCAGT 240
 AACTGCCCCA GCGTACACAA CAATCACTTC GGGATCAAT GCCACAAATC GTGGACGGGC 300
 AAGCGCACCT ATCGTACCGA CGATGCGCGG AACGAATGCT TCCGCAGCTA TTCGGCCGCT 360
 CGCGAATCGT ATGAAGATCA TTCCCGATTT CTGCTCCAAC CACGCTATCG TCCCTGTTC 420
 AACTCGACA GAGAAGACTA TCGGGGCTGG GCTACGGGGT TGCAACGCTG TGGCTATGCC 480
 55 ACCAATCGGG GCTATGCCAA TCTGCTGATC AAGATGGTGG AGCTGTATGA GCTATATGCT 540
 TTGGATCGCG AGAAGTACCC CTCATGGTTC CACAAGTCTT ACCCGGGGTC CAACAAAAAA 600
 TCCCATCAAA CGACCAAGCA GAAGCAGAGC GGAATCAAGC ACGAAGCTTA CTTCAGCTAC 660
 GGACTGCTCT ACATCATAGC CAAGCAAGGC GATACCTTCG ATTCTTTGGC CGAAGAGTTC 720
 GACATGAGAG CCTCCAAACT GGCCAAATAC AACGATGCTC CCGTGGATTT CCCGATCGAA 780
 60 AAGGGCGATG TGATCTATCT GGAGAAAAAG CACGATGCT CCATCTCCAA ACACACACAG 840
 CACGTAGTGC GTGTGGGCGA TTCGATGCAC AGTATCTCCC AACGCTATGG CATCGGATG 900
 AAGAACCTCT ACAAGCTCAA CGACAAGGAT GGCGAATATA TACCCCAAGA GGGCGATATA 960
 CTGCGCTTGC GC 972

65 (2) INFORMATION FOR SEQ ID NO:13
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1599 base pairs
 70 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
 (ii) MOLECULE TYPE: DNA (genomic)
 75

WO 99/29870

PCT/AU98/01023

8 / 490

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
10 (B) LOCATION 1...1599

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13

15	AGGATCCCCG ACGAGCAGAC CGGACGTATC ATGGACGGAC GTCGATATTC GGATGGCCTC	60
	CATCAGGCTA TCGAAGCCAA AGAGCATGTG AAAGTAGAGG CTGCGACACA GACATTGCA	120
	ACTATCATT TGCAGAACTA TTTCCGCATG TATCATAAGC TGGCAGGGAT GACCCGTA	180
	GCTGAAACTG AAGCGGGAGA GCTTTGGGAC ATCTACAAAC TGGACGTTGT AGTTATTCCG	240
	ACAAACAAGC CTATCGCCCG TAAGGATATG AATGATCGTA TCTATAAGAC GGCACGTGAA	300
20	AAATATGCG CAGTTATCGA AGAGATTGTA CGTCTGTGCG AAGAGGGCAG ACCTGTACTT	360
	GTGCGTACTA CTTCGGTGGG AATATCCGAA TTGTTGAGCC GTATGTTACG CTTCGGTGGC	420
	ATCCAAACAA ATGTACTCAA TGCCAAATTG CATCAGAAGG AGGCGGAGAT GTAGGCTCAG	480
	GCCGCTCAGA AAGGAACGTG TACCATCGCA ACGAACATGG CCGTCTGTGG TACCGACATC	540
	AAGCTCTCTG CCGAGGTTAA GAAAGCCGGG GGTTCGCTA TCATTGGTAC GGAAGGCAC	600
	GAATCCAGAC GAGTGGACAG ACAGCTTCGT GGTCTGTCG GCGTCAGGG TGATCCCGGT	660
25	TCGTCCATAT TCTATGTTT CTTGAAGAT CATCTGATGC GCCTCTTTC CACAGAAAAG	720
	ATTGCTCAT TGTATGATCG TTTAGGTTT AAGGAAGGAG AAGTGTCTGA AAACAACATG	780
	CTGAGTAAGT CCGTGGAGCG TGCTCAAAAG AAGGTGGAAG AGAACACTT CGSTATCCGT	840
	AAACATCTCG TTGAGTACGA TGATGTAATG AATTCGCAGC GTGAAGTCAT TTATACCCGT	900
	CGCCGTCATG CTTTGATGGG AGAGCGTATC GGTATGGATG TACTCAATAC CATATACGAC	960
30	GTATGTAAGG CTCTGATTGA CAATTATGCA GAAGCCAATG ATTTGGAAGG CTTCAGGAA	1020
	GATCTGATGC GTGCACTCGC GATAGAATCT CCIATCACGC AAGAAATATT CAGAGSTAAG	1080
	MAAGCAGAAG AGCTGACCGA TATGCTTTTC GATGAAGCTT ACAAGTCTT CCAACGTAAG	1140
	ATGGATCTGA TCGCAGAAGT GGCACCACCT GTGGTTTCATC AGGTATTCGA GACCCAAGCC	1200
	GCCGTGTAGC AGCGCATTCT AATCCCCATT ACGGATGCTA AACGTGTCTA TAACATAGGA	1260
35	TGCAATTTGC GTGAAGCGGA TGAACCTCAA GGGAAAAGCA TCATCAAGA ATTGAGAAA	1320
	GCTATCGTAC TGCATACTAT CGATGAGTCT TGGAAAGAAC ATCTGCGTGA GATGGACGAG	1380
	CTTCGTAAT CCGTTCAGAA TGCCAGCTAC GAAACAAAG ATCCACTACT TATCTATAAA	1440
	CTGGAATCTT ACGAACTGTT CCGCAAGATG GTAGAAGCCA TGAACGTA GACCGTAGCG	1500
40	ATCCTAATGC GTGCTCGGAT ACCGGTACCG GAGGCTCCTT CCCAAGAAGA GCTGGAACAC	1560
	AGGCGGCAAA TAGAAATCCG ACATGCAACC CAACAACGT	1599

(2) INFORMATION FOR SEQ ID NO:14

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

50 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

55 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

60 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14

65	AAATCTTGCC GTGTTATTGG CCAGACGAGG CGATACGGAT GCTGCCCTGT CGGACTACGA	60
	CCGTGCCATC AAAGCCTATC CGGAGTTTGC CGATGCCTAT TTCAATCGCG GCCTGCTGTT	120
	GCTTTGCGCG GGAAGGGCCA AAGAAGGCAT CGCCGATCTG AGTCGGGCG GCGAATACGG	180
	GCTCTACAAG GCGTACAACA TCATCAAAAG AATGAGCAGC AAGTCATGAT CTCGCTCAAT	240
70	AACCTGACTG TCGATTTCGG CACCCGTCCT CTCTTCGATC AGGTATCATT CGTCATCAAC	300
	AGGCGCGACC GTATCGCTCT TGTAGGGAAG AACGGTGCCG GCAAGAGTAC GCTGCTCAAG	360
	CTGATTGCGG GCATGGAAGA ACCGAGATCC GGACACATAG CACGCCCAA GGGGATCCGC	420
	ATAGGCTATC TGCCCGAGGT GATGCGTTTG CAGGACGGAC ACACGGTTTA CGAAGAGGTC	480
	GAGCAGGCTT TCAACGATAT TCGCCAAATA GAGGAAGAGA TACGGCTCT GTCCGATGAA	540
75	ATGCGCGGAC GTACGGACTA CGATCGGAT GACTATATCC GACTGATAGA GCATTATACG	600

WO 99/29870

PCT/AU98/01023

10 / 490

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1965 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16

ACAAACGAAAG	AAAACGAGAC	AACAACAAAA	AACGAATATA	GAATTATGGG	AAAAATCATT	60
GGAAATTGACT	TAGGCACAAC	GAACCTCTGT	GTCTCTGTAT	TGGAAGGTAA	CGAACCTATC	120
GTTATTACAA	ACAGTGAGGG	CAAGCGCACA	ACGCCCTCGG	TAGTGGCTTT	TGTGGATGGT	180
GGCGAGGCTA	AGGTGGGCGA	TCCGGCCCAAG	CGTCAGGCCA	TCACCAATCC	GACCAAGACG	240
ATATACTCTA	TCAAACGCTT	CATGGGCGAA	ACTTACGATC	AGGTTCCAG	ACAAGTGGAG	300
AGAGTGGCAT	TCAAGGTAGT	ACGTGGGGAC	AATAATACTC	CGCGCGTAGA	TATAGACGGT	360
CGTCTCTATA	CGCCGCGAGG	AATTTGCGCC	ATGATCCTTC	AGAAGATGAA	GAAGACGGCC	420
GAAGACTACC	TGGGTGAGGA	AGTAACGGAG	GCCGTGATCA	CTGTGCCCGC	ATACTTCAAC	480
GACGCTCAAC	GTCCAGGCAAC	GAAAGAAGCA	GGAGAGATCG	CGGGCTGAA	AGTTGCGCGT	540
ATTGTGAACG	AGCCTACGGC	AGCTTCTCTG	GCCTACGGTC	TGGACAAGTC	CAATAAGGAT	600
ATGAAGATCG	CTGTCTTCGA	CTTGGGTGGC	GGTACCTTCG	ATATCTCTAT	CTTGAATTG	660
GGCGACGGCG	TTTTCGAAGT	GAAATCGACC	AACGGTGATA	CGCACCTCGG	AGGAGACGAC	720
TTCCGACCAG	TGATCATTGA	CTGGCTGGCA	GAAGAGTTCA	AGTCTCAGGA	AGGTGTGGAT	780
CTTCGCCAGG	ATCCTATGGC	TATGCAGCGT	CTGAAAGAA	CTGCCGAAAA	AGCCAAGATA	840
GAGCTCTCCA	GCACTTCATC	TACGGAGATC	AACCTCCCCC	ATATCATGCC	GGTGAACGGC	900
ATCCCAAGC	ACTTGGTGAT	GACGCTTACA	AGGGGCTAAGT	TCCAGCAGTT	GGCCGATCGT	960
CTGATTCAAG	CATGTGTGGC	ACCCTGCGAA	ACGGCCTTGA	AAGATGCCCG	TATGTCACGT	1020
GGCGATATCG	ATGAAGTGAT	TCTCGTAGGT	GGTTCACAC	GTATCTCTGC	TATTCAGGAG	1080
ATTGTGGAGA	AGATCTTCGG	TAAGGCTCCG	TCCAAGGGTG	TGAATCCCGA	CGAAGTGGTA	1140
GCTGTGGGTG	CCGCTATTCA	AGGCGGTGTT	CTGACCGGTG	AGGTAAGGA	TGTCTTGCTG	1200
TTGGACGTTA	CCCCCTTGTC	GCTCGGTATC	GAGACTATGG	GAGGCGTGAT	GACTCGCTTG	1260
ATCGATGCCA	ATACCACTAT	CCCGACGAAG	AAGAGCGAAA	TCCTTACCAC	AGCAGTGGAC	1320
AATCAACCTT	CGGTAGAGAT	TCATGTACTT	CAGGCTGAGC	GTCTTTTGGC	TAAGGACAAT	1380
AAGAGCATCG	CGCGTTTCAA	CTTGGACGGT	ATTGCTCCGG	CGCCCCGTCA	GACACCGCAG	1440
ATCGAAGTAA	CGTTTGACAT	CGATGCCAAC	GGTATCTGTA	ATGTAACGGC	TCATGACAAA	1500
GCTACCGGCA	AGAAGCAGAA	TATCCGCATC	GAAGCCTCCA	GCGGTTTGTC	CGATGATGAG	1560
ATCAAGCGCA	TGAAGGAAGA	GGCGCAGGCC	AATGCCGAAG	CAGATAAGAA	AGAGAAAGAA	1620
CGTATCGACA	AGATCAATCA	GGCCGACAGC	ATGATCTTCC	AGACGGAAAA	GCAGTTGAAG	1680
GAGTTGGGAG	ACAAATTCCC	GGCCGACAAG	AAGGCTCCGA	TGGATACCGC	TCTCGACAAA	1740
CTGAAAGAAG	CACACAAGGC	ACAGGATGTA	GCTGCTATCG	ATACAGCCAT	GGCCGAAGCT	1800
CAAAACCGCTC	TTTCCGCAGC	GGGCGAAGAG	CTTTACAAGA	ATGCCGGAGC	AGCCCAAGGT	1860
GGCCGACAAAC	CCGGTCCGGA	CTTCGGCGGT	GCTCAAGGTC	CCTCTGCCGG	TGATCAGCCC	1920
TCTGACGACA	AGAACGTCAC	AGACGTAGAC	TTGAGGAAG	TGAAG		1965

(2) INFORMATION FOR SEQ ID NO:17

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1401 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
 (A) NAME/KEY: misc_feature

(B) LOCATION 1...1401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17

5 AAGTGGGCGC GTACAACTAC TTAAAGGATA TCGAACGCCA CAATCTATAA AACTATGCGC 60
TACGACTTAG CTATCATCGG TGGAGGGCCG GCGGGTTATA CCGCTGCCGA ACGTGCTGCC 120
AAAGGTGGCC TGAACACCTT CCTAATTGAG AAGAATGCTC TCGGTGGTGT ATGCTCAAC 180
GAAGGATGTA TACCGACCAA GACGCTACTC TACTCGGCCA AAGTGCTACA TCAAAATGCT 240
ACGGCATCTA AATATGCAGT AAGTGGAAAG GCGGATGGAC TTGACCTCGG CAAGGTGATT 300
10 GCCAGAAAAG GTAAATCAT TCGCAAGCTG ACTGCAGGCA TCCGTTCACG CCTGACAGAG 360
GCCGGAGTAG AGATGGTGAC GGCAGAAGCT ACGTAAACGG GATGCGATGC AGACGGCATC 420
ATCGGCATTA CTGCGGGGCA AGCAGAGTAC AAGCTGCGCA ACCTGCTACT ATGTACCGGT 480
TCGGAGACGT TTATTCCACC CATCCCGGGA GTGGAGCAGA CAGAGTATTG GACAAACCGT 540
GAAGCTCTAC AGAACAAGA GATTCCGACC TCTCTCTCA TCATCGGTGG TGGAGTGATC 600
15 GGAATGGAGT TCGCTTCTTT CTTCAACGGT ATCGGTACGC AAGTGCAAGT GGTGGAGATG 660
CTGCCGGAAT TACTCAACGG TATCGATCCC GAACATGCAG CTATGCTACG CGCTCACTAT 720
GAAAAAAGAG GAATCAAAAT CTACCTCGGG CACAAAGTAA CATCGGTTCG CAACGGAGCT 780
GTTACGGTAG AATACGAAGG AGAAAGCAA GAGATCGAAG GAGAAGCTAT CCTGATGAGT 840
GTGGGACGTC GCCCGCTGCT GCAAGGATTC GAGTCGCTCG GATTGGTGCT TGCCGGCAAA 900
20 GGTGTAAAGA CTAATGAGAG GATGCAAACT TCCCTGCCCA ATGTCTATGC TGCAGGTGAT 960
ATTACAGGCT TCTCGCTTTT GGCACATACG GCTGTACGGG AAGCAGAGGT AGCAGTAGAT 1020
CAGATTTTGG GCAAAACAGA CGAAACGATG AGCTACCGTG CCGTACCAGG TGTGGTGTAC 1080
ACCAATCCCG AGGTGCGCGG TGTGGGAGAG ACGGAAGAAT CGCTTCGCAA AGCAGGACGT 1140
GCCTACACTG TTCGTGCGCT TCCTATGGCC TTCTCCGGTC GATTGTAGC AGAAAACGAA 1200
25 CAAAGCAATG GAGAGTGCAA ACTACTACTT GATGAAGAGA ACCGCTTGAT CGGAGCACAC 1260
CTCATTCGCA ATCCGCGCGG CGAACTCATC GTAACCGCTG CCAATGGCCAT CGAGACCGGC 1320
ATGACGGATC GACAAATCGA ACGAATCATA TTCCCTCATC CGACTGTAGG CGAAATCCTA 1380
AAAGAAACTC TCGCGGAGG T 1401

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(2) INFORMATION FOR SEQ ID NO:18

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 2835 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

45

(v) ORIGINAL SOURCE:

- (A) ORGANISM: PORPHYROMONAS GINGIVALIS

(ix) FEATURE:

50

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...2835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18

55 CCTAAGATAC TTATGGAAT GAAAAGATT TTATCACTTG GTCTTCTGCT TGTGGGATTC 60
ATTCGGATGA AGCTTTCTGC CCAACAGGCT CAGCCACTCC CTACAGATCC GGCTGTTCGT 120
GTGGGTAAAT TGGACAACGG ATTGACTTAT TTATCCGTC ACAACGAGAA CCGGAAAGAT 180
CGTGGGATT TCTTTATCGC ACAAAGGTA GGTCTATTTC TTGAAGAAGA TAGCCAGTCC 240
GGTTTGGCTC ACTTCTTGA ACACATGGCT TTCAACGTA CGAAGAACTT CCGCGTAAG 300
60 AACTTGATCA ACTATCTCGA AACGATCGGT GTACGTTTCG GTCAGAACCT GAACGCTTCT 360
ACCGGATTCG ACAAGACGGA ATATACGATA ATGGATGTGC CGACTACACG TCAGGGAATC 420
ATCGACTCCT GCTTGCTTAT CCTGCATGAT TGGAGTAACA ATATTACCCT CGACGGGCAT 480
GAGATCGACG AGGAGCGCGG TGTGATCCAG GAAGAGTGGC GTGCTCGTCG CGATGCCAAC 540
CTTCGTATGT TCGAGGCTAT ACTTGCCAA GCTATGCCGG GTAATAAATA TGCAGAACGC 600
ATGCCCATCG GTCTGATGGA CGTCGTGCTC AACTTCAAGC ATGATGAGCT GCGCAACTAT 660
65 TATAAGAAAT GGTATCGTCC CGACCTGCAA GGTCTGTTGA TCGTGGGAGA TATCGATGTG 720
GACTATGTGG AGAACAAGAT CAAAGAATCT TTCAAGGACG TTCTCTCTCC CGTGAATCCA 780
GCAGAGCGTA TCTATACGCC GGTAGAGGAC AACGATGAGC CTATCGTAGC CATGTCTACC 840
GAGTCTGAGG CTACTACCAC GCAGCTCTCC ATCAGCTTCA AGAGCGACCC CACTCCTCAA 900
GAAGTGGGAG GATCGATATT CGGACTTGTG GAAGACTATA TGAACAGGT GATCACTACA 960
70 GCCGTGAATG AGCGTCTGTC CGAGATTACT CACAAGCCTA ACAGTCTTCT CCTCAGTSCA 1020
GGAGCTTTCT TCTCTAATT CATGTACATC ACCCAGACTA AGGACGCATT CAATTTTGTT 1080
GCCACGGTTC GTGAGGGTGA AGCGGAGAAA GCGATGAACG CATTGGTGGC AGAGATAGAA 1140
AGCCTCGCTC AGTTCGGTAT CACCAAGGCG GAATACGATC GTGCACGCAC GAATGTGCTC 1200
AAGCGATACG AGAATCAATA CAACGAAAGA GACAAAGCTA ABAACAAATG TTATSCCAAT 1260
75 GAATACTCCA CCTACTTCAC CGATGGCGGC TATATCCCGG GTATTGAGGT GGAATATCAG 1320

WO 99/29870

PCT/AU98/01023

12 / 490

ACGGTGAAATG CTTTGTCTCC TCAGGTTCCCT CTGGAAGCAT TCAATCAGGC TATTGCCCAA 1380
 ATGATCGATC CGGTGAAGAA TGCTGTGTT ACCCTCACCG GTCTTCAAA GGCTGAAGCC 1440
 AAGATCCGGA GCGAAGCAGA CTTCTCGCT GCTTTCAAAG CTGCTCGTCA GCAGAAAGTA 1500
 5 GAAGCCAAAG AAGACGAAGT CTCCGACCAA AAATTGATGG AGAAAGCTCC TAAGGCCGGA 1560
 AAGATCGTTT CCGAGAAGAA AGATCAGAAG TTCGGTACCA CGGAACCTAC CCTTAGCAAT 1620
 GGCATCAAA TATACCTCAA GAAGACCGAT TTCAAATCAA ACCAAATCCT GATGAGTGCT 1680
 CTCAGCCCGG GTGGTATCCT CTCCGGAAG CATGCTCCCA ACCAATCTGT GATGAATTGG 1740
 TTATGAACG TGGGTGGCTT GGGCAACTTC GATGCTATCC AGCTGGATAA GGTGCTGACA 1800
 10 GGTGCTCTG CTTCCGTATC TCCCTCTTTG TCTCTGCTCA GTGAAGTCT TTCGGGCAAA 1860
 ACYACTGTAG AAGATATGGA AACTTTCTTC CAGTTGATCT ATCTCCAAAT GACTGCTAAC 1920
 CGCAAGGATC CCGAAGCGTT CAAGGCCACA CAGGAAAAGT TGTACAATAA CTTGAAAAAT 1980
 CAGGAAGCCA ACCCGATGGC TGCGCTTATG GACTCTATCC GTCATACCAT GTACGGCGAT 2040
 AATCCGATGA TGAACCCAT GAAAGCTGCT GACGTGGAGA AAGTAAATTA CGATCAGGTA 2100
 ATUGCTTTCT ACAATGAGCG ATTCTGTGAT GCCGGCGACT TTATGTTCTT CTTTATCGGT 2160
 15 AATCTGGATG AAGCCAGAT GAAGCCATTG ATCGAAACTT ATCTTGCTTC ATTGCCCAAC 2220
 CTCAGCGTG GCGATAAGAT GAATAAGGCT CAGGTACCGG CTGCCGTTT GGGAAAGATC 2280
 GATTGCAAGT TCGAAGAGGA AATGGATACT CCTTCGACTA CTATATTCGA TCTCGTGCTC 2340
 GGAATGTGG AATATACGCT CAAGAACAGT CTCCTGCTGG AAGTCTTCTC AGCCGTAATG 2400
 GATCAGGTGT ACACGGCTAC CGTTCGCGAG AAGGAAGCGG GTGCATACAG TGTGGCTGCA 2460
 20 TTCGGCGGTC TCGAGCAATA TCCTCAGCCC AAGGCTCTGA TGCAGATCTA TTCCCCACG 2520
 GATCCTGCTC GTGCCGAGGA AATGAATGCT ATCGTTTITG CTGAGTTGGA GAAGCTTGCC 2580
 AAGGAGGGCC CCAATGTGGA ATACTTTAAG AAGACTATCG AAAACCTGAA TAAGCAGCAC 2640
 AAAGAAAGTC TGGGTGAGAA TCGTTTCTGG CTCGAAGCCA TGAAGGCGTC TTCTTCGAA 2700
 GGAATGACT TCATCACAGA CTACGAATCC GTACTGAACG GTCTTACTCC TGCTGAATTG 2760
 25 CAAAAGTTT CCGCAGACCT CTTGAAGCAG CAGAATCGGG TTGTTGTCAT GATGCTCCT 2820
 GTTGCAAAGG CTCRA 2885

(2) INFORMATION FOR SEQ ID NO:19

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2058 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
 (ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...2058
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19

TACACTATGA GTAAGAAAGG AACATCGGG GTAACGAGG ACAATATATT CCCGTCATC 60
 AAAAAATTCC TGTACAGCGA CCATGAGATA TTCCTGCGTG AGATCGCTTC CAATGCCGTG 120
 GATGCTACGC AGAAGCTGAA AACGCTTACA TCGCTCGGCG AATTCAAAGG CGAGACGGGT 180
 55 GACCTCGCGG TAACGGTCAG CGTGGATGAA GTGGCAGGCA CGATCAGGT CAGCGACCGC 240
 GCGGTAGGGA TGACCGAAGA GGAGGTGGAG AAGTACATCA ATCAGATTGC TTTCTCCAGT 300
 CGCGAAGAGT TTCTTAAAA GTACAAAGAC GACAAGGCCG CCATTATCGG CCACCTCGGA 360
 CTCGGATTTT ACTCGGCTTT CATGGTGTCC GAGCGAGTGG ACGTGATCAC GCGCTCTTTC 420
 CGAGATGATG CTACGGCGGT GAAATGGAGC TGCGACGGAT CGCCCGAATA CACGCTCGAA 480
 60 CCTGCGGACA AGGCTGACCG TGCCACCGAC ATCGTGATGC ACATCGATGA GGAGAATAGC 540
 GAGTTCCTCA AAAAAGAAVA GATAGAGGGG CTCCTCGGCA AATACTGTAA GTTCTTACC 600
 GTGCCGATCA TTTTCGGCAA GAAGCAGGAA TGGAAAGACG GCAAGATGCA AGATACGGAC 660
 GAGGACATC AGATCAACGA CACACATCCT GCCTGGACCA AAAAGCCTGC CGACCTCAAG 720
 GACGAAGACT ATAAGGAATT TTACCGTTCG CTCTATCCCA TGTCCGAAGA GCCTCTCTTC 780
 65 TGGATCCACC TCAATGTGGA CTATCGTTTC AATCTGACAG GTATCTCTTA TTTCCCGAAG 840
 ATCAAAAACA ACTTGGATCT GCAGCGCAAC AAGATTGAGC TCTACTGCAA TCAGGTTTAC 900
 GTCACCGATG AAGTACAGGG TATCGTGCCG GACTTCTCA CCTCTGTCA CGGGGTCTATC 960
 GATTGCGCGG ATATTCCCTT CAACGTATCG CGCTCCTATC TGCAGAGCGA TGCCAAATGTG 1020
 AAGAAGATCT CGTCTCATAT CACCAAGAAG GTGGCAGACC GTCTGGAAGA AATTTTCAA 1080
 70 AACGACCGCC CCACATTCGA GGAGAATGG GATAGTCTGA AGCTCTTCGT CGAATACGGT 1140
 ATGCTGACGG ATGAAAGTT CTATGAGCGT GCAGCCAAAT TCCTCTTTT CACCGATATG 1200
 GACGGACACA AGTACAGGTT CGACGAATAC CGAACGCTCG TCGAAGGTGT ACAGACGGAT 1260
 AAGGACGGAC AGGTAGTGTA TCTCTATGCT ACGGACAGC ATGGACAGTA CAGCCACGTG 1320
 AAACGTGCAT CCGACAAAGG CTACAGCGTG ATGCTGTGG ATGGTCAGT GGATCCGCAT 1380
 75 ATCGTGAGCC TGCTGGAGCA AAAGTTGGAG AAGACACACT TTGTCGTGT CGATAGCGAT 1440

WO 99/29870

PCT/AU98/01023

15 / 490

(2) INFORMATION FOR SEQ ID NO:23

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1119 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

10 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

15 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

20 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...1119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23

25	GGGTCTTGTG GAAGTAGCCC AGCAATGGGC CGATCAGGGT GTTCGGCTTG TGATCSCCGG	60
	ATTGGACATG GACTTTCGAC GTCAGCCTTT CGGACCTATG CCGGGCTTGT GTGCCATAGC	120
	CGACTCCGTG ACCAAGTTC ATGCCGTGTG TGTGGAATGC GGCCGATTGG CCAGCTATTC	180
	TTTCGGTCGT GTCCAAGGCG ATCAGCAAGT GATGCTGGCG GAACTGAACG AATACAGTCC	240
30	CCTCTGCAGA ACCTGCTACA GGAAATGCAG TTCTCCCCCA CAAACAGAAG AAATCCATTC	300
	GACAATATGA ATAGCAGACA TCTGACAATC ACAATCATTC CCGGCTCTCT CCTCTTTGTA	360
	CTGACATTGG GCGGCTGCTC CGTAGCCCAA CAAGATACGC AGTGGACTCT CGGCGGAAG	420
	CTCTTTACTT CCGCGTGGAT ACAACGTTTC GCCGAATATC AAGCGCTTTG CATTGAGGCA	480
	TACAACATCG CTACGGAAAG AGTGGACGCT CTACCGGCAG AACGTAACA AGGAGATAGG	540
35	TATCAGGCTC TCAGGGGCAA GGATTATGAT GAAGAGACTT GGGGGAAATG GTGTGCACAG	600
	GCCGATGCCG ACACACTGGC AGGAGCTTTG TCTTTCTTCC TCCATGCAGC GAACAAGGGG	660
	ATCGAGGCTT TTTACGTCAC CAACCGCAGA GACAATCTGC GCGAAGCAAC TCTTCAGAAC	720
	CTTCAGCGTT ACGGATTCCC CTTTGCCGAT GAAGAACATT TGCTTACGAC CCATGGGCCA	780
40	TCCGACAAAG AACCCCGTCG GCTCAAAATA CAAGAACAGT ATGAAATAGT ATTGCTCATA	840
	GGAGACAACCT TGGGCGACTT CCACCACTTC TTCAATACGA AAGAAGAGTC CGGACGCAAA	900
	CAGGCTCTGG GCCTGACAGC CGGGGAGTTT GGGCGGCACT TCATCATGCT GCCCAATCCC	960
	AACTACGGAT CTTGGGAACC GGCATGGTAC GGGCGGAAGT ATCCGCCACT GCCCGAAAGA	1020
	GACAAAGCAC TTAACAACCT GCACTCACAG AACAGCAGA	1080
45		1119

(2) INFORMATION FOR SEQ ID NO:24

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1278 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

55 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

60 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...1278

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24

70	CGTTGGGGTT TTTCTAATTT TGTGGCCATG AGCACCATA TAGATGTACA ACAGATCAAA	60
	CAGCGTTTCG GCATCATCGG TAGCAGTCCG CTGATGGAAC ATGCCATACG AGTGGCAGCA	120
	CAGGTGGCTC CTACCGACAT GTCCGTCTCT GTGACGGGAG AGAGCGGTTT CCGGAAAGAG	180
	TTCTTCCCGA AGATAATCCA CTAATACAGC GCGCGGAAAC ATCATAGCTA CATTGCAGTC	240
	AATTGCGGAG CCATCCCGCA AGGAACCATC GATTCGGAGC TGTTCCGACA CCGCAAAAGT	300
75	TCCTTTACCG GAGCCGTATC GGATCGCAAG GGGTACTTCG AAGAAGCATC CCGCGGCACG	360
	ATCTTTCTGG ACGAAGTGGG CGAACTGCCT TTGCCACGC AGGCGAGGCT GCTGAGGGTG	420

WO 99/29870

PCT/AU98/01023

16 / 490

5 CTGGAGACGG GCGAGTTCAT CCCCCTAGGA GCCAGCCAGT CGCAGAAGAC GGATGTCCGT 480
ATCGTAGCGG CGACGAATGT GAACCTCAAG GAGGCGGTAG CGAACGGGAA GTTCCGGGAA 540
GACCTCTTCT TCCGGCTCAA TACGGTACCG ATCGAGGTGC CTGCGCTGCG TATCGGACCG 600
GACGACGTGC CCTTGTCTTT TCGCCGATTC GCGCCGACA GCGCCGAGAA GTATCGGATG 660
CCTCGCTGCG GCCTATCGGA CGAAGCCCGT ACCATATTAA TCGGTACCG CTGCCCCGGC 720
AATGTGCGAG AGCTGCGCAA TATAACCGAC AGGCTGAGCA TCCTGGAGGA GGAGCGGACG 780
GTATCGGCAG AGACCATCAC TCGCTACCTG GACGCTGAGG GGATGCAAGA CCTCCACCCC 840
GTCGTGATCC GACGGAACGA AACGACCGAA GCGACAAAC AAATCCCCCA TTACGAGCGC 900
GAAATCATCT ACCAGGTGCT ATACGATATG AAGAAAGAGA TAGCCGATT GAAGGGGATG 960
10 ATGAACCGCC TGGCGCAUCA CGAACAGCCC TCATGGCCTG TAGGGTCGGA CGTCTGGGGC 1020
AACGACGACA AGCGCACCGC AGATCCGAAG TGGGGCGTCA GCACGCACAA GGCCCCATC 1080
GCGAACCGCG CAGAACCCGT GGAGCCGATA CAGGAAGCCA GCGAATACAC CGAGGATCCG 1140
GTTTCGCTGG AGGAGGTAGA GAAGAAATG ATTTCCCTTG CATTTGAACG CCACGGCGGA 1200
15 GTTTCGCTGG AGACGCGGA GGAAGTGAAG ATTTCCGAGC GGACACTATA CCGTAAATC 1260
AAGGAGTATG GACTGGAA 1278

(2) INFORMATION FOR SEQ ID NO:25

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1959 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 25 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 30 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: FORYPHYROMONAS GINGIVALIS
- 35 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1959
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25

40 AAAATCTTC CGAGGTACCG TCCGGCATTT GGCAGAAATC GTAAAAGGGA ACAACCTGAC 60
CCTGACAACG ATGATAGTCG TGGGAGAAGC CATAGACAAT CGGGAAGGGC TGTCACGGTT 120
GTATGCCGAC GAATTCAAAC ACCTCTTCCG CACATGATCC TACTCTTCGG CGGTACTACG 180
GAAGGCCGTG CCGCAGCTCG CGTGTGGAT GAAGCGGGA GTCCGTTTT CTACTCCACC 240
45 AAAGGCAATC TCGAAGAGAT CCAGAGTAGC CACGGCCATC GTCTGACAGG AGCCATGAGC 300
GTTGCCGACA TGGTTTCGTT TTGTCCGAAA GAAGAGATCC GACTGATCGT GGACCCCGCT 360
CATCCTTTTC CCGAAGAATT GCACGCTTCA GTGGCAGAAG CTTCTGAACA AACAGGTATC 420
CCCGTAGTAA GATACGAGAG ACAATACCCCT CCACGCGAAG AAGSTATCGT CTGGTGTGCA 480
AACTACGATA CGGCTGCCGA GCGGATGCTT GCGGATGGCG TGCAGCGTCT GCTGATGCTC 540
50 ACAGGAGTGA ATACGATCCC CAAGCTGGCT GCTTCTGGA AAGAGCGCAC CACCTTTTGC 600
CGCATATTGA AGCGAGACGA ATCGTTGCT TTGGCAGAGA AGAAGCGCTT TCCTGCGGAG 660
CGCATCGTTT TCCTCGAACC GCATGCGGAC GAGGAGCTGA TCGAAGCCGT TCGCCCCGAT 720
GCCATTATCA CAAAAGAAAG CGGAGAGAGC GGTACTTCC GAGAAAAGAT AGAAGCTGCC 780
CGACGGATGG GCATCCGTAT ATATGCCGTC GTACGTCCCC CTTTGCCTCC TTCACTCATC 840
55 CCCGTAGGCG GGCCTGTCCG TTTGAGACGG GCGGTAGAAG GCCTCGTGCC GGGATTCCTT 900
TACCTCCGAA GCGGATTCAC TACCGGCACC ACAGCTACCG CTGCAGTAGT AGCAGCCATG 960
TACCGATTGA TGGGGCTTGG CTCTCTCGCC GAAGCTCCCG TAGAATTGCC TTCGGGCGAA 1020
ATAGTCAGTC TGCCCATAGC GGAATTCGA GAGGAAGAAG ATGCTGTGCT ATCCGCGATC 1080
CTGAAAGATG CAGGTGATGA TCCGGATGTG ACCAATGGCA TGGCGGTATG CGCTACGATC 1140
60 AGGCTCAATC CCGAACATGA GGAAGTCCGC TTCCTGCAGG GTGAAGGGGT GGGGGTAGTG 1200
ACGCTCCCCG GCCTCGGTCT GGAGGTCCGA GGTCCGGCTA TCAACCTCGT ACCTCGACGA 1260
ATSATGACAG CAGAGGTACG CCGACTCTAT GCGCAGGGAG GTGTGGATAT TACGATTAGC 1320
GTACCCGAAG GCGGAGAGGC TGCTACCCAG ACATTCATC CCGGACTCGG CATAUGGGAC 1380
GSCATCTCTA TTATCGGAAC ATCGGGAGTC GTGAAACCTT TTTCCGCGGA AGCGTTCGTT 1440
65 GGTGCCATCC GTAAGCAAGT GGGTATTGCC ACCGCTTGG GAGCCAATCA TATCGTCTC 1500
AATTCGGGAG CCAAGAGTGA GCGTTATGTA AAAGGAGCCT ATCCGCACT CATTCACAG 1560
GCCTTTGTGC AGTATGGCAA TTTCGTGCGC GAATCACTCA GTTGTGTAGC TTCCTTCCT 1620
TCTGTCCGTT CGGTAACGGT AGGAATCATG CTCGGCAAAG CAGTGAAACT CGCCGAAGGC 1680
TATCTGGATA CGCACAGTAA AAAGGTAGTG ATGAATCGGG ATTTCTGCA CGAAGTGGCT 1740
70 CGTCAGGCAG GTTCTTCGGA AGACATCCAT GCCATAATAG ACAGCCTGAA TTTGGCTCGT 1800
GAGCTATGGA CTATGCCGAG TGGCGAGGAC AGCGATCGAC TGCTACGAAA GATTGCCGAA 1860
CGATCTTGGG AAATTTGCCG CCCATCGGTA CCATCGGCGG AATTAGAACT CTTGCTGATC 1920
75 GATGAGTCCG GAGCGATTCC TTTTCGTAAC GGTGGAGAA 1959

WO 99/29870

PCT/AU98/01023

17 / 490

(2) INFORMATION FOR SEQ ID NO:26

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1353 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1353

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26

25	CAACAAAGAC CACATAGAAT TATTATGTTG AGGACTTTCC GAATCGGTGG TATTCACCCC	60
	CCCGAAAACA AGTTGTCCGC AGGCAAGCCC GTAGAGGTGT TGCCTATCCC CTCACAGGTA	120
	GTATATCCCTC TTGGTCAGCA CATCGGTGCA CCGGCAACTG CCACGGTCAA GAAAGGGGAT	180
	GAAGTTAAGG TCGGGACTAT CATTGCTCAG GCCGGAGGAT TCGTATCAGC TAATATCCAC	240
	TCATCTGTGT CGGGTAAGGT GCTGAAGATC GATAACGTAT ACGACTCAAG CGGCTATCCC	300
30	AAGCCCGCAG TCTTCATTAG CGTAGAAGGT GACGAATGGG AAGAGGGCAT CGATCGCTCA	360
	CCCGGTATTG TGGGTCTTGG CGGTGCTACC TTCCCTACCC ATGTGAAGCT GTCCCTCCT	420
	CCGGGCAACA AAGCTGAGAT CCTGATCATC AACGCCGTAG AGTGGGAGCC TTATCTGACG	480
	AGCGACCATG TCCTTATGCT GGAGCACGGC GAAGAGATCA TGATCGGCGT GAGTATCTGT	540
	ATGAAAGCCA TTCAGGTAAA CAAGGCCGTC ATCGGAGTTG AGAATAATAA GAAAGATGCT	600
35	ATTGCTCACC TCACCAAACT GGCCACTGCA TATCGGGGCA TAGAGGTAAT GCCGTGAAG	660
	GTGCAATATC CTCAGGGCGG TGAGAAGCAG CTGATCGATC CAGTGATCCG CAAGCAGGTA	720
	AAAAGCGGTG CCTTGCCTAT CAGCACAGGT GCCGTAGTAC AAAACGTGGG TACGGTATTC	780
	GCCGTGTACG AAGCAGTACA GAAGAACAAG CCTCTGGTCG AGCGCATCGT GACGGTTACA	840
40	GGAAAAAAC TGCTCTGTCG GTCTAACCTC CTCGTTCGTA TAGGTACTCC TATTGCGGCT	900
	TTGATCGAAG CAGCAGGTGG CTTGCCGGAG AATACGGGCA AGATCATCGG CGGAGGTCCG	960
	ATGATGGGAC GCGCTCTGCT GTCAACCGAT GTGCCGTGTA CCAAAGGCAG CTCGGAGTA	1020
	TTGATCTCTG ATAGAGAAGA GGCAGTTCGC AAGCCTATGC GCGACTGTAT CCGATGGCGC	1080
	AAGTGGCTCG GAGTGTGTCC GATGGGACTC AATCCGGCTT TCCTTATGCG CGACACCTTA	1140
	TATAAGAGCT GGGAAACAGC GGAAAAAGGC AACGTGGTTG ACTGTATCGA ATGCGGTTTC	1200
45	TGCAGCTTCA CTTGTCCGGC CAACCGTCTC CTGCTGGATT ATATCCGCCA AGCCAAGAA	1260
	ACTGTGATGG GTATCCAAAG AGCAGGTAAG CAA	1320
		1353

(2) INFORMATION FOR SEQ ID NO:27

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1467 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27

50	ATGAACCTCTC AAAAGAAAGA GGCTTTTAAT ATGAAAGAA TACAACCTAAC TCTTATCGCT	60
	CTCTTCGCCG CTGTTGCCGG TTTGGTCGCT CAAAATGCTT ACGAGGGAGT AATTTTCATAT	120
55	AAAATTTCTG TGGACAAAAC CGGAAACAAG GTTGTACTGA ATGGTGGGCG AGATATGAGT	180
	AATTTAAAGC TCAAGAGCAC TCAGATGATC ATTGTTACCG CTATTCCTCG TTCAGAAGAT	240

WO 99/29870

PCT/AU98/01023

18 / 490

5 GGTACCAGCC GGGTGGAAAT TCCTTCGGTA GTCATTACAG GCCGCAATAG AACAAAAGCT 300
CTCAAGCGTG AAATCGCATT TAGTTCGGCT TTGCCCAAG CAAAACATGC AGCTCAATAC 360
ATTCCCGCTC ATAATGGGAA GAGCGAGCAG TTGCTTTTA CAGGAGAACA TGCTTATGCA 420
TCATGGATGA TGGATGCCAA GTTTGTGGTT CGTGAGGAGG TACGAGGTTG TGCTAAATGC 480
CCTGTAGGTC TCTCGAGTAA TATGTTCCT TTGATCCAC TCTTCAATCC GGCAGAGGCT 540
CCTTATTTGT TGGCACACAT TACTCCGGCA GAAGAAGTGG AAAACACGCG AGAGTCCAGC 600
TTCCGATGCT ATATCAACTT CAAAGTCAAT AAGGCAGATG TCCTTCCTGA GTATCGCAAC 660
AATAAGGCGG AGTTAGAGAA AATCAAAGAA TTGTAAAGCA CCGTTAAGGC TAA'CCAAAC 720
TATTCGGTCA ATAAAATGAT CATCGAAGGG TTGCTTCTC CCGAGGCTTC AATAGCCAC 780
10 AATAAGGCTT TGTCGGAGCG CCGTGTCTAA AGACTCGCGG AAGAATTGGT GCGTAAGTAT 840
GGCAAAACAT TGCCGAATAT AACCCTGAA TTGSCCGTG AAGATTGGAA GGGGCTGAA 900
CTGGCTATCG AAAAGAGTGA TATAGCGGAT CGTGACCGCG TATTGGAGAT AATCAACTCC 960
GATAAATATG CCGATGATGA TGCACGTGAA CAGGCTCTGA AGCAACTTTC GTCTTATCGT 1020
TATATCTTGG ATCAGATCTA TCCGAATTG CGTCGCAATA CGATAACCAT GGGGTATATC 1080
15 GTTCGTGATT ATACCCTCGA AGAAGCTCGT GAAATCATTA AGACTGCTCC GAAAGAACTT 1140
AGTGAGGCGG AAATGTACCG TGTGGCAATG TCTTATCCTG AGGGGCACCA AGAGCGTTTG 1200
TTTGCTCTGA ATACGACCTT TAAGTATTTT CTTGAAAGTG TAAAGGGCGG AATCAATTTG 1260
GCTGTAGCCG C'ITTTAATGG TGGAGACGTT CAACAGGCAA TTGCTCTGTT GAGTCCGATT 1320
CAGACAGAAA AGGGTGTAA GAAATCTCTT GGAGCTGCTT ATGCTCGTAC GGGAGATTTT 1380
20 GCTCGTCCG AAACCTTCTT CCGTAAGGCC GTTGCAGAAG GAGATGCAAA TGCGCAGCGC 1440
AACCTCGATA TGCTGCTTGG CAAAAAG 1467

(2) INFORMATION FOR SEQ ID NO:28

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...1152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28

50 GACATGGCAG AAAAAGAGA CTATTACGAA GTCCTCGGTG TATCGAAGAA TGCCACCGAC 60
GATGAACTGA AAAAAGCATA TCGCAAGAAG GCTATCCCAT ACCATCCTGA TAAGAACCCC 120
GGTGACAAGG AGGCCGAAGA GCACCTCAAA GAGGTAGCTG AAGCCTACGA CGTATTGAGC 180
GATCCGCAGA AGCGCAGTCA ATATGACCAG TTGCGCCATG CCGGATTGGG CCGAGCTGCC 240
GGTGGAGGTT TCAGCGGAGG CCGTATGTCC ATGGAGGATA TTTTCACTCG CTTGGGTGAT 300
CTATTCGGTG GGTTCGGCGG TTTCCGGCGA TTCTCCGATA TGGGCGGTGG CAGTCGCAGA 360
CGTGTTCGCA GAGGGTCTGA CCTGCGAGTA CGAGTGAAGC TTTCTTTGGC CGATATAAGT 420
AAGGTGTGG AGAAGAAAGT GAAGGTAAAA AAGCAGGTAG TGTGCAGCAA ATGTCGTGGC 480
55 GATGGCACGG AAGAAGCCAA TGGCAAGACT ACCTGCCAGA CTTGCCATGC AACCGCGCTG 540
GTTACACGTE TGAGCAACAC TTTCTTGGG GCCATGCAGA CCCAGAGCAC TTGTCCCACT 600
TGCCACGGAG AGGGTGAGAT CATCACGAAG CCATGCTCCA AGTGTAAAGG CGAAGGTGTG 660
GAGATCGGCG AAGAGGTGAT CTCATTCCAC ATCCCTGCCG GTGTAGCCGA AGGAATGCAA 720
ATGTCCTGTA ACGGCAAGGG AAATGCCGCG CCCCAGGAG CCGTGAATGG CCACTTGATA 780
60 GTCGTGATCG CCGAGGAACC GGATCCGAAT CTGATCCGCA ATGGCAACGA TCTGATATAC 840
AATCTGCTTA TATCCGTTCC GTTGGCTATA AAAGGAGGTA GTGTGGAAGT GCCGACGATA 900
GACGGACGAG CCAAGATCCG CATCGAGGCG GGGACACAA CCGGCAAGAT GCTCGGTTTG 960
CGCAATAAGG GGTTCGCCAG CGTAAACGGC TATCCCATGG GAGACCAACT GGTGAATGTC 1020
AATGTCTATA TCCCGGAATC GATCGATGCC AAAGATGAGC AGGCTATCGC AGCGATGGAA 1080
65 AACTCGGACA GCTTCAAACC TACCGATGCT GTCGTAAAG ATATAGACAA GAAATACAGA 1140
GAGATGCTGG AT 1152

(2) INFORMATION FOR SEQ ID NO:29

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

WO 99/29870

PCT/AU98/01023

19 / 490

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29

CGATTGCGATT	CAACAACTAA	TGCTCACA	ATTAAATTTAA	GAACAGAGAT	GAAGAACTG	60
ATTTTAGCGA	CITTTGGGACT	TATGGCCATT	GCCATGCTCT	CATGTTCAAG	CAACAACTAA	120
GATTTTGAGA	ACAAAGGGGA	GGCTACTCTT	TTGGTAACGT	TTGGTAGCTC	CTATAAAGCT	180
CCACGGGAAA	CCTATGCCGA	GATTGAGAAG	ACTTTTGCCG	CAGCTIATCC	CGATCAAAGG	240
ATAGCTGGA	CATACACGTC	TTCTATTATC	CGAAAGAAAC	TGGCTCAGCA	GGGTATTAT	300
ATCGATGCTC	CGGATGAGGC	TTTGGAGAAA	TTGGCTCGTC	TGGGTATATA	GAAGATCAAT	360
GTACAGAGTC	TTCATGTGAT	TCCCGGCCGA	GAATATGATG	AGATGATCGA	CTTTGTCAAT	420
AAGTTTAAGG	CAGCACATAG	TGATATTACT	GTGAAGGTAG	GGGCTCCGCT	TTTGGATACC	480
GATGAAGATA	TGCGGAGGT	GGCAGAGATC	TTGCACAAAG	GTTTTCAGCA	AACGATAGAG	540
AAAGGTGAAG	CTATTGTATT	CATGGGACAC	GGCACCAGAG	ATGCTGCCAA	TGACAGGTAT	600
GCCCGTATCA	ATAAGATCAT	GAAGAATAT	AGCAAGTTCA	TGATCGTCGG	AACCGTCGAG	660
TCCGATCCCT	CTATCAATGA	TGTTATTGCC	GAAGTAAAG	AAACCGGTGC	CACGGCCGTA	720
ACAATGATCC	CGCTGATGAG	TGTGGCAGGC	GACCATGCTA	CGAATGATAT	GGCGGAGAT	780
GAGGACGATA	GCTGGAAGAC	GTTGCTGACC	AATGCCGGCT	ACACAGTTTC	TATAGACAAG	840
CTGGACATG	GCAATTCTC	AGCTCTTGGG	GATATAGAAG	AGATCCGGAA	TATCTGGCTC	900
AAGCATATGA	AAGCCACCTC	TGCTCGC				927

(2) INFORMATION FOR SEQ ID NO:30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1473 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30

CGGAGAGATG	CGCGGAGGCA	ACTGGTACGC	CGTAGGAGGA	AAGAGCTATC	TGGCACAGCA	60
AATACCGGAT	GCCGGAGGAG	AGTATTTCCCT	GAAAGACGAT	CAGCGATCCG	GTGGTGTTTC	120
CCTCGACTTC	GAGACGGTCT	ACAGCCGATC	CGATTCCGGT	CGCTACTGGC	GAATCCTCAA	180
CAGCTATCCC	GGGGAGTTTC	GTTACGAAGC	TTTGAAAGCC	GAAGACAGCC	GATATGCCGA	240
TTTCAGGGCA	TTCAAGGAAA	AAGGCGTGAT	ATACTGCAAC	CTGAGGGAAA	CAGCCTTCTA	300
CGAATCATG	CCCATGCCATC	CCGATTGGGT	GCTGGCCGAT	CTTATCGCTA	TCITGACACC	360
CGGACTACTT	CCCGACCAAC	AACCGCATTT	CTATTATTTC	CTCCAATGAC	ATCCGTGAGC	420
CACTTACGTA	CAATTCTCT	CGCAGGTATC	CTGGCTGCGC	TGGGAGGGGC	TGTAATCATT	480
CTCTTCGGGG	TTAATCTCTT	CCTCGGCTCG	GTGGCTATTG	CGATGAGCGA	GATCTTCCGA	540
CATCTTTTTT	CAGATCGTCC	CGAAGGAGGA	GAAGCACTCG	TGCACTACAA	TATCCTATGG	600
AAATCCCGCC	TGCCCGAAGC	CCTCACGGCT	GCTTTTGCCG	GCGCAGGTTT	ATCCGTTAGT	660
GGCTTCGAGA	TGCAGACCGT	CTTTCCGAAT	CCTTTGGCCG	GTCCGTCCGT	TCTCGGCATC	720
AGCTCCGGTG	CCAGTTTGGG	TGTTGCTTTG	GTGTTCTGTC	TGAGCGGGTC	GCTGGGAGGA	780
GTGGCATTCG	GTAGCCTGGG	TTATATGGGC	GAGGTGCCCA	TGAATATAGC	CGCTGCCGTA	840
GGCTCGCTGG	CAGTAATGGG	GCTGATCGTT	TTTGTGAGCA	CCAAGGTGCG	CAGCCACGTT	900
ACGCTGCTCA	TTATCGGCGT	TATGATCGGA	TATGTAGCCA	CTGCCGTGAT	CGGGGTATTC	960
AAGTTTTTCA	GTATCGAAGA	AGATATTCGG	GCATACGTAA	TTTGGGGGTT	GGGCAGCTTT	1020
TCCCGTGCCA	CGAATTCGCA	ACTGAGTTTC	TTTGCCATTC	TGATGTTGAT	CTTTATTCCT	1080

WO 99/29870

PCT/AU98/01023

20 / 490

5 GCGGATATGC TCCTTGTCAC GCAGTTGAAAT CTCTTATTGC TGGGAGAAAG CTACGCACGT 1140
AATCTGGGAC TGAATACTCC TCGGACACGG CTGCTCGTSA TCTCTTCCGC CCGTTTGTCTC 1200
ATCGCTACCG TCACGGGCTA TTGCGGTCCT ATCGGCTTTT TGGGGATGGC TGTGCCACAC 1260
TTGGCACGGG TTATCTTTCA CACATCGGAT CATCGGATCC TGATGCCTGC TACCTGTTTG 1320
ATTGGAAGTG CTCTGGCTCT TTTCTGCAAT ATCATTGCTC GTATGCCGGG GTTTGAGGGG 1380
GCTTTGCCCG TCAATTCCGT AACGGCTTTG GTGGGAGCAC CTATTATCGT CACCGTTTTC 1440
TTCCGGCGCA GACGCTTCAA GGAAGAAACC GAC 1473

10 (2) INFORMATION FOR SEQ ID NO:31

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2289 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
(11) MOLECULE TYPE: DNA (genomic)
(111) HYPOTHETICAL: NO
(1v) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2289
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31

35 CATTTTTTAG TAACGATTAT GCGGACAAAA ACTATCTTTT TTGCGATTAT CTCTTTTATT 60
GCTCTATTGT CGTCTTCTCT GTCGGCTCAG AGCAAAGCCG TTTTAACCGG TAGTGTGTGG 120
GATGCCGAAA CCGGAGAGCC TCTTGCCGGT GCTCGAATCG AAGTCAAACA CACCAACATA 180
GTAGCCGGTG CCGATGCCGG CGGACATTTC GAGATCAAGA ACCTGCCGGC AGGGCAGCAT 240
ACTATTATAT GTTCGTTGGG GGGGTATGGA CAGAAAGAGG AGGTGGTTGC CATCGAAGCC 300
GGACAGACCA AAACGATCTC TTTTGCAATG CGACTGCGAA CGAACAACTT GGAGGAAGTC 360
GTCCGTACCG GTACCGGTAC ACGTTACCGC TTGGTCCGAT CTCTGTGGC AACGGAAGTC 420
CTTACCGCTA AGGACATAGC CTCCTTCTCG GCTCTACTT CCGAGGCGTT ATTGCAGGGG 480
CTGAGTCCGT CTTTGTGACT CGGCCCCAAT CTGATGGGCT CTTTCATGCA GCTGAACGGC 540
CTTAGCAGTA AGTATATCCT CATCCTTATC GATGGTAAGC GTGTGTACGG CGATGTAGGC 600
GGTCAGGCGG ATTTGAGTCG TATTTCTCCT GATCAGATCG AACGGATCGA ACTGGTGAAA 660
GGTGCTTCGA GTTCGCTCTA CGGATCCGAT GCCATCCGGC GGGTAATCAA TGTGATCACA 720
AAAAAGATA CGAATCGACT GAGTGCATAT ACGTCAATC GCATATCGAA GTACAACGAT 780
CGGCAACCA ATACTTCGCT CGATATAAAC ATCGGTAAGT TCAGTAGCAA TACCAACTAT 840
TTCTTCTACC ATACGGATGG CTGGCAGAA AGTCCGTTCC AAATAAAAAA GAAAAAAGGA 900
TCCGCGCAAC CGGTCTTGA GGAACGSTAT AAGAAACTT TCTGTGCACA GGAATATCAG 960
GGTGTAGGCC AATCGCTTTC CTATTATGCA ACTAACATC TTAGCTTCAG CGGAAATGTG 1020
CAGTACATAA AACGTGAGAT CTTCACTCCG ACTTTTCCG AAAAGAAGGC CTATGACATG 1080
GATTATCGTG CPTTGACGSC TTCACTCGGT ACGAACTATC TTTTCCCAA TGGTCTGCAT 1140
ACGCTTTCTT TCGATGCCGCT CTACGATCGC TTCCGTTTCG GATATTGTGA TCATGACAA 1200
GACAGCAGTG AGAGCCTGAT CAACAACCAA GGTGAGCCG AGCAACCCAC ATTCTTTCCG 1260
GGTCAGCTAC GCAATAAAAA CGATCAGATC CGATACAGCG CAGAGGCTCG CGGTGTATTT 1320
55 ACACTGCCTT ATGCGCAGAA ACTGACCGGC GGTTTGGAGT ATTTCCGTGA GGAATTGATC 1380
TCTCCCTATA ATTTGATTAC CGACAAGSCA GATGCTTCCA CGCTCTCTGC TTATGTACAA 1440
GATGAATGGA AACCGCTCGA TTGGTTCAAT ATGACAGCCG GTTTCGCTCT GGTACACCAT 1500
CAGGAGTTTG GTACACGAAT GACGCCTAAG GTATCCATAC TCGCCAAATA TGGGCGCGTG 1560
AATCTCCGCG CTACGTATGC TAACGGCTAT AAGACTCCCA CGCTGAAAGA GCTTTTGTGA 1620
60 CGGAACGAAC TCACCACTAT GGGTTCCGAC AATCTCTATC TCGGCAATGC GGATCTTAAG 1680
CCACAGATGT CGGATTATTA TGCTTTGGGC TTGGAGTACA ATCAAGGCCC TATCTCGTTC 1740
AGTGCAACGG TTTATGACAA TGAATTCGCG AATCTGATCT CCTTTATGGA TATACCGACC 1800
TCACCCGAGC ACGAAGCTCA GGAATCAAG AAAACCAAGC AGTATGCCAA CATAGGAAAA 1860
GCTCCGAGCC GCGGCTTGA TGCTCTATGT GATGCTCTA TCGGTTGGGG TATCAAGTTA 1920
65 GGAGCCGGAT ACAGCCTCGT GGAAGCTAAG AATCTCCAGA CGGATGAGTG GCTGGAAGGA 1980
GCTCCACGTC ATGCTGCCAA TGTGCACGCT GATTGGGTTT ACTACTGGGG TCAGTATAGA 2040
CTTGCGCTGA GCCTTTTCGG CCGTATTTCG AGCGAGCGTT ACTACAAAGA CGGCAATGCT 2100
CCGCACTATA CCTGTGGCG ACTCGCCACA TCGCATCGTT TCGCTCATTT CCGCCACATC 2160
ATCCTGGATG GAACGCTCGG TATAGACAAC CTGTTTGAAT ACGTGGATGA TCGTCTATG 2220
70 GGTGTCAATT ATGCTACCGT AACGCCGGGA CGTACTTTCT TTGCTCAAT AGCGATTCCA 2280
TTCAACAAC 2289

75 (2) INFORMATION FOR SEQ ID NO:32

WO 99/29870

PCT/AU98/01023

21 / 490

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1095 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32

25	TGCTGCGCAA GGCTTCGGGA CACCTCTCCC CGGAAGAAGT CGTTTCGGAA TGATACCGTT	60
	TTTCCTTATT TCCTTATTCA TCTGATCAAA CATATTATCA TTATGACGGA CAACAAACAA	120
	CGTAATATCG TATTCCTGGC GTTCTCTCTC TTGCTGGGAG TCATCGCAGT GGTGACGATC	180
	GTTGGTTTTT TCATGCTCAG ACCGGCCGAG GAGATTATCC AAGGACAGAT AGAAGTGACC	240
	GAATACCGAG TGTCAGCAA AGTGCCCGGG CGCATCAAGG AACTTAGGAT ATCCGAGGGA	300
	CAGCAGSTGC AGGCCGGCGA TACCTCTGGT CTCATCGAAG CCCCAGAGT AGCGGCTAAG	360
	ATGGAGCAGG CAAAGGCTGC CGAAGCAGCT GCACAGGCTC AGAACGCCAA GGCTCTCAA	420
30	GGAGCAGGCA GCGAACAGAT ACAGGCGAGC TATGAGATGT GGCAGAAAGC TCAGGCCGGC	480
	GTAGCCATAG CGACCAAGAC ACACGAGCG GTGCAGAAC TCTATGACCA GCGAGTGGA	540
	CCGGCTCAGA AGTTGGAAGA AGCCACTGCC CAGCGCGATG CGGCCATCGC TACGCAAAA	600
	CGGCCCGAAG CCCAGTACAA TATGGCTCGC AACGGTGCCG AACGCGAAGA CAAGCTGGCA	660
	GCTTCTGCC TCCTCGATAG AGCGAGAGGA GCGCTGCGG AGGTGGAGTC GTACATCAAC	720
35	GAACCTACC TCATCGCCCC ACGGCGAGG GAAAGTGTCG AGATATTCCC CAAAGCCGGC	780
	GAACCTAGT GTACCGGGCG ACCTATCATG AATATCGCG AGATGGGCGA TATGTGGGCC	840
	AGCTTTGCCG TTCGTGAGGA TTCTCTCAGC AGCATGACCA TGGGAGCCGT TCTGGAGCT	900
	GTGGTCCCGG CTCTGAATGA AGAAAAAGTA CGCTTCAAGA TCACATTCAT CAAAGACATG	960
	GGTACCTATG CTGCGTGGAA AGCGACCAAG ACAACAGGGC AGTACGACCT GAAGACCTTC	1020
40	GAGGTAAAGG CCACCTTGC GGATAAAGAC AAGGCACAAA AGCTACGCCC GGGTATGTCC	1080
	GTGATCATAC GCAAG	1095

(2) INFORMATION FOR SEQ ID NO:33

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 960 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33

65	CCGCAATCCT CTCTGATCG AAGAAGCTTC CAAAACGTCA TGAATAAATA TCATTCTCAA	60
	AGCGTTTTAG AGGTGCGGCA AATTGGGATT GTGATTATCT TTGCGCCCAT AGTACGGAAT	120
	GTACATCAAC AACCCCTTTT TTAAAGCCAT AAATCAATTA TGCGTATTGT CAGTAATTTT	180
	TTGTTCTGCT CTTTTCTGGT TTGCTTTTT GCATCATGCC GTTCCGACGG AGAAAAGGTC	240
70	CTTTACCTGC AAGATATCCA AACTTTTAAT CGGGAGATTA TCGCTAAACC ATATGACGTA	300
	AAAATTGAGA AGGACGATGT GCTGAACATC CTGTCAACCA GTAGAGACCC GGAGCTTTCA	360
	ACGCCCTACA ACCAAGTGTT GACCACTCGT GCACTGGCCC GCAACGGCTA TGGAAACGAAC	420
	TCGAACGAAG GCTTCTTGGT CGATTTCGAA GGTACATCA ATTATCCTAT TTAGGCCAG	480
75	ATCTATGTAG AGGCCTTAC TCGTACCGAA CTGGAGAAGG AGATAAGAA GAGGATTATT	540
	TCCAGTGGAT TTATCAAGGA TCCTACGGTA ACGGTGCAGC TTCAAAATTT CAAGGTGTCT	600

WO 99/29870

PCT/AU98/01023

23 / 490

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2955

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35

5	60	120	180	240	300	360	420	480	540	600	660	720	780	840	900	960	1020	1080	1140	1200	1260	1320	1380	1440	1500	1560	1620	1680	1740	1800	1860	1920	1980	2040	2100	2160	2220	2280	2340	2400	2460	2520	2580	2640	2700	2760	2820	2880	2940	2955										
15	20	25	30	35	40	45	50	55	60	65	70	75	80	85	90	95	100	105	110	115	120	125	130	135	140	145	150	155	160	165	170	175	180	185	190	195	200	205	210	215	220	225	230	235	240	245	250	255	260	265	270	275	280	285	290	295				

(2) INFORMATION FOR SEQ ID NO:36

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

WO 99/29870

PCT/AU98/01023

24 / 490

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(1v) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
    (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
5
(ix) FEATURE:
    (A) NAME/KEY: misc feature
    (B) LOCATION 1...3138
10
(x) SEQUENCE DESCRIPTION: SEQ ID NO:36
GACTTCCCTT GGGTTAGGCT AAAACCGGAG AAGAAAGGAA AACAACATAA CAGTAATAAT    60
TTTAAAGTTT ACGCAAAAGA AAGTCTATG AAAAGAATGA CGCTATTCTT CCTTTGCTTG    120
CTGACGAGCA TTGGGTGGGC TATGGCCAG AATAGAACCG TGAAGGGTAC AGTTATCTCC    180
TCCGAGGATA ATGAGCCCTT GATCGGCGCG AATGTCGTGG TTGTCGGAAA CACCACTATC    240
GGTGTGCAAA CCGACTTGGG TGGCAACTTC ACGCTTAGCG TGCTGCCCAA TGCCAAAATG    300
TTGAGAGTGT CCTATCCGG TATGACTACC AAAGAGGTCT CCATCGCTAA TGTGATGAAG    360
ATCGTACTGG ATCCGGACTC TAAGGTTCTG GAGCAGGTAG TTGTATTGGG TTACGGTACG    420
GGACAGAAAC TCAGCACTGT TTCGGTTCTT GTGGCCAAAG TGTCACGCGA AAAGCTCGCG    480
GAAAAGCCCG TTGCCAATAT CATGGATGCC CTCGAAGTTC AGGTAGCCGG TATGCAGGTT    540
ATGACTACAT CCGGTGACCC TACTGCCGTC GCTTCTGTGG AGATCCATGG TACAGGGTCG    600
TTGGGGGGCAA GCTCTGCACC ATTGTATATC GTGGATGATA TGCAAACTTC TTTGGATGTT    660
GTGGGTACGA TGAATCCGAA TGAATTTGAA TCTATGTCCG TTTTGAAGA TGCTTCTGCA    720
ACATCTATTT ATGGAGCTCG TGCTGCAAAAC GGAGTCTGTT TCATTCAAAC GAAGAAAGGT    780
25
AAAATGAGCG AGAGAGGTCT TATTACCTTT AATGCCAGTT ACGGGATTTC TCAATCTCTG    840
AATACTAAGC CCCTTGATTA TATGATGACT GGAGATGAAT TGCTGGATT TCAAGGTGAAG    900
GCAGGTTTTT GGGGGAACAA TCAACCGGTT CAGAAGGTTA AAGATATGAT CCTTGCCGGA    960
GCTGAAGATT TGTATGGCAA TTATGATTCT TTGAAGATG AGTATGGTAA GACATTGTTC    1020
CCAGTGGATT TTAATCATGA TGCAGACTGG CTCAGGCTTT TGTTTAAAC AGCACCCACC    1080
30
AGTCAAGGTG ATATTTCTTT CTCGGGAGGG TCTCAGGGAA CTTCATATTA TGCCCTCTATA    1140
GGCTACTTCG ATCAGGAAGG TATGGCTCGT GAACCGGCAA ATTTTAAAGC CTATAGTGGC    1200
CGGCTCAACT TCGAAAGTCG TATCAATGAA TGGCTGAAGG TTGGTGCAA TTTGTCTGGT    1260
GCGATAGCGA ATAGACGATC TGCCGACTAT TTTGGAAAGT ATTATATGGG GTCAGGTACT    1320
35
TTCCGTGTGT TAACGATGCC TCGTTATTAT AACCTTTTG ATGTGAATGG GGATTAGCA    1380
ATGTTCTATT ACATGTATGG AGCTACGAGA CCTTCATGA CAGAACCCTA CTTCGCAAAA    1440
ATGAGACCGT TCAGTTCCGA ATCAGATCAG GCCAATGTAA ATGGTTTCGC CCAGATTACT    1500
CCGATCAAGG GCCTTACTTT AAAGGCACAG GCTGGTGTGG ATATTACTAA TACTCGCACT    1560
TCTTCTAAGA GAATGCCCAA TAATCCGTAT GATTCTACTC CTCTCGGGA AAGAAGAGAA    1620
40
AGAGTCTATC GAGATGTTAG CAAGTCTTTT ACAAATACGG CTGAATATA GTTTTCAATT    1680
ATGAAATAAC ATGATCTTAC AGCATGTATG GGGCATGAAT ATATTGAATA TGAAGGGGAT    1740
GTTATTGGGG CATCTTCTAA AGGATTGAA AGTGATAAGT TGATGTTACT GAGCCAGGGA    1800
AAAACCGGAA ATAGTTTGTG TTTGCCCTGA CACAGAGTCG CTGAATATGC CTATTTGTCT    1860
TTCTTTAGTC GTTTTAATTA CGGTTTGTAC AAATGGATGT ATATAGATT CTCTGTTCTG    1920
AATGACCAAT CCTCTCGATT CGGATCCAAT AATAGAAAGC CGTGGTTCTA TTCTGTCTGG    1980
45
GGAAATGTTG ACATATATAA TAAATTCATT CAAGAAAGTA ATTGGCTCAG TGATCTTCTG    2040
CTGAAATATG GTTATGTTAC AACGGGTAAC TCGGAGATTG GTAATTACAA CCACCAAGCA    2100
CTCGTTACTG TGAACAATTA TACTCAAGAT GCTATGGGGC TTAGCATTTT TACAGCAGGC    2160
AATCCCGACC TCTGTGGGA AAAGCAGTCT CAGTTCAACT TCGGTTTGGC TGCAGGGGCT    2220
TTCAATAATC GCTTATCTGC AGAGGTAGAT TTCTATCTCC GCCTACGAA TGATATGTTG    2280
50
ATTGATGTCC CGATGCCCTT TATCAGTGGT TTCTTCTCAC AGTATCAGAA TGTAGGCTCT    2340
ATGAAAAATA CGGGTGTAGA CCTTCTCTTT AAGGGGACGA TCTACCAAAA TAAGGACTGG    2400
AATGTATATG CTTCTGCGAA TTCAACTTAC AATAGACAGG AATAACAAA GCTTTTCTTC    2460
GGTCTCAATA AGTACATGTT GCCTAATACC GGTACTATAT GGGAAATTTG GTACCCCAAT    2520
TCGTTCTATA TGGCTGAATA TGCTGGAATC GACAAAAAAA CCGGTAAAGCA GTTGTGGTAT    2580
55
GTTCTGTGTC AAGTCGATGC GGTAGGTAAT AAAGTTACAA CAAGCCAGTA CTCAGCTGAC    2640
TTGGAGACAC GAATGATAA GTCTGTTACT CTTCTTACTA CAGGTGGTTT CTCCTTAGGT    2700
GCTTCTTGGA AAGGACTTTC TTTAGATGCT GATTTTGCTT ACATCGTTGG TAAATGGATG    2760
ATCAATAATG ACCGTTACTT TACAGAGAAT GCAGGTGGAT TGATGCAATT AAATAAGAT    2820
AAAATGCTAT TGAATGCCCT GACAGAGGAT AATAAAGAAA CAGATGTTCC AAAATTGGGA    2880
60
CAGTCTCTTC AGTTTGATAC GCATTGTTG GAGAATGCTT CTTTCTGCG TTTGAAGAAT    2940
CTCAAACTCA CCTATGTACT CCCCATAAGT CTTTTTGTG GGCAGAAATG GATTGGTGGG    3000
GCTCGTGTCT ATTTGATGSC GCGCAATCTG TTAATCTCTA CGAAGTATAA AGGCTTTGAC    3060
CCTGAAGCAG GGGGAATGT GGGAAAAAT CAATATCTTA ATTCTAAGCA GTACGTTGCG    3120
65
GGTATTCAGT TGTCTTTC

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(2) INFORMATION FOR SEQ ID NO:37

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(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 2607 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: circular

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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...2607

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37

15	TGGCATAGGA ATATTTTAT CTTTGCAGT ACATTAGCC CGAAAAATAT GCTCCCACTG	60
	CCATACCGTT ATGCAAAAC CGAGCACCTT TTTCTCGCAA AAGGATACTG CAAGAATCCA	120
	ATAACAAACA TAATTATCCT ATTTATGAAG AAAAAGAATT TTTTGCTTCT TGGCATTITC	180
	GTTCCTTTTC TGACTTTCAT CGGCAGCATG CAGGCACAC AGGCCAAGA TTATTTCAC	240
20	TTTGACGAAC GGGGCGAGGC CTACTTCICA TTCAAAGTGC CTGATAGGGC CGTCTACAA	300
	GAGCTGGCTC TGATCATGTC CATCGACGAG TTTGACCCCG TAACCAATGA AGCCATTGCC	360
	TATGCCAGCG AAGAGGAGTT CGAGGCATTG CTGCGCTATG GGCTCAAGCC TACATTCTTG	420
	ACTCCTCCAT CCATGCGACG CGCTGTCGAG ATGTTGCACT ACCGCTCAGG AGAAAAATAC	480
	GAATGGAATG CTTACCCAC CTATGAAGCC TATATCAGCA TGATGGAAGA GTTCCAAACA	540
25	AAGTATCCAT CACTTTGTAC TACTTCCGTC ATTGGCAAT CCGTAAAGGA TCGTAAACTG	600
	ATGATTGGCA AGCTGACGTC CTCTGCCAAT ACAGGGAAAA AGCCTCGCGT GCTCTATACT	660
	TCTACGATGC ACGGAGACGA AACGACCGGA TATGTGGTAC TGCTCCGACT CAGAGCCAT	720
	CTGCTGTGCA ACTACGAATC CGATCCGAGG ATTAAGAACA TTCTGGATAA AACGGAAGTA	780
	TGGATCTGCC CTTTGACCAA TCCGGACGGA GCATACAGAG CCGGAAACCA CACCCACAA	840
30	GGAGCTACTC GCTACAATGC CAACAATGTC GATTGGAACC GTAACTTCAA GGATGATGTA	900
	GCCGGTGATC ACCCGGATGG AAAACCTTGG CAGCCGGAGG CAACCTGCAT CATGGATTTG	960
	GAAGGAACA CCTCTTCTGT GCTCGGTGCC AATATACATG GAGGAACAGA GGTGGTGAAC	1020
	TATCCATGGG ATAATAAAAA AGAAGACAT GCAGACGATG AGTGGTACAA ACTGATCAGT	1080
	CGCAACTACG CAGCGGCTTG TCAGAGTATT TCCGCCAGCT ACATGACCTC CGAAACCAAT	1140
35	TCGGGAATCA TCAACGGTTC AGACTGGTAT GTAATTCGCG GAAGTCGTCA GGCAATGCA	1200
	AATTATTTCC ATCGTCTGCG AGAAATTACC CTTGAAATCA GCAACACGAA GTTGGTGCGG	1260
	GCCTCTCAAC TTCCAAAGTA TTGGAATCTG AACAAAGAAT CTCTGCTTGC TCTGATCGAA	1320
	GAATCCTTAT ACGGCATCCA TGGTACAGTG ACTTCCGCTG CGAAGCGACA GCCTCTCAA	1380
	TGCCAGATCT TGATAGAAAA CCATGACAAG CGCAACTCCG ATGTTTACTC CGATGCTACC	1440
40	ACAGGCTACT ACGTACGTC TATCAAAGCC GGCACCTATA CGGTGAAATA CAAAGCCGAG	1500
	GGTTATCTTG AGGCAACTCG TACCATTACG ATCAAGGACA AAGARACCGT CATCATGGAC	1560
	ATTGCATTGG CCAACTCGGT TCCTCTGCCT GTACCCGATT TCACAGCTTC TCCTATGACC	1620
	ATCTCAGTAG GCGAAAGCGT CCAATTCCAA GATCAAACGA CAAATAACCC CACGAATTGG	1680
	GAGTGGAGCT TCGAAGGCGG ACAGCCTGCC ATGAGTACAG AGCAGAATCC GCTCGTATCC	1740
45	TATAGTCATC CCGGTCAGTA CGACGTTACG CTCAAAGTGT GGAATGCAAG TGGTTCRAAC	1800
	ACGATTACGA AAGAAAAATT CATCACTGTC AATGCCGTTA TGCCGTAGAC TGAATTCGTC	1860
	GGTACCCCGA CGGAAATAGA AGAGGGCCAG ACGGTATCTT TCCAAACCA ATCCACCAAT	1920
	GCCACCAACT AGSTATGGAT ATTGATGGC GGCACCTCCG CTACCACTGA AGACGAAAC	1980
	CCGACTGTGC TTTACAGCA AGCCGGCCAA TACGATGTCA CGCTCAAGGC GATCAGTCT	2040
50	TCCGTTGAAA CCGTGAAGAC GAAAGAAAAA TACATCACTG TCAAGAAAGC TCCGTTCCCT	2100
	GCTCCGGTAG CCGACTTCGA AGGAACACCT CGAAAAGTAA AGAAAGGCGA GACAGTTACT	2160
	TTCAAAGACT TGTCTACGAA CAATCCGACT TCATGGCTTT GGGTGTTCGA AGGCGGCTCT	2220
	CCTGCCACCA GCACGGAGCA AAACCCGGTG GTCACTACA ATGAACAGG CAAGTACGAT	2280
	GTCCAGCTGA CTGCCACCA CGAGGGCGGA AGCAATGTGA AGAAAGCAGA AGACTACAT	2340
55	GAGGTTATCC TCGATGACAG TGTCGAGGAC ATAGTGGAC AGACGGGTAT CGTCATTCTG	2400
	CCGCAAAACG GAACGAAGCA GATCCTCATA GAAGCCAACG CTGCTATCAA AGCGATCGTT	2460
	CTCTATGACA TCAATGGACG GGTCTACTC AAAACTACTC CGAATCAGCT CCGCTCGACC	2520
	GTAGATCTTT CCATCTGCC CGAAGGAATC TACACCATCA ATATCAAAC GGAATAATCC	2580
60	GCTCGCACGG AAAAGATCCA TATCGGG	2607

(2) INFORMATION FOR SEQ ID NO:38

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

WO 99/29870

PCT/AU98/01023

26 / 490

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38

CTTCGTACA	GTGGAGAGAG	CGATGCAAAA	GAGTCTGATC	AGAATTGCCG	GAAATGTACC	60
TTTCATUGGCT	TTGAAAAACG	AGTAAATACG	ATGCGACTGA	TCAAGGCTTT	TCTCGTGCAA	120
CTCTTACTGC	TCCCATTTT	CTTCTACAAG	CGCTTTATAT	CGCCGCTTAC	ACCGCCTTCA	180
TGCGGGTTTA	CCCCCTCATG	TTGCTCTAT	GCCATCGAAG	CCTTACGTAA	ATATGGCCCG	240
GGCAAAGGAC	TATTGCTGAG	CATCAAGCGT	ATTCTCCGCT	GTCACCCGTC	GGGTGGAAGT	300
GGCTATGACC	CCGTTCGG					318

(2) INFORMATION FOR SEQ ID NO:39

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2583 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...2583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39

TTAGAGATGG	CATACGACTT	TACACAAACA	TTCCGCAACA	GCCTGGAGTA	CAGCTATCAG	60
GAAGCAACCC	GTCTCGGCGT	CGTAGCCGTG	ACGCCAAGATA	TGCTCGTACT	CGGTATCATT	120
CGCGACGGAG	ACAAATGGCGC	GATCGACATC	ATGCGGCACT	ATGGGATCAA	CTTGTACGAA	180
CTCAAACGGT	TGATCGAGTT	GGAAGCCATC	GCCGAGAGTT	TGCTGCTTC	GCCTGAGGGA	240
TGCCCCATCT	TCACCCCTTC	GGCTCGGGAG	GCTATCGATG	ATGCCACAGA	CATCTGTGCC	300
GACATGGAGG	ACGAGGCCGT	CAGCCCGGTC	CATCTGTTGC	TGAGTATCCT	CAACTCGACA	360
CAGGAGAGCT	TAGTACAAAA	GATAATTATG	AAACAAGGTA	TAAATACGA	CACCATCCTG	420
TCGGATTACT	TCGGACAGCG	CAACCCCTCC	GAAGGGAAGT	CTCCCTCCGA	AATGGAGATC	480
CTCGACGGGT	ACCAAGACAA	CGACTTCGAC	GACGAAGAGG	ACGAATCCTC	TCCGCCTTCC	540
GGGAATAGCG	GGACAGGCGG	AGGCTCCGGC	GACGCCCCCG	AACAGARTAC	CGGCCGAGGC	600
GATACTACCA	CCACGACACG	GAGTGGAGGC	GACACGCCCTG	CACTGGACAC	CTTCGGCACC	660
GACATCACTG	CCATGGGCGC	AGCAGGCAAG	CTCGACCCGG	TAGTGGGTCC	GGAGCAGGAG	720
ATCGAAAGGG	TGATACAGAT	ACTCAGCCGG	CGCAAAAAGA	ACAATCCGGT	GCTCATCGGC	780
GAACCCGGTG	TAGGCAAGAG	TGCCATCGTG	GAAGGACTGG	CCGAACGCAT	CGTGAACAGG	840
AAGGTGAGCC	GTATTCTTTT	CGACAAGCGG	ATCATCAGCC	TGGATTGGCC	TCAGATGGTA	900
GCCGGCACCA	AATATCGCGG	ACAGTTCGAA	GAGCGGTGTA	AAGCCGTGCT	CGATGAGCTG	960
AAGAAGAATC	CGCAGATCAT	CCTCTTCATC	GACGAGATAC	ATACCATCGT	GGGAGCAGGC	1020
TCTGGAGCCG	GATCGATGGA	TACGGCCCAT	ATGCTCAAAC	CCGCTCTTGC	CCGTGGACAG	1080
GTACAGTGCA	TCGGAGCCAC	TACGCTGGAT	GAGTATCGTA	AGAACATAGA	AAAGGACGGA	1140
GCATCGAAC	GCCGCTTCCA	GAAGGTGCCG	ATAGCCCCCT	CGACTGCAGA	AGAAACGCTG	1200
ACCATCCTGC	AAATCATCAA	AGAGAAATAC	GAGGACTATC	ACGGTGTACG	CTATACGGAC	1260
GAAGCGATCA	AAGCGGCAGT	GGAAGTGAAC	GATCGCTATG	TATCCGATCG	TTTCTTCCCA	1320
GATAAGGCGA	TAGATGCCAT	GGACGAGGCC	GGCGCGAGCG	TCCATATCAC	CAATGTGGTG	1380
GCTCCGATAG	AAATCGAGAT	ACTGGAGGCC	GAATTGGCAT	CGGTGCGAGA	GAACAAGCTC	1440
TCGGCCGTAA	AGGCTCAGAA	CTACGAACATG	GCTGCCTCCT	TCCGCGATCA	GGAGCGGCGC	1500
ACTCAGCAGC	AGATAGCGGA	AGAGAAGAAA	AAATGGGAAG	AGCAGATGTC	CAAGCACCGC	1560
GAGACCGTGG	ACGAGAATGT	AGTGGCGCAT	GTAGTGGCGT	TGATGACAGG	CGTTCCGGCT	1620
GAGCGGCTGA	GCACGGGCGA	AGGCGAAGCT	CTGCGCACGA	TGGCAGATGA	TCTCAAGACC	1680
AAAGTAGTAG	GTCAGGACAC	AGCCATCGAA	AAGATGGTGC	ATGCCATCCA	CGGCAATCGT	1740
CTGGGACTTC	GCAATGAAAA	GAAACCGATC	GGTCTTTTCC	TTTTCTCTCG	CCCCACGGGG	1800
GTAGGCAAGA	CCTATTGGCC	CAAGAAGCTC	GCGAATACC	TGATCGAGGA	TGAGAATGCC	1860
ATGATCAGGG	TGGATATGAG	CGAGTATATG	GAGAAGTTCT	CGGTTTCGCG	TCTCGTGGGT	1920
CGCCCTCCGG	GATATGTGGG	CTATGAAGAA	GCGGCCAAC	TGACGGAGCG	CGTAAGACGC	1980
AAACCTTATT	CCGTGGTTCT	CTTGGATGAG	ATCGAAAAGG	CGCATGCCGA	TGTCTTCAAT	2040
CTGCTCTTAC	AGGTGATGGA	CGAAGGTCAG	CTGACCGACA	GTCGTGGAGC	GGCGGTGAAT	2100
TTCAAGAACA	CCGTGATCAT	CATCACCTCC	AACGTGGGTA	CAGGCCAGCT	CAAGAGACTTC	2160

WO 99/29870

PCT/AU98/01023

27 / 490

5 GGGCAGGGTA TCGGGTCCG TTCGGAAAAA GACGAGGAAG CGAACAAAGGA GCATAGCCGT 2220
TCCGTGATCC AAAAAGCTCT GAACAAGACG TTCAGCCCGG AATTTCTCAA CCGTTTGGAC 2280
GATATCATCC TCTTCGACCA ACTGGGCAAG ACGGAGATTC GCCGGATGGT GGACATAGAG 2340
CTTAAAGCCG TCTTGGCGCG CATCCATCGT GCCGGATACG ACCTCGTCCT TACCGATGAA 2400
6 CCCAAGGATG TGATAGCGAC GAAGGGATAC GACCTCCAAT ACGGAGCAGC ACCGCTCAAG 2460
CGCACACTCC AGAACCAAGT GGAGGATCGC CTCACGGATC TTATCCTCTC CGGACAGATC 2520
GAGAAAGGSC AGACGCTTAC GCTCTCTGCT CGCGATGGCG AGATCATCGT ACAAGAACAA 2580
GCA 2503

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(2) INFORMATION FOR SEQ ID NO:40

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1368 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

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(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION: 1...1368

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40

35 AGACGAGGAC AAATCUGCCG ACACCATACC GATTCGTCAA GGGGATCGGA CAGCAAAAGCC 60
TGCCGCTTCT CTTTTTCATG CGAGACCATC GGTTCCTCCA ACCACCAAAG AGCAAAATG 120
AATTACCTGT ACATACTGAT TACACTTTTA CTCTCCGGCT TTTTTCGGG TGCTGAGATT 180
GCTTTCCTTT CTTCCGACAA ACTCGCTCTT GAGTTGGACA GGAATAGAGG CGATCTCACA 240
GGCAGAGCST TAAACTTGCT GTATCGACAT CCGGACCAAC TGGTGACTAC TCTCCTTGIG 300
GGTAATAATA TCGTTTGGT AGTCTATGGT CTGCTGATGG CGGGATIGCT GGCCGCACCT 360
40 TTGGCGCAAT GGATTGATAA CGATGCTATG ATCGTCGTTT TCCAATCTGT CTATCCACT 420
ATCATCATAC TGTTTACCGG GGAATTTCTA CCCAAAGCCA TTTTCAAGAC CAATGCCAAT 480
ATGATGATGA GGGTATTTCG CCTCCCTATC GTAGCGATCT ATTATCTGCT TTATCCTCTG 540
TCTAAACTCT TCACUGGTTT ATCTCGCTCT TTTATTCTGC TGGTGGACAA GAATTATGTG 600
CCTACACAG TAGGGTTGGG GCGCGTAGAT CTGATCATT ATTTGGCAGA AATATGTGCC 660
45 GGAGAAACG AACAGAACGA CTTGACTACC GAAGTGAAGA TCATCCAGAA TGCGCTGGAT 720
TTTTCCGGTA TTCAGTGGG AGACTCCATG ATCCCACGCA ATGAGATGAT AGCATGTGAG 780
TTGCAACCGG ATATTGAAGT ACTCAAAACG ACTTTTATCG ATACCGGTTT GTCCAAAGATC 840
ATTATCTACA GACAGAACAT AGATGACGTA GTAGGATATA TCCATTGCGG CGAAATGTTT 900
CGTGGGCAAG ACTGGCAAAA ACGTATCAAT ACTACTGTAT TCGTACCCGA AAGCATGTAT 960
50 GCCAATAAAC TGATGCGACT ACTCATGCAG CGCAAGAAAA GCATTGCGAT CGTCATCGAT 1020
GAACCTGGAG GTACGGCCGG AATGTCACA TTAGAGGATT TGGTAGAAGA GATTTTCGGT 1080
GACATTGAGG ACGAACACGA CACTCGCAAG ATCATAGCCA AACAGCTCGG CCTCATACC 1140
TATCTGCTCA GTGGTCGTAT GGAATAGAT GATGTGAACG AACGTTTGG GTTGTCTTG 1200
CCTGAGTCTG ACGACTACCT TACCGTGGCC GGATTATCC TGAATAGCCA TCAAAATATC 1260
55 CCACAGCCCA ATGAGTCTGT GGAGATTGCT CCTTATACTT TTACCATTCCT CAGATCTTCT 1320
TCCACCAAGA TCGAATCTGT GAAATGTCC ATCGACGACC AATCGAAC 1368

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(2) INFORMATION FOR SEQ ID NO:41

65 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 897 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

70

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

WO 99/29870

PCT/AU98/01023

28 / 490

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION: 1...897

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41

TTAAAAAGG AGATAACTAT GAAACAGAAC TACTTCAAAA GAGTCTGCTC ACTGCTTTGG 60
CTGGTTTAC CCATGCTTAT TATGCCATTG GAAGTAGCAG CTCAGAGAT TATTCCGAAC 120
GAAGAGGTGT TGAATCATT GACTTTCGTT GCACCGGTTG AGGAGACAGA CGCAATAGAG 180
10 GCAGAGGTAG AAGCTCTGCA GGAGATAGTC GCTACTGAGG AGATTGCGGA GCAGGCTGTT 240
CGTTCTTATA CCTACACGGT CTATCGTGAT GGCGTGAAGA TTGCTTCAGG ATTGACTGAG 300
CCCACTTTTC TCGATGAAGA TGTTCTGTCG GCGGAACATA CCTACTGCGT AGAAGTACAG 360
TATCAGGGAG GCGTATCCGA CAAAGTATGC GTGGACGTAG AGGTGAAGGA CTTCAAACCG 420
15 GTTACCAATC TCACCGGAAC TGCTTCCAAT GACGAAGTTT CTTTGGACTG GGACGGGTGTG 480
GAAGAGAAAG CTGAAGAGCC GGCAAGTGAT AAAGCAGTCA GCTACAACGT CTACAAGAAT 540
GGAACCTTGA TCGGTAATAC AGCTGAAACT CATATATGTT AGACCGGTGT AGCCAATGGT 600
ACATACATCT ACGAAGTGA AGTAAAGTAT CCTGACGGTG TATCTCCGAA GGTGSGCTGA 660
ACCGTGACCG TGACCAACAG CTCATTGAGC AATGTAGATG GACAGGCTCC TTACACATTG 720
CGAGTAGAAG GCAAGAAGAT TATTGCGGAA GCCCATGGTA TGATCACGCT CTACGACATC 780
20 AACGGACGTA CCGTGCCGT AGCCCCGAAT CGATTGGAAT ACATGGCGCA AACCGGTTTC 840
TATGCAGTGC GCTTCGATGT GGGGAATAAA CACCATGTAT CGAAAATACA AGTAAGA 897

25 (2) INFORMATION FOR SEQ ID NO:42

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

35 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORPHYROMONAS GINGIVALIS

40 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION: 1...1131

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42

TTGTTAATC ATAAAAAATC ATGGTATGAA ACATTTCAAT TTTATCTCGT TGTTTCCGC 60
TCTGGCTTTA TTCTTTTGTG TGAATAATACC CTTGCACAAC AAAAAACAGA GGAGTTTGCA 120
CCTGTGTCCG ATTTACGTGC AGAAGCGTAC GGCTCTACCG TTTTCTCCA CTGGACTCCG 180
50 CCGTATGACA ATCCGATGAT TCCTCTAAGC GAGAGTTTTG AATCAGGTAT TCCAGCTATA 240
TGAAGACCA TTGACGCAGA TGGCGATGGC TATAATTGGA TGCATTGAC CAATTTCAG 300
GGACAGAGTG GTCTCTGTGT CTCTTCGGCT TCATACATAG GCGGCGTCGG AGCTTTGACT 360
CCGACAATT ATCTGATAAC ACCCGAATTA AAACATACCCA CAGACGCGTT GGTGAAAATA 420
ATCTATTGGG TATGTAACA AGATCTCACT GCTCCATCGG AGCACTATGC CGTTTATTC 480
55 TCTTCTACAG GCAATAATGC TGCTGACTTT GTTAATCTCT TATATGAAGA GACTTTGACT 540
GCCAAACGGA TACAATCCCC CGAGTTGATC CCGGGAATC GGACACAAGG TGTTTGGTAT 600
CAAAGAAAGG TGGTACTCCC TAACGATACT AAATATGTTG CTTTCCGCCA TTTTAATTC 660
ACGGATAATT TCTGGCTCAA TTTGGATGAA GTATCTATCC TGTATACCCC TCTTCCCGA 720
AGAGCTCCGT GTCCGCATCC GGGTGGTTAC ACTTATCTCT TATTCCGTGA TGGACAAAAG 780
60 ATAGCGAGTG GATTGTCCGC ATTGGCATAT ATCGATACGG ATGTACCGTA TGGGACTCAA 840
GACTATTGTG TCCAAGTCAA TTATCTGCAA GGAGACTCGT ATAAAGTCTG CAAAAATATA 900
GTGGTGGCAA ATTCTGCAA CATCTATGGG GCGGATAAGC CTTTTCGTT GACCGTGGTT 960
GGCAAGACCA TTGTAGCGAG TGCTTTCAAA GGAGAGATCA CTCTTATGA CATTGCTGGC 1020
CGGTGATAG CTTCCGGCTG CGATACGCTT AGGTACAAA GCGAAAATGG TTTTACCTC 1080
65 ATTAATAATC AGGTAAACGG AACTGTCTAT ACTGAGAAA TCCAAATCCA A 1131

70 (2) INFORMATION FOR SEQ ID NO:43

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2547 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
75 (D) TOPOLOGY: circular

WO 99/29870

PCT/AU98/01023

29 / 490

(ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
 5 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS
 10 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...2547
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43
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TTCCGGAATAT	CACCTTCAAT	GAAGAAAGT	TTTCTTTTAG	CCATAGTAAT	GCTCTTTGGC	60
ATTGCCATGC	AGGGACATTC	TGCTCCGGT	ACGAAAGAGC	GAGCTTTGAG	TCTGGCTCGG	120
CTGGCTTTGC	GACAGGTATC	CTTGCGAATG	GGACAAACAG	CAGTATCTGA	CAAGATTTC	180
ATCCGATTACG	TTTATCCGCA	AGGAGATGCT	GAGAGGGGTA	TCACATCACA	AGAGGAAGGC	240
TCCTCTGCAT	ATTTTATGT	AGCTAATCGT	GGAATATATG	AGGGCTATGC	TCTTGATGCA	300
GCAGATGACA	GAATACCGAC	AATTTTAGCC	TATTCACCCA	TTGGCCGTTT	CGACATGGAC	360
AGTATGCCGG	ACAATCTTCG	CATGTGGCTA	CAAAATTACG	ATCAGGAAAT	AGGCCTGATA	420
CTTTCCGGAA	AAGCTCAGCT	CAATGAAGAG	ATATTACGTA	CCGAGGGCGT	ACCGGCTGAA	480
GTACATGCTC	TGATGGATAA	CGGTCAATTT	GCCAACGATC	CCATGCGATG	GAATCAAGGT	540
TACCCATGSA	ACAATAAGGA	ACCACTGCTT	CCTAATGGCA	ATCATGCTTA	TACCGGCTGT	600
GTTGCTACTG	CTGCAGCACA	AATCATGCGC	TACCATAGCT	GGCCGCTTCA	AGGTGAAGGC	660
TCTTTCGATT	ATCATGCAAG	TTCATTAGTT	GGCAACTGCT	CCGGCACATT	TGGTGAATATG	720
TACGACTGSA	TCATATGCC	CGGAATCCC	GACCTTGATA	ATCTGACTCA	ATCTCAAGTG	780
GATGCCATCG	CCACACTGAT	CGGTGATGTG	AGTGCACTG	TTTCGATGAG	TTTTTATGAA	840
AATGGAAATG	GTACGTACAG	CGTTTATGTA	GTAGGAGCCT	TGCGAAACAA	CTTTGCTACT	900
AAGCGTTTAC	TGCAGCTACA	TGTACGCGCC	TTATATACCT	CACAGGAGTG	GCACGATATG	960
ATCCGCGGGG	AACCTTGCCTC	CGGAAGGCCG	GTCTATTATG	CAGGGAATTA	CCAGAGCATA	1020
GGACATGCTT	TCGTTTCCGA	TGTTTATGCT	TCGGATGGTA	CTTTCCATTT	CAACTGGGGT	1080
TGGGGAGGTG	TTTCCAACGG	CTTCTACAAA	CTAACACTCC	TCTCGCCGAC	TTCTTGGGT	1140
ATCGGAGGTG	AGGGAATAGG	TTTTACCAAT	TATCAAGAGA	TCATCACCGG	TATCGAACCG	1200
GCTAAGACTC	CCGCTGAAGC	CGGTACAGAT	GCCTTGCCGA	TCTTGGCACT	GAAGACATA	1260
GAAGCCGAGT	ATAAAAGTGA	ATCCGGATTG	AACGTAGGGT	ATTCGATATA	TAATACAGGT	1320
GAAGAGCAAT	CAATCTTGA	CCTCGGATAC	AGATTGAACA	AGGCTGACGG	AGAAGTCATA	1380
GAGGTGAAAA	CTTCTATCTAT	CAATATCTCT	TGGTACGGAT	ACGGAGAGCA	TCCCGAGAGT	1440
TTCTCATTTG	CACCTAATCA	GTTGTCACAA	GGAATCAACA	CCATCACCTT	ACTTTATCGT	1500
CGCACAGGCA	CCGAACAGTG	GGAGCCGGTA	CGGCATGCAC	AGGGAGGATA	TGTCAATAGC	1560
ATTAAAGTAA	ATACGACAGA	CCCGAACAAT	GTCTAGTCA	CGGTAGATAA	TAACGAAGGC	1620
AAGCTCAGTA	TGCTCCCAA	CAGCTTTGTC	GCAGATCTGA	ATTCTTATGA	ACATAGTACG	1680
ATTACAGTAC	AGTTCAATAG	CGACAGCCCT	GATGAGATCC	GTACACCCGT	AGCCTTTGCT	1740
CTATCTACAG	GAGCTACTGC	GGACGATGTA	ATATCTTTGG	GCTGGGTAAT	GGCTGAAGTT	1800
CCGGGCGGTA	GCAGCAACTA	TCCGGTGGTT	TGGTCTAAAG	ACGTTCTCAC	TCTCTCGGAA	1860
GGCGACTATA	CATTGTGGTA	TAGATTTTCC	ATCAACAACC	AAAAGGATGA	ATGGAAAAAG	1920
ATCGGAAGCG	TGTCAGTAAA	AACACCGACA	GAGTATACGC	AUCCCTTATT	CGAAGTGGCC	1980
CATAATCAAA	CTTCTACCTA	TACGCTGGAT	ATGGACACAC	ACAGAGTATT	GCCCGACTTT	2040
ACACTCAAAA	ATCTCGGATT	GCCTTTCAAT	GGTGAGTTGG	TTGTTGTTTT	CCGCCAAACA	2100
CAATCCTCAT	CGGGGCTTTT	ATGGGACAGT	CAAGAAACAG	TACATATCAA	GCAAGGAGAA	2160
ACTTTGCTAT	ATAAACCTGT	TGTCGAAGGC	CCTATACCTG	ATGGATCCTA	TCGTGCGACC	2220
CTCCATGCAT	TGTAACAGCG	ACAACAACAG	TTGTACCTCA	AGGGGAAAAG	GAATACACG	2280
GTGAAGATCG	TCAATGGTAC	AGCGGTAGAA	GCAATAGAA	CGTCAGAGA	GATCAGAGTA	2340
TTCCCTAATC	CGGCACGCGA	TTATGTGGAA	ATATCGGCAC	CTTGCAATTC	CCAAGAAACA	2400
TCTATCATTC	TTTTCGATCT	GTCAGGCAAG	ATTGTCATGA	AGAATAGTTT	ATCAGCGGGG	2460
CATGGCAGAA	TGGATGTCAG	CCGACTTCCT	AATGGGGCCT	ACATCCTTAA	GTTGGATGGA	2520
TATACGACGA	AAATAAATAT	AGTGCAC				2547

(2) INFORMATION FOR SEQ ID NO:44

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 885 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

WO 99/29870

PCT/AU98/01023

31 / 490

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

5 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION: 1...1026

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46

1	ATCAGGAACA	GAATATGTC	GAATAAATCG	ATCCTTCTGC	TTTGCTGTTT	GCTGTGCTTC	60
2	ATTTCGTCTA	CGAAGGCTGT	GACCCCCCTC	AGAAATGTGC	GCAATAGCCA	AGTGAACAGC	120
3	AAAGCAAAGA	CGAACGTAC	AAAGCCCTCG	GACTCTGTAC	GGTACATTAG	CAACATGATT	180
4	GCAGATCGGC	TGGAGTCCG	CAACAAGATT	TCTTCCGAAA	AAGAGGTAAG	AAAAGCCGAA	240
5	TATGAAAATC	GGCTGGCGAT	GGAAGCACTC	AATTACCCCTG	CCATAGATTT	ATATGGTGAA	300
6	GATTCTTGGA	GCGAGTATGT	AAACCCCTTC	GTGGGTGCAG	GAACCGATGT	CGAAATTCGG	360
7	AACTCCTATG	ACATTGATGT	CTCTTCCTTC	GTGATGCCCG	TGGAAGATAA	GCAGGTCACC	420
8	TCTCAATTTG	GCTACCGTCG	GCGTTTCGGA	CGGATGCACT	ATGGTATTGA	TCTTTCAGTG	480
9	AATCGTGGCG	ATACGATACG	AGCAGCCCTT	GACGGGAAAG	TTCGTGTACG	CAGCTATGAA	540
10	GCAGGTGGGT	ATGGCTACTA	CATAGTCTTG	CGCCATCCGA	ACGGACTGGA	GACTGTGTAC	600
11	GGACACATCA	GTGCGCAATT	GCTAGACGAG	AATCAGATCG	TTCGAGCAGG	ACAACCGATC	660
12	GGATTAGSAG	GCAGCACGGG	TGCAAGCACG	GGTCCTCATC	TTCACCTCGA	GACCCGCTTC	720
13	ATGGGTATTG	CCATCAATCC	GAGTACCATT	ATAGACTTCG	ATAACGGAGT	GCCGCTCCGA	780
14	GCACATTACA	CAATCAAACG	AGGGAGCAAT	TCTCGCTATG	CAAAAGCCTC	TAAGACTTCT	840
15	TCTCGCTATG	CAAAAAAAGG	GAAGAAAGGC	AGACAAGCTT	CTTCTCCTAT	GACCTATAGA	900
16	ATCAAAAAAG	GCGATACTTT	GGAACAATA	GCCAAAGGC	ACGGCACTTC	TGTTCAGAAA	960
17	CTCTGTGCTA	CCAATGGCAT	TGGCAAGAGT	AAATTTTGA	CTCGGGCAA	AGCCTTGAGG	1020
18	ATCAAA						1026

30 (2) INFORMATION FOR SEQ ID NO:47

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 477 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

35 (ii) MOLECULE TYPE: DNA (genomic)

40 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

45 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION: 1...477

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47

1	CCGAGCAAAA	CGATAATTAA	GACAATGGCA	AAAATCAATT	TCTATGCTGA	AGGCGTCAGC	60
2	CTTCTCTCGA	TCAGAAGACG	GATCGTCGGT	AAGTGGATAG	CCGAAGTATG	CAGCCGATAT	120
3	GGGAAAGCGG	TGGGAGAAAT	CTCCTATCTT	TTCTGTGATG	ACGAATATAT	CCTGAAAGCC	180
4	AATCAGGAAT	TTCTCGATCA	TGACTACTAC	ACCGACATCA	TCACTTTCGA	TTCCTGCGAA	240
5	GCGGATACGG	TGAATGGCGA	CCTGCTTATC	AGTCTCGATA	CCGTACGCTC	GAATGCCCGT	300
6	GCTCTTGATC	TTGATACGCA	AGACGAACTG	CATCGTGTCA	TTATCCACGG	CATCTGCAAT	360
7	CTTTGCGGAT	TGAAAGACAA	GAGCAAAAAG	GATGAAGCCC	AAATGCGTGC	AGCCGAAGAG	420
8	AAAGCCCTTG	TCATGCTGCG	AGAAACCATC	GGATCGGAGC	TTTCCCTATT	GCATACA	477

65 (2) INFORMATION FOR SEQ ID NO:48

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1185 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

70 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

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WO 99/29870

PCT/AU98/01023

35 / 490

	ATCAAAGGAA	ATACTGTCGT	GTACGAAGAC	GTAGTACGCC	GAGAGCTTTA	CACAAAGCCC	1260
	GGCCAGCTCT	TTAGTCGCGA	GGATATCATT	AACTCTATTG	GTCTCATCAA	TCAGCTTGGG	1320
	CATTTTCGATG	CCGAAAATC	TATTTCCCGT	CCGATTCCCA	ATCCCGAAAC	AGGAACAGTG	1380
5	GATATAGAGT	ATGATTTGGT	GCCGCGTAGC	AGTGACCAAT	TGGAGCTTTC	TGTCGGTTGG	1440
	AGTCAGTCCG	GACTTCTGTT	CCGAGGAGCC	ATTAAGTTCA	CGAACTTCTC	TGTCGGCAAC	1500
	TTGCTCCATC	CCTCGATGTA	TAAGAAAGGG	ATCATTCCGC	AAGGGGATGG	GCAAACACTA	1560
	TCAGTGAGTG	CTCAGACCAA	TGGAAAGTAC	TATCAGCAGT	ATAGTGTCTC	ATTATGGAT	1620
	CCATGGTTTG	GGGGCAAGCG	GCCGGATATG	TTCAGCTTCA	GTGCATTCTA	TTCCAAGACT	1680
	ACGGCGATTG	ACTCCAAGTT	CTACAATAGC	AATGCCGGCA	ACTACTATAA	TGCCCTACTA	1740
10	AATAGCTACT	ACAACAACCTA	TAATAGTTAT	TACAACGGTA	TGTCGAACTA	TACCGGCGAC	1800
	CTCTATACTC	AGGCCAGCGA	TCCGGATCGT	TCGCTTCAGA	TGTTAGGTAC	TTGGATCGGT	1860
	TACGGTAAGC	GTTTGACTTG	GCCGGACAAT	TGGTTCCAGA	TTTATACTTC	TCTGAACCTAC	1920
	ACCTACTATA	GACTGCGAAA	TTGGAGCTAC	AATACCTTCC	AAAAATTTCCA	TCATGGCTCG	1980
	GCTAATGATC	TCAACTTGGA	GCTGCGTCTC	TCTCGTACTT	CCATCGATAA	TCCTATTAT	2040
15	ACCAGAAGCG	GATCGGATTT	CATGGTTTCT	GTTCGTGCTA	CTCTTCCTTA	TTCTTTGTGG	2100
	GACAATCATG	ACTATGCCAG	CCAGAACCTC	AGCGTAAGCG	ATCGTTACAG	ATTATCGAG	2160
	TATCAACAAT	GGAGTTTAG	AGGACGAGTT	TTTACTCCAT	TGCTCAATCC	TGCTACGCAT	2220
	AAATATACAC	CGGTGCTCAT	GATCCGAGTG	GAAGSAGCAG	TTCTTGGTTC	GTATAATTCC	2280
	AATAAGAAAT	CTCCTTTCCG	TACTTTCTAT	ATGGGAGGTG	ATGGTATGTC	CAGCTATTAT	2340
20	GGTGGCTACA	TGAATGAGAC	TATAGGTTTG	CCTGGTTATA	AGAACGGATC	TATTGCCGGT	2400
	AATAACTACG	ACTATGCATA	TGCTTATATG	CGGCTTACGA	TGGAACTACG	TTTCCCGATT	2460
	CTGTTTGAAA	ACTCATTCAA	TGCGTGGCTC	TTAGCTTTTG	CCGAAGCAGG	CAATGCCGTGG	2520
	CGCAGTATCG	ACAATTATAA	TCCCTTTAAC	CTGAAGCGAT	CGGCCGGTGT	AGGATTGCGT	2580
	GTAACTTTAC	CGATGGTCGG	AATGCTCGGT	ATCGATTGGG	GATATGGCTT	TGACCGTCCG	2640
25	GACAATTCTC	TACAGCGAGG	AGGAAGCAAT	GTCCACTTTG	TGCTCGGACA	GGAGTTT	2697

(2) INFORMATION FOR SEQ ID NO:53

30	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 531 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
35	(D) TOPOLOGY: circular
	(ii) MOLECULE TYPE: DNA (genomic)
	(iii) HYPOTHETICAL: NO
40	(iv) ANTI-SENSE: NO
	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PORPHYROMONAS GINGIVALIS
45	(ix) FEATURE:
	(A) NAME/KEY: misc feature
	(B) LOCATION 1...531
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53

	CAATAAACA	TGAATGGCGA	TATGAAACGG	TTTTTGATTI	TGATCGGCTT	TGCACTGGCG	60
	GTAGCTTTCT	COGGTTTTTC	CCAAAAGTTC	GCTTTGGTAG	ATATGSAATA	TATCCTCAGG	120
	AATATTCCTG	ACTATGAGAT	GATGAACGAA	CAGCTGGAAC	AGGTGTCCAA	GAAATGGCAA	180
	AATGAAATCG	AAGCTCTCGA	AAATGAAGCC	CAATCTATGT	ATAAGAAGTA	TCAGAGCGAT	240
55	CTCGTATTCT	TGCTGCTGCG	ACAGAAGAAA	ACCCAAGAAG	AGGCTATCGT	AAAGAAAGAG	300
	CAGCAAGCAT	CCGAGCTCAA	GCGGAAGTAT	TTCCGCCCGG	AGGGGGAGCT	GTATAAGAAA	360
	CGCTCCGATC	TGATGAAGCC	TATTCAGGAT	GAGATTGGGA	ATGCTATCAA	AGAGATTGCC	420
	AAGCGTAACA	ACTATCAGAT	GGTGCTTGAT	AGAGGTACGT	CCGGAATTAT	CTTTGCCAGT	480
60	CCGTCTATTG	ACATTAGCGA	CCTGTACTG	AGCAAGATGG	GCTTTAGCAA	G	531

(2) INFORMATION FOR SEQ ID NO:54

65	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 510 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: circular
70	(ii) MOLECULE TYPE: DNA (genomic)
	(iii) HYPOTHETICAL: NO
75	(iv) ANTI-SENSE: NO

WO 99/29870

PCT/AU98/01023

36 / 490

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(vi) ORIGINAL SOURCE:
    (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(1x) FEATURE:
5   (A) NAME/KEY: misc_feature
    (B) LOCATION 1...510

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54
10  CGAATAAATA AACACACGA AATGAAGAAA TTTTCTCTCA TGCTTCTGAT GGCTCTTCCT    60
    TTGAGCCTCT TGGCACAAA GGTGGCAGTG GTAAACACTG AGGAGATCAT TTCCAAAATG    120
    CCGGAACAAAG TAGCTGTAC CAAACAGCTC AACGAATTGG CCGAAAAGTA TCGCCTTGAT    180
    CTCGAAGATA TGGACGATGA GTTTGCCAAA AAGACAGAAG AATTGTGAAA GGAAAAAGAC    240
    TCTCTACTGG AGAACATCCG CAATCGTCGT CAGCAGGAAC TTCAGGATAT TCAAACCTCGT    300
15  TATCAGCAGT CATACCAAAC GATGCAGGAG GATTTGCAAA AGCGCCAAAC ACAGCTTTT    360
    GCTCCTATCC AACAAAAGGT GGCTGATGCC ATCAAGAAAG TGGGTGACGA AGAAAACTGT    420
    GCCTACATCA TGGAGGCCGG TATGATGCTT TACACCGGAG CTACTGTAT TGAATTGACC    480
    GCAAGGTAA AAGCGAAACT CGGAATCAAG    510

(2) INFORMATION FOR SEQ ID NO:55

    (i) SEQUENCE CHARACTERISTICS:
25  (A) LENGTH: 2484 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: circular

    (ii) MOLECULE TYPE: DNA (genomic)
30  (iii) HYPOTHETICAL: NO
    (iv) ANTI-SENSE: NO

35  (vi) ORIGINAL SOURCE:
    (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

    (ix) FEATURE:
40  (A) NAME/KEY: misc_feature
    (B) LOCATION 1...2484

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55
45  ATCATGAAGG AAGCTATTCC CCGAAAGAAC AAGTATATAA AGCTCAACGG TATATACAGA    60
    TTGTCATTCA TTCTGCTATG CTGCTCTCAGG CAGCTATGGC ACAAGGCGTC    120
    AGGGTATCGG GCTATGTGCT CGACCGTGGG GAAAAGCCGA TCCCGTTCCG CGGAGTCAAA    180
    GTGCGTGTA CCGGGACAGG CGCAACGACG AATCTGAAGG GATACTACGA GTTTCGGATG    240
    AAGGCCACGA CGGACAGCAT CACGATCGAG TTCAGCTCCA TGGGGTACCA AGGGGTAAGT    300
    CGCAGCTTTC CGTCTCTGAC CAAGGACACT CGGCTGAATG TTCGTTTGGC AGAGGCGGAG    360
50  ATGGAGCTTT CGAGCGTGAC GGTACAGGCC ACAAAACGCA GACTCAACAC GATGGAGCGC    420
    GTCAATACCC GAGACCTTCG TGTCATGCA GGGCCTACGG GAGGGGTGGA ATCGCTCATC    480
    AGTACCTACG CAGGAGTAAC GCAGAACAAAT GAACTAAGCT CGCAATACTC GGTTCGCGGA    540
    GGAAGCTACG ATGAGAATAT GGTCTATGTA AACGGAGTGG AGGTTTATCG CCCGCTGCTG    600
    GTTCGCTCTG CACAGCAGGA AGGTCTGAGC TTCGTCAATC CGGATCTGAC ACAATCCGTA    660
55  CASTTCTCG CCGGAGGTTT CACGGCCGAC TATGGCGACA AGATGTCTC CTGACTGGAT    720
    ATTGCTTACA AGCAACCGCA GGAGAAGGAA GGAGCGGTAC TCCTCGGGAT GCTACAATCG    780
    AGTGCCTACT ATGGCAGCAG TCCCGGAGCC TTCAGCCAAA TCACGGGTGT ACGCTACAAG    840
    AGTGCCAAAT CGCTCTTGGG CACTACGGAC ACGAAAGCCG AATACGATCC GATCTATGCG    900
    GACGACAGCA CATTCATGAC GTACCGTTTC AGCCCCAAGC TGTCGGTTAG TTTCTCGGCG    960
60  AATATTTTGC AACTCGCTA CAAGTTTGTC CCTCAGACCC GTGAGACGAG CTTGCGTACA    1020
    CTGAGCGATG CCAAAAAGTT GAAGATCTTT TTCGACGGTC AGGAACAGA TCGTTTCCTG    1080
    ACCTACTTCG GTGCCCTCAG CATGAACTTC GTGCCGAGCG ACAAACAGCG GCATACGGTT    1140
    ACGCTTTTCG CCTTCAACAG TAACGAACGG GAGACCTACG ATATTACAGG AGAATACTTT    1200
    CTGAACGATG TGCAGCTGGG GCGGACGGA ACTGCTTCGA TGGCTTCGGG CTCAGACAAC    1260
65  TCCAACGCTT TGGGCATCGG GCGCAATCAC GAGCATGCGC GCAACAGGCT GAGCTACCGC    1320
    GTGCTGAACA TGGGTTACAG AGGGGAGATG AAGCTGAACG AGAAGCATCG CCTGCAAGCC    1380
    GGGGTATCGG CACAGATGGA GAAAATAGCC GACCATATCA CCGAATGGGA ACGGAGGGAT    1440
    TCGGTAGAT ACAAACCTACC TCACTCGGAG ACCGTATTGC TGATGTACAA TAACCTATAT    1500
    GCCGATACGC AGATGAGGGG AACCGGCTTG TCGGCATTCT TAAGAGATCG ATTCAACTTC    1560
70  AGCATGGGAG GAGGTACATT TTCTCTCAT CCGGGTATCA GAGCTTCGTG GTGGAGCTTC    1620
    AACAAAGGAT TGCTCTGTCAG CCCACGTATC AGCGTGGGTT ATTCTCCGGA AAGCAACCGG    1680
    GCTTTGTGAC TGCGTGCAGC CGCCGGACTT TATTATCAGG CACCGTTTTA CAAAGAGCTA    1740
    AGGCAGACGC ATAAGGATGC CGAAGGCAAT AACGTGGTTG TCCTCAACGA GAAGATCCGC    1800
    TCTCAGGAGG CTTTTCACAT TCTCGCAGGA GCAGACTATA CCTTCGAAAT GGGGGGGCGA    1860
75  AAATACAACT TTACGGCAGA GGCTTACTAC AAGAGCCTGT TCAACATCAA CCGGTATATA    1920

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WO 99/29870

PCT/AU98/01023

37 / 490

5 ATAGAGAACG TGAAGATCCG CTATCTGGGC GAAACATCG GTTCGGGTTA TGCTGCGGGT 1980
ATCGATCTCA AGCTCTTCGG CGAACTGGTA CCCGAGTGG ATTCGTGGCT GACGGCTTCC 2040
ATTATAAAG CCCGTCAGAA ACTGGATGGC TACGGTTCTT TACCACTGAT GAACGCACCC 2100
ACTTACAAAT TCTCTTCTT CCTTCAGGAG TACGTGCCGG GCAATAAACG CATCACAGCC 2160
ACCTGCGGG CTGCACTAAG CGGAGGATTG CCCAGCTCA ATCCGAGCAA AGGGCTTAGC 2220
TCGCCGGCCT TTACCGCACC GGCCTATAAG CGTGTGATC TGGGGGTAAT GTACAAATGG 2280
CTCGACCCGG ATGACTCTT TGCCGGCCGA AGCAAAATGG TAATGGGAGT AAAAGGGGCC 2340
TACATAGGGG CTGACCTCTT CAATCTGTTC GACATGACCA ACGTCAATTC TTACTACTGG 2400
10 GTGTGCGGATG CCTACCAACA GCAATACGCC GTACCGAACT ACGTGACAGC CCGCCAATTC 2460
AACCTGCGTC TCCTCGTCGA ATTC 2484

(2) INFORMATION FOR SEQ ID NO:56

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2037 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
20 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
25 (iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
30 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...2037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56

35 CCTATCCCTT TTCTTCTTAA TATGTACAGC GGACATCATA AAATCCATTA TCCTTTTCTT 60
ATCCTGTGG TATGCCTTGC TTTTGCTGCC TGCAAGAGCG TGAAGTTGAA AGATGCGGAG 120
AAGGCACATG ATCGCCCAAG GTATACCAAG GCTGCCGATA GTACAAATAC ATTATACAGG 180
CGTACCCGAC GAAAGCAGGT GGAGATGAAA GCTTATACCG CTTCGCGATC CGGTGAAAC 240
40 TATCGTGCGG CCGGCAGACA AGCCAAAGCT TTGCGTGGCT ATCTGAATGC CAGACGCTAC 300
GGGTATCCGG ATTCTGTGGT ACTGCTCCGT TTGGCACAGA CTTATCAGCA AGGAGGTAAC 360
TATAAGGAAG CCGAGGTACT CTTCGGTGGG TATCTGGAAG CTTATCCGAA AAGTTATTTT 420
GCAGCTATCG GTTTGGAGGG GTGCTCTCTT GCCCGCCAGC AAAAGGAATA TCCTACACGT 480
TACCGGATAC GCGAGCTGC CGAGTGGAA TCGGCACGGG GCGACTTCGG CCCGGCCTAT 540
45 GCACCGATG CTTCGGCTCT CTATTTTACA TCGAGCAGAA GCAAAGACGA CGGTTTGGAT 600
AATAGCAGCA TAACGGGACT GAAACCCAAC GACATTATA TCATCAACG AGATGCACAA 660
GGACGATGGG GACGTCCCGA TAGCGTGTCC GGAGGAATCA ACACTCCATG GGATGAAGGC 720
GTGCCAACGA TCACGCCCGA TGGTAGTACC ATATATTATA CGTTGGGCA GCAAGGAGCC 780
GATTACGACC GTACGGTACA GATCTATTCC GCGCTCCGGA GCGGAGAAGG CGGTTGGAGC 840
50 AACGGTTCGC TCGTGGACAT TATGCCCGAT TCGCTCCGTA TGGCTGCTCA TCCCTCTATG 900
TCGGCATCCG GCGATTACCT GTATTTCTGC AGCAATATAC GCGGTAGCTA TGGCGGCAAG 960
GATATTATC GTGTCAAGGT GTGCGGATCGT TCTTATGGTT CACCGGAGAA TTTGGGGCCT 1020
GATATCAATA CGCCGGGGGA CGAAATGTTT CCCTTCATAG ATGGGGATAG TACCCTTTTC 1080
TTGCTTTCGG ACGGACACGC CGGTCTGGGA GGACTGGATA TTTTCAAAGC CACGCTGGAC 1140
55 TCTACCGGCC AATGGCATGT AGTCAATATG GGACAACCGG TCAATTCCTC TGCCGATGAT 1200
TTGCGCTTGG CTGTGGAGCC TAAAGGCAAA AACAAAGAAG AAGCTTTGCC GGACAACGGA 1260
GTCAAAAGTG TATTTTGTTC CAACCGAGGC GATGCACGCG GATGGCCGCA CCTCTTCCAT 1320
TTGAACTGC CGGCTATCTA CACCGAGATT CAAGGTTATG TGATGGACAG AGAAGAAAAT 1380
CCCATAGCCG GAGCCACTGT CAGGATCGTA GCGCAACGCG GCCCGTAGG ACAGGGATTC 1440
60 GTGACTACTC GTGACGATGG CTCCTATAAG ATGAGCGTGC AGGGCGATAC TCGCTATGTA 1500
ATGCTTGCCG GAGCATCGGG TTATTTGAAT CAGTACGTAG AACTCAAGAC CGATACCCCC 1560
AAGCAGAGTG AGACCTACTA TGTGGACTTT TTCCTTGCA TCGCTGAGAA AGCCGAGGGC 1620
TTGCAAAATA TTTTCTATGA TTTCGATAAA GCTACTCTTC GCCCGGAAAG CATGAAGAGC 1680
65 TTGGACGAAC TGATTCGTAT CCTCACGGAC AATCCGGAAT TCGGATCGA ATTGGGTTCC 1740
CATGCCGACA GGAAAGGCCCG CGATGCTTAC AACCTCGGAC TATCTGACCG CAGAGCCAAA 1800
TCCGTGGTGG ATTACCTCAC GAGTGTGGC ATAGCGGCCG ACAGGCTTAC GTGGAAAGGC 1860
TACGGTAAAG CTGTGCCCCA GACCGTGACA GCCAAAATTG CCGAACGGCA CGATTTCCTG 1920
AAGGAAGGCG ATGTGCTCAC CGAGGAATTC GTAGCACCTT TGACCGAGGA GCAGCAGTCA 1980
70 GTCTGGGACC AACTGAACCG TCGTACCGAG TTCCGTGTGA TCGAAGAAGA GTTGGCT 2037

(2) INFORMATION FOR SEQ ID NO:57

75 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2316 base pairs

WO 99/29870

PCT/AU98/01023

38 / 490

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

5 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
10 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
(ix) FEATURE:
15 (A) NAME/KEY: misc feature
(B) LOCATION 1...2316
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57

20 CCTGCACAGC CGAAAACATA TTGCATACGA TACTTTCCGA GAGAGGTATC TCCGAGGAGG 60
CAAAACAGAAA GGACATTGTA TGCGGACAAAG ATGCGCCGGC ATATCGTCAA GTGCTGTCCC 120
TCTGCCTCCA TACTCTTGCA AGAATACTCC ACAACAGAAT TATTCATTCA TCACTTTAAC 180
ATATCAATAA TTATGAAAAA GTTTTCTTTC GCGCTACTAT CGATTGGTAT TTCAGCGCAG 240
GCTTTTGCCA AGACGSACAA CGTCCCGACA GATTCGCTAC GAGTACACAA TCTTCAGACC 300
25 GTCACGGTCT ATTCTACAGC CACGGCCGTA CCTCTGAAAA AGATACCGGC CAAGATGGAA 360
CTCATCTCAT CGCGCAACAT CAAGCACTCC GCTTTAACA ACATGACCGA CATCCTCAAG 420
ACGCAAAATT CGCTCGATGT CATACAATAC CCGGGCTTTA GTTCGAACAT CGGTATCCGC 480
GGTTTCAAGC CCTCCGGCAA GTATGTAACC GTATTGGTAA ACGGCATCCC TCGGGGAACG 540
GACAAATCTT CTACGCTCAA CACGAGCAAC ATCGAACAAA TCGAGATCCT CAAAGGCCCG 600
30 TCTCTTCCA TCTACGGCAC CAATGCCATG GCGGTGTGG TGAACATCAT CACCACACAA 660
TCCNAGGACA AGATCCATGG CAACGTTTCT CTCTCGGCG GTAGCTACCA GACCATGGCC 720
GGATCATTCA ACTTGGGTGG CCGCTTCGAG GATATTTTCT CATTCGATCT TAGTCTGGGC 780
TTGGACAAGC AGAACAAGGA CTATAAGACC GGATCAAACA ATTTCTATC CCTGAGCAA 840
CTGGAAGAAG CTATAGTAGA TGTAAATGCT ACCAAAAACA AGAAATGAA GGGGAGCGAC 900
35 TATACTGTAG CAACGGGACG TCTGCGTTTC GGTATCGACT TCACGCCCA ATGGTCGCTG 960
AATCTGTATG AAACCGTATC CTCTCGGAGT GCGATCCCCG TAGGAGGATC TATATGGGGC 1020
GTTTACGGAG AATCCAAAAA AAATCTGAAT CGTCTTCGA CCTCTTCGA GCTGCTCGGC 1080
AAACATGGCT GCCACAGCTC TCATTTCTCC CCTACTTCA ACATAGAGAA ATCGGAGAAC 1140
40 TATAACAATG CCGATCCACG CGGTTTCATC AACTACAAAA GCGACTACTA CACCTATGGT 1200
GCCCTACTCC AGGACAAGAT TTCCCTTGGG GGACAAAAATA TCGTACTCGG TGTCGACAGC 1260
CGAAACATGA CGATGGAGTC AGAAAGATTG GAGCAGGCAG GAGTGAATAC AAAGCCATAC 1320
AACCCTGGAT ATGCCACGAA CAATATCGGT TTGTTCCGAC AGGCCAATTT CTACCTGCTG 1380
AACGATGCTC TATCGATATC TGCCGGTGCA CGTGGCGACT TCATGTTCTT TGACCTGAAA 1440
45 GCGAACGAGT ATCTCAACAA TGAAGCCAAA CAGGAAACTC ATAACGTAAT CAATCCGAAT 1500
GTCCGAATCA AATATGAGTT TGTGAAAGGC CTTACAGCTC ATGGTACATT CGGTAGTGCA 1560
TTCAGTGCTC CCGATGCTTT CCAAAAAGCA GGCCCAATAC TAGGCCCGTT CGGCACGACC 1620
ATAGGCAATC CTGACCTGAA ACCCGAAAAG TCCATGACCT GGGACTTCGG TATCGGATAC 1680
AGCAATGACG GCTGCGGGAT CCAAGCCGAC GTAACCTTAA CCTATTTCGA CACCGACCC 1740
AAGATCTGA TCTTGTCAG CCCTGACTAT GCTAATAATA TCACCACATA CATCAATGCC 1800
50 GACAAGGCTC GTATGAGCGG TATCGAGGCC CTTTGTGCTT ATGACTTCGG CAGCCTCTTT 1860
GCCAACAAAT TCTCTCTCCG CGCATTTGCG AATGCCACGA TCATGCTCAA TTCGAGATG 1920
AAGAAAAGCC AGACCGATGC CCTTGGAGC GAAATGTACT ACGTTCGCAA GCAGAATATC 1980
ACCTTCGGTA TCGAATATCG TGGCAAGAA GGACTTGAAG TGATGCTCAA CGGTGCTTC 2040
ATGGGACGCA GGATCGAGCA AAACCTGGTAT GCTTACTACC CCGAAGTTCG CCCCAGACTC 2100
55 CAGCAACTGC TTGCAGCAGA AGAGCCTGAA TTGGCTGCTC AGGGACTGCT CCGTCATCCG 2160
CAGCAATGG TGTTCATGC CTCTGCTTAC TACCACATGA ACAAGTATCT CACCTTCGGT 2220
GTGAACCTGA ACAACATCTT GGATGAGCTT TATACGGAGA AAGACGGCTA CCACATGCCC 2280
GGACGTAACA TCATGGGTAA GGTATGCTC AACTTC 2316

(2) INFORMATION FOR SEQ ID NO:58

65 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1452 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

70 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
75 (vi) ORIGINAL SOURCE:

WO 99/29870

PCT/AU98/01023

39 / 490

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58

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10  GGCCGGGCGCT CTTCCCTTAA CAGGCAAATG GATGGCATAC TAAACGATGA ATATAGACAA    60
    GCATCTATGA ACAGGTTTTC AAATCATTGG CCCTGCATCC TCGTGGGGTT TGTACTCTGG    120
    TTTGTATCGG CGAGTCGGAC TGTGGCACA AACGCTCCG AAACGACGGT ATCGTACGAT    180
    ACGGATACCG CCGTACTCTC CGAAGCCGAT GTGCTTCGSA TCGCTCTTAG TGAGAATGCC    240
    ACAGTGAAGG TGGCCGATAT GGATGTGCGC AAACAGGAAT ATGCACGTAG GGCAGCACGT    300
    GCGGATCTCT TCCCGAAAGT AGACCTCAAT GCGCTTTACA GCCATACGCT AAAGAAGCAG    360
    GTCTTATATA TAGATATGCC CCGTTTCAGC AGTAGCGAAG GTATCGAAAT GGGCGGTACA    420
    CACAATACGC AAGGAGGGGT GAACGTCTCC ATGCCATTGG TGTCGGCACA GCTTTGSAAG    480
    AGCATTGCCA TGACUGGAGA ACAGCTCGAT CTGGCTCTGG AGAAAGCTCG CAGCTCCCGA    540
    ATCGATTGGG TGGCAGAGGT GAAGAAGGCT TACCTCAGTG TATTGTTGGC CGAGGACTCT    600
    TATGGCGTAT TCAAGCGCAG CTATGACAAT GCTCTGGCCA ATTATAAGAA CATATCCGAC    660
    AAGTTCGATC TGGGACTTGT GCGCGAGTAT GATAAGATTC GAGCCAAATG ACAGGTACGC    720
    AACATCGAGC CTAACTCTTT GCAAGCGCAG AACTCCGTAG CCCTTGCTCT CTGGCAGCTC    780
    AAGTCTCTGA TGAGCATGGA AGTGGAACCT CCGATCAGAC TCTCCGGTTC ATTGTCCGAC    840
    TATAAAGAAC AAGTCTATAC CCGCTATTTT GCGCGCGATA CGCTTATTTC CAACAACTCC    900
    TCCCTGCGTC AGCTCGATAT ACAGCGTCGT CTGGCTGTCA GTGCAGACAA GCTGAACAAG    960
    TAGAGCTTCC TGCTACACT CAATCTGGGA GGGCAGTACA CCTATTCGCT CAACAGCAAC    1020
    GACATCAAA TCTGGGGCGA GGGACAACGC TGGACGCCCT TCTCCACCAT ATCGCTCAGC    1080
    CTGTACATTC CTATATTCAA TGGAGGGCAA CGTCTGTACA ACGTGAAGCA AAGTGCTTTA    1140
    TCGATCCGTC AGATCGATCT GCAACGACGC CACATAGAGC AATCCATCCG AATGGGAATC    1200
    AAGAACCAAA ATGACCGTCT GCGTACCTGT ATGCAGAGAT TTGTGGCCTC GGAAGAGGCT    1260
    30  GTCCGAAGTG CAGAAAAGGG CTATCAGATA GCACAGAAC GCTATCAGAC AGGCGAAGGC    1320
    ACTCTCGTCG AGCTCAACGA TGCCGATGTG GCTCTTTTGC AGGCTCGACT CAATTATAAT    1380
    CAGGCCATAT TCGACTTTAT GACCGCAAAG GCCGAATTGG ACAAGATGAA CGGCATGGGG    1440
    ATTCCCGAAC AA
    1452

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(2) INFORMATION FOR SEQ ID NO:59

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1620 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59

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60  TTTCATAACT TTGACTTCCT AAACGCTATA AAATTGTTT CGATGGCAAA TAATACTCTT    60
    TTGGCGAAGA CTCGACGTTA TGTCTGCCTT GTCGGTTTCT GTTGGCTCAT GGCATGATG    120
    CACCTCTCTG GCCAGGAAGT CACTATGTGG GGGGACAGCC ATGGAGTGGC GCCGAACCAA    180
    GTGGCGCGAA CGCTGGTGAA GGTAGCCTTA AGTGAATCCC TCCCTCCGGG TGCAAAACAG    240
    ATTCTGTATC GATTCTCTCT TCCGAAAGAA ACGGAGGAAA AAGTCACCGC CCTATATCTC    300
    CTTGTGAGTG ATTCTTTAGC GGTGCGCGAC TTGCCGSACT ACAAGGGGCG AGTCTCTTAC    360
    65  GATAGCTTCC CGATCTCAAA GGAAGATCGT ACCACAGCCC TTTCTGCGGA TTCGCTAGCC    420
    GCACGCCGCT TCTTTTATTT GGCTGCGGAT ATAGGGCCCTG TTGCTTCTTT TTCCCGATCC    480
    GATACGCTGA CTGCCCGTGT GGAAGAGGTG GCTGTGATG GCGGCCCTTT GCCGTTGAAA    540
    GAGCTGTCCG CTGCCCTCCG TCGTCTGTAT AGGGGGTATG AGGCCCTCTT TGTACCCGGT    600
    GATGGCGGAT CGCGGAACCT TCGTATCCCG GCCATTTTGA AAACGGCTAA TGGAACTCTC    660
    70  ATAGCGATGG CCGACAGACG AAAATATAAT CAGACGGATC TGCCGGAGGA TATAGATATA    720
    GTCATGCGGC GCAGTACGGA CGGAGGSAAG TCGTGGAGCG ATCCCGAGAT TATCGTACAG    780
    GGAGAGGGGC GCAATCATGG CTTTGGCGAT GTAGCCCTGG TGCAAAACCA AGCAGGAAAG    840
    CTCCTGATGA TCTTTGTGCG TGGAGTAGGC CTGTGGCAGT CTACCCCGCA TCGTCTCTAG    900
    CGCACTTATA TATCGAAAG TCGGGACGAA GGACTGACTT GGTGCGCTCC TCGGATATA    960
    75  ACCCATTTCA TCTTCGGCAA GGATTGTGCC GATCGGGAC GCACTGCTG GTTGGCCTTC    1020

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WO 99/29870

PCT/AU98/01023

40 / 490

5 TTTTGTGCTT CGGGACAAGG GCTTGTGCTG CCATCCGGTC GTATCACGTT TGTGGCTGCC 1080
 ATCCGCGAAT CAGGGCAGGA GTACGTCTTG AACAACTATG TCCTCTATAG CGACGATGAG 1140
 GCGGATACAT GGCAGCTTTC CGACTGTGCA TACCGCCGTG GCGATGAGGC AAAGCTTTCA 1200
 TTGATGCCCC ATGGCAGGGT ACTGATGAGC ATACGCAATC AGGGACGGCA GGAGAGCCGA 1260
 CAGCGTTTCT TCGCTCTCTC CTCCGACGAT GGCCTTACTT GGGAGAGAGC CAAGCAGTTC 1320
 GAGGGCATCC ATGACCCCGG CTGTAATGGA GCTATGCTTC AAGTGAAAAG GAACGGAAGG 1380
 GATCAAGTGC TGCACCTCCT GCCTCTCGGC CCGGATGGGC GTCCGATGG AGCTGTCTAT 1440
 CTCCTCGATC ATGTCTCCGG CCGCTGGTCC GCTCCCGTTG TTGTCAATTC AGGATCGACT 1500
 GCCTACTCGG ATATGACTCT GCTGGCGGAT GGAACGATCG GTTATTTCGT CGAAGAGGGC 1560
 10 GATGAGATCT CATTGGTTT CATTGCTTC GTCCITGAGC ATCTCTTCGA TGTCCGGCAA 1620

(2) INFORMATION FOR SEQ ID NO:60

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 879 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
 20 (ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
 25 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS
 30 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...879
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60
 AAGTCTCCGA GCGATTCCGC TTGCGGTCG GTATGGAGCG CGAATACAAT ATCTGGACTC 60
 GTCGGTGGGA AACGCATTAC TTGCTTATC CTGTATTCTA TGGCGATAAG AAGTAGTAAT 120
 ATAGAATCAA TACAGTGCTT TGTGATGAAA AAAGAAAAAC TTTGGATTGC GATCGTCGCC 180
 GGTTTGGCTT TCGTATTGGG CCTTTATGCT CTGCGCGCA GTGTCGCTCA GCTACGCCGC 240
 40 TCTCAGCCTT CGGTGACTGT GACCGGTATG GCGAGCGTA ATTCAAAATC CGATCTGATC 300
 GTTTGGACTG CTTCTACCA GCTCCAGATG ATGGATCTCG AATCGGCCTA CAAGGCTTTG 360
 AAGGAAAAAC AGATATTGGT AGCAGACTAT TTGAAAAACA AGCAGCTGCC CGATTCTGCT 420
 TATATCTTCT CAAGCGTAGC CATCTCTAAA GAATACAACT ACTATTACGA TCCTCGGCAG 480
 GAACAAAACG TCAGGACCTT TGCCGGGTAT CTGCTCAGCC AGACAGTTAC GGTGACCTCA 540
 45 CAGGACATCG AATATGTGGA GAAAAATATC CGCGATATAA CCGAGCTGAT CAATCAGGGG 600
 GTAGAGATTA CCTCCGACCG TCCGGCCTAT TACTACACCA AGCTCAATGA TCTGAAGGTC 660
 GAGATGCTGC GCAATGCCCT CGAAGACGCT TTCAATCGTG CTTGGGTCTT TCGGAGGGGG 720
 AGCGGTTCCT CCGTGGGTAA GATGCTATCT TCTTCGATGG GCGTGTTCGA GATAGTGGGG 780
 50 CTCAACTCGA ACGAAGATTA TAGCTGGGGA GCTTCGTTC AATCGTCTTC CAAGATGAAG 840
 ACGGCAAGCA TAACGGTTAA GGCTTCTTTC GCTTTGAAG 879

(2) INFORMATION FOR SEQ ID NO:61

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 840 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
 60 (ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
 65 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS
 70 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...840
 75 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61

WO 99/29870

PCT/AU98/01023

41 / 490

5 GGGAACTCC AATGAAAA AACAAATGCA ATTATCGCCT CAGCCCTCTT GGCTTTAGGA 60
GCCGTCGGCT GTAAGAAAA TGCTGACACT ACCGCTGTCA GTGAAAAGGA TAGCATAGCC 120
TTGTCCATGG GTATTTTGTG CGGACAGGAT TTTGCCAATC AGTTCGAAAT GTCCCGCTTG 180
CAAGGCCAGC CGATTGATTC GGTAGCTTTC TTGGACGGTT TCAAAATATGG TATCGATACG 240
ACGCGCTTCT CGTACAATCT GGGAGCCATC TATGCTTCCA ATATAGCTCG TCAGCTGGCT 300
CATGATTCCA TCATATCGA CAAGTTCTAT GCAGCCATGC GTGCGGCTCT TCTTAAAGAC 360
ACCGTATCTA TCGCCATGAA GCCTGCAGAT GCACAGGCTT TCATGCAACG AATCCAAGCC 420
AAAAAGCAGC GAGAAAAA TATGAAGCAG TTTGGCCAGA ACATCGAAAA GGGTAATGAA 480
TACATCGATA CCTTTAAAA AGAAGATGCT GTAACGTGTA CGACAACTGG TCTGGCATAC 540
10 AAGACTCTTC ASGAAGGTAC GGGAGCTACT CCCTCTTTGG CCGATACTGT ACGTGTCAAG 600
TATGTGGGTA CTCTGGTCGA TGGTAAAGAG TTCGACAAAA ACGAAGAAGG AATCGAATTT 660
GCCGTTACCG GTGTGATTAA AGGCTGGACG GAGATGCTCC AACTCATGAA GGTGCGTCAG 720
AAAGTTCGCG TGGAATCCC ACAGGAGCTG GCTTATGGGG AGACCGGCAA CTATACCATC 780
15 GAACGTTCT CTACCTGAC GTTCGAGATG GAACCTATCG GGATCAAGCC CGGAAAAAG 840

(2) INFORMATION FOR SEQ ID NO:62

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2409 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
25 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
30 (v) ORIGINAL SOURCE:
(A) ORGANISM: PORPHYROMONAS GINGIVALIS
35 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2409
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62

40 TGTGGAAGC AGAAGCTCTC AAACCCGAAG AGGAGCCGGT ATCCGTGCAG ACGGATATCA 60
TTCCGACAAA GCGATAAGAA TCCGATGAAA GTATTACGGC AAGTATTCCT CCCCATCTTT 120
TTTGTCTTAC TGACAGGTGC CTGCTCCACC ACAAGAATC TGCCGGAAGG CGAACAGCTG 180
TATATCGGAA TGGGCAAGAC ACAGATACTC CGGCAGGACA AGAGCCACGC CGGCCAACAG 240
GCTCTGACCG AAGTGGAGAG TACACTGAAA GTTACACCCA ATGGAGCTAT TTTGGGCACT 300
45 GCAAGTGCCT CCTTACCCAA GATACCATTC GGGCTATGGC TATACAACAG CTTCGTGGGG 360
GATTCCACTG TCATTTCGAA ATGGATATTC GACAAGTTTG CAGCCCAAGCC GGTTCCTATC 420
AGTCAGGTCA AATCCGATAG CCGGGCTAAG GTGGCGACGA ACATCCCTCG CGAACACGGG 480
TACTTCGATG CTAAAGTAAA AAGCAGTGTG ACCACTCTGA AAAAGGACTC GCTCAAAGCC 540
AAATCTCCT ATACGGTGGG TATGGCTCTC CCTTATCATT ACGACAGCAT CATTCCTTTA 600
50 CCGATCAGCA CTTTCCCGCA CAGCATTCTG GCTTACAGGC AGACTCCGTC TTTGATCAGG 660
AAAGGAGACC AGTTCAATTG GGCAAGCTG CACGAAGAGC GTCAGACCAT CAGTGCCCTG 720
CTGAGAGACA ATGGTTACTA CTAATTCGCG CCACAGGATA TTATCTACGA AGCCGATACC 780
CTCCTCGTAA GAGGTGCCGT ATGCTTGCGA GCCAAGCTCT CGGAAGATAC TCCACCCCAA 840
GCCATGCGCC CGTGGAGGAT AGGGAACCGG ACAGCAGTCC TGCTCGGAAT GAACGGAGAA 900
55 AGCCCGACAG ACTCGCTCGA AGTGGAGGAT ATGAAAGTCC TTTACTATCG TAAATGCGG 960
GTTCCGCCCC AGATTTTGGC CAAACGCTTT CGTTTCTTCT CCGGCAATCT GTATCGGCAG 1020
AAAGACGATG AGACGACACG CAAATCCTTG GCTCGTTTGG GAGCCTTCTC CGTTATCGAT 1080
CTCAATTTT TGCAACGCGA TTCCATTTCC GGCCTTTTGG ATGTGCGACT GCTAACCCAC 1140
CTCGACAAAC CTTGGGATGC ATCATTAGAG ACCTTGTTCA CGAGCAAAAG CAATGACTTC 1200
60 ATCGGTCCCG GACTGAATTG TGCTCTTGCT CGGCGCAATG TATTGCGCGG AGGAGAAAT 1260
CTTCTTGGGA ATATCGGTGG ATCGTATGAG TGGGAGACCG GCAATCGTCC CGAAAATAGC 1320
AGCAATCGGC TGATCGATAT AATTCGTAC AACATGAATA CGGCCGTGAA CCTCTCGTTT 1380
CCCTCGATTG TATTTCCCGG TCTGCTGGAT AAATACTATT ACTACCCAC GACTACGACT 1440
TTTCAGGCTT CTGCCACCGC GCTGAACAGG GCACACTACT TTAGCATGTA CTCTTCGGGC 1500
65 TTTTCGACCA CCTACGAATT TCAGCCCTCC AAGGAACACC GGCATGCTAT TTTCCCGCTC 1560
AAGCTCAACT ACAACCTCCT GGGGCATCAG ACAGAACTT TCCAGGCCAT TACGGCGAAC 1620
TAAGCTATG TGCTGCTCAG CCTTCAGAGT CAGTTCTTGG CTCAAATGGG GTATATCTAT 1680
ACGTCAACA AATCCGTTTC AGAGAAAAGT CCTCATCATC TTTGGATGCA ATTCGGACTA 1740
TCCGAGGCAG GCAATCTCCT GAATCTGATC TATCTGGCAG CCGGCAAGAA GTACAGCGAC 1800
70 ACCAAGAAAT TCGTCGGCGT CCCCTTCTCT CAGTTCTATCA AAGCCACGGG AGAAGTGGC 1860
TATTCCTATA CCATAGACCG CAATCAGTCA CTGGCAACCC GTTTCGGGAC AGGCGTGATA 1920
TATAGCTATG GCAATATGCG AGTGGCAACC TATAGCGAGC AGTTCTATGT AGGCGGTGCC 1980
AATAGTATCA GAGCTTTCAC CGTCCGTAGC ATCGGCCCGG GACGGTTCAA TCCGATATCC 2040
GACAAACAGT ATTCCTATTG GATCAGGTG GCGGAATCA AACTCGAAGC CAACGTGGAA 2100
75 TATAGAGGCA AGCTTTTCGG GGATCTCCAC GCAGCCGTTT TCCTCGATGC GGGCAACGTT 2160

WO 99/29870

PCT/AU98/01023

42 / 490

5 TGGCTCTTGA GGGAGGATTC TTCCCGTCCG GCCGGTGCTC TGTCCGAAGT GGGATCGGTG 2220
AGCAATTTCC TGAATAGCAT CGCTCTCGGC ACCGGTGTGC GCCTTCGCTA CGATCTGGCA 2280
TTTCTCGTGG TTGCTGTGCA GTCTCGGCTTC GGTCTCCACC TTCCTTACAA TACGGGTAAG 2340
AAAGGTTACT ACAATATCCC ACGCTTTAAG GATGCCATCG GTTCCATTG GGTGTGCGC 2400
TATCCCTTC 2409

(2) INFORMATION FOR SEQ ID NO:63

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2349 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 15 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 20 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORPHYROMONAS GINGIVALIS
- 25 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2349

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63

30 TCTCTCTCCG CGTATATCCG TTTCTCTATG TCCTCGCATT CCGTTCGGTA TCTAATCGGC 60
ATTGCCGGCT GCTTGCTCCT CATGCTTGCT TCCTCCTGCT CGGTACCCCG TTATGTGCCG 120
GACGGTAGCA GACTATTAGA CAGGGTAACG ATCGCAAGCG AAACGGGCAG TATCGCTCTG 180
CCGGAAGATA TTCCGGGACTA TACCTCCAG CAACCCAATT ACAGACTGTT CGGGATGACT 240
CGCTGGCTAC TCGCGCTCTA TAGCAGCTCG AATCCGAACA GCAACAGCTG GTGGAACCGT 300
TCGCTCCGGA AATGGGCGGA ACCGCTGTC CTCATCGATT CTGTCCTCAC CGATCGTACT 360
GCCAACCGTC TGGCAAAGGC GATGGCCGGC GATGGCTTTC TCGATGCTAC TGCTCGTGCC 420
GTGGTAGACA CCGGCTTGTA CAAGAAAGCT CGCATTACTT ATCTGATTCA GCCCGGAAGC 480
CGTTATTATA TAGCCAATAT GGCTTTGGAT GTGAAGAATC CACTCCTTCC TCCCGTTGCG 540
CTTGGCAATT CGCTTCCTTC GGCATACAAG GTCGGSAACA GCGAGGGTTC TCCCTTGTCG 600
CCCATCGTAC TCGATGAAGA GAGAAAGGCG ATAGCTCGTC ATATGCGCAA CAACGGCTTC 660
TGGAAGTTCT CCGCCGAGGA TGTATTATG GAAGCAGATA CTACCGTTTC AGGAGGATCG 720
GGTACGAAAT CTGCCGATCT GAAATTAGTG GTCAATGGCA TCGGGCGTTA TCCATATCGG 780
ATCGGCAGGG TATTCCTTCA TGCCGATTAT GATCCTCTCG AATCGGACTT CAGAGTTTCA 840
GAGCTTGCAC GTATCGATTG GATTTCGCGT GGGGATTACA CTGTTTACTA TGGGAGTAGG 900
GGAGCTTATA TCCGGGCATC GGCTCTCAGC CGGTTCGGTG CCGTTACACC GGGAGCTTTT 960
TTCTGCGAGG ATGATGTGGA ACGCTCTTAT ATCAAGCTGA ATGCGCTCCC TATCGTTCCG 1020
AACGTGAATA TCGGATTTGT GGAGCACAAT GGTAAGGATG AGATTGCTCT GCGGATAGC 1080
TCTCGCCTTG TGGACTGTCT TATTCTTACC GTTCGGGCA AGAGCAAATC GTTCGAAGCC 1140
GAAGTCCTCG GCACCAATTC CGCTGGAGAC TTCGGGCGCG CTTGCTCTCT CCGTTTCAAC 1200
GATCGCAATT TGTTCGTGG GGCAGAGATG TTCATATCA AACTCAAGGG TGCTTACGAA 1260
GCCATTCCGA AGGTTTCGCA CAGCTTCATG GAATATGGGG TGGAAAGCTC GCTCCGTTTC 1320
CCTCGTCTCC TCTTCCCATT CATTTCTGAC GAAACGCGCC GCGGCTACG GGCATCCAGC 1380
GAATGGAAGA TCGGGTATAA TTACAGACA CGTCGGGAGT TTGATCGGGT GATTCTCTCC 1440
GCTCAACTCA ATTATTATG GCAGACCTAC CTGCACAATC GTCTGCGTCA TACGATCCGC 1500
CTGCTGGATG TCGATTATCT CCATCTCCG TACATCGATC CCGACTTCGC CCAATCCCTT 1560
CCGCTACGGA CTGCACTGTA TAACTACAGC GAGCAGTTTA TCTCGGCTC GGCATATATA 1620
CTGAACATA CCAAGCTTC GTCCATGGAG CGTACCGTAT CCAATCCTTT TACGGCACGG 1680
TTCAGTATCC AGACAGCCGG CAACCTGCTG CAAGCCATTT CTTATCTGAC CGATTCTCG 1740
AAAGACGAAC ACGGGTTGTA TAAATGTTT GGTCTGCACT ATGCTCAGTT CGTCAAGCTC 1800
GATCTCGATC TGGCTAAAC CGTTCTTCTC GAAAAGGACA ATACTTTGGC ACTGCATCTG 1860
GATTTCCGAC TGGCTTTCCC TTATGGCAAT GCTCGCCATA TACCTTTGA GTTACGTTAC 1920
TTTGCCGGAG GATCGAAGC CGTTGCGGCG TGGAGTGTCC GTACCTTCG CCGGGGAGT 1980
ATGAAGATGA CTCCGGACAA GACCTTCTTC GATCAGATGG GTGATATCG TCTGGATCG 2040
RATGTGCAAT ACAGGACAAA GCTGTTCTGG AAGTTTCGCG CAGCAGCTTT TGTGATGCC 2100
GGCAATGCTT GGACGATAAA GAGATATGAG AATCAGGAGG ACGGTCTCTT TCGTTTCGAT 2160
CGCTTCTACA AGGAAATAGC TTTGGCCTAC GGTCTGGGCG TTCGTCTCGA CTTGATTAT 2220
TTCCTTGTGC GGCTGGATGC CGGACTGAAA GCCTACGATC CTCAGCAGAC AGGGCGTTAC 2280
AAATGGGCTA TCACAGCGCC AAACCTTTCT TCCATATTCG CTGCGCACAT TGCAGTAGGC 2340
TATCCGTTT

(2) INFORMATION FOR SEQ ID NO:64

- 75 (i) SEQUENCE CHARACTERISTICS:

WO 99/29870

PCT/AU98/01023

43 / 490

(A) LENGTH: 2625 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

5 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

10 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORIPHYROMONAS GINGIVALIS

15 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2625

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64

21	GTCSAATCTA	AATTGTTATG	TCTTATGAGA	AAAAGAATTC	TACAACTTTT	CCTGACCGCA	60
22	TTGCTGCTGG	CATTAGGCTC	CTCTCTCGCC	ATAGCGCAAA	CAGTGGTGAC	CGGTAAGGTG	120
23	ATCGATTGAG	AAACGTCGGA	ACCGCTCATC	GGTGTATCCG	TAAGCACCGG	TCAGGAGGCA	180
24	TCCCTCCGCG	GTGTAACCCAC	CGATATGGAT	GGTGGCTTCC	GATTGGAAGT	ACCGGCCAAA	240
25	TCTGTCTTGA	CTTTCCGTTG	CGTAGGTTAT	GCTACCGTAA	CTCGCTCTAT	AGGCAGAGGT	300
26	TCTCAAGAAG	ACCTCGGTAC	GATTCTCCTC	GATCCCCAGG	CCATGGGCTT	GGATGAGATT	360
27	CAGTAATAG	CCTCTGTGGT	GCCCAAAGAC	CGTATGACGC	CGGTACCCGT	TTCCAATATC	420
28	CGTGTGGCTG	ATATTGAGGC	AGCATCGTTG	AATGTCGAAT	TTCCCGAACY	GGTTAAATCC	480
29	ACTCCCTCTA	CCTATACGAC	AAAAGGAAGC	GGAGGTTTCG	GTGATGGTCG	TACCAATGTG	540
30	CGTGGATTGG	ACACTTACAA	CTTCGGTGTA	CTCATCAACG	GAGTTCCTGT	CAATGGTATG	600
31	GAAGACGGGA	AAGTATATTG	GAGCAATTGG	AGTGGTCTGA	TGAATCAAGC	CAGTACCATT	660
32	CAGATTGAGC	GCGGACTCGG	AGCCTCCAAG	CTCGGTATCA	GCTCGGTAGG	TGGTACGATG	720
33	AACATTATCA	CGAAGACTAC	GGACGCCAAC	ACCGGAGGTT	CGGCTTATGT	CGGTATGGGT	780
34	AATGATGGAT	TGCACAAAGA	ATCGTCTCC	ATTTCTACGG	GTATGAACGA	CGGTGGGGCT	840
35	ATCACCATTG	CAGGCTCCCA	TATGACGGGT	CTGGGTTATG	TGAAGGGGCT	GAAGGGACGT	900
36	GCATTCTCTT	ACTTCTTCAA	CGTTTCGAAG	AAGTTCATATG	AACGTCATAC	CCTCTCTCTT	960
37	ACCGGATTGG	GTGCACCCCA	ATGGGCACAA	CAACGTTCTT	CCAAATATTC	TGTAGCCGAC	1020
38	TATGACAAAT	ACGGCATCCG	TCACAATCAA	TCCTTCGGCT	ATCTGCGAGG	CGAAGTGAAT	1080
39	CCTACGGGCT	ATGCTTACAA	TACGTACCCAC	AAGCCCCAGT	TCTCGCTGAA	CCACTTCTGG	1140
40	AAGATGGATG	AAAATACCTC	TCTTTATACG	GCANCTACG	CATCTTTGGC	TACCGGTGGA	1200
41	GGTCGTCCGG	CTTATGGAAA	GAACAGTAAG	TGGGTATTGA	TCAACTACAA	CACCGGACAA	1260
42	CCCTATGAAC	AAACAAAGGT	GACTCCCGAT	GGACTTATCG	ACTACGATGC	CGTACTGGCT	1320
43	GCCAATGCTG	CGGCGAGCAA	TGGCTCGGAA	GCAATTTTTC	CCCTTGGCTC	CAACTCTCAC	1380
44	AAGTGGTTCG	GTCTACTCTC	TTCATTCAAG	AAGAACTTAA	ATAGTTCGCT	GACTTTGACA	1440
45	CCCGGATACG	ATGGGCGTTA	CTACCGTGGC	GACCACTATG	ACAAGATCAC	CGATCTGCTC	1500
46	GGCGGTAGCT	ACTACATAGA	GGATCCCAAG	ACAAAGCTCG	CATACCATGC	GGAGGTGAG	1560
47	CAACTGAAAG	TGGGTGACAT	TGTAAATCGG	GACTACACAG	GCGAAATCAT	GTGGCACGSC	1620
48	CTCTTCGCAC	AGATGGAGCA	TTCGTCCGAA	TGGATCGATG	CATTCGTATC	AGGATCTATC	1680
49	AACTACGAAC	TATACCGCAA	TCACAATAT	GGCGGTAGCA	AGTCCACGGG	CTACCTGCCC	1740
50	GGCGTATCGC	CGTGGAAAAG	CTTCCTTCCG	TGGAGTGGCA	AGGCAGGTCT	GAGCTACAAG	1800
51	TTCGCACAGG	GACACAATGT	ATTCGCCAAT	GGCGGTTTCT	TCACACGTGC	ACCACTCTTT	1860
52	GGCAATATCT	ATGCTGCGGG	GGCTATCATT	CCCAATGACA	AAGCCAATAT	GGAAAAGGTG	1920
53	CTACAGGAG	AGGTGCGGTA	TGGATTACAG	AATCACAAAA	ACTTCGAGTT	CAATATCAAC	1980
54	GGATACTATA	CGAAGTGGAT	GGATCGCGTG	ACCTCGAAGA	GAATCGGAAA	CGAGTATGTT	2040
55	TATCTCAATG	GCGTTGATGC	TGTTCACTGT	GGGGTAGAGG	CTGAGGTCAG	CTATCGTCTT	2100
56	ATTGCTCAGA	TGCACCTTCG	CGGTATGTTT	TCTCTCGGTG	ACTGGACTTG	GCAAAACAAT	2160
57	GTAAGTTACA	CTTCTTACGA	CGAAGCCGGC	AATGAGACAG	GGCAGGATAT	AACCTATATC	2220
58	AAGSGTCTTC	ACGTGGGAGA	TGCAGCACAG	ATGACGGCTG	CTGTATCGGC	AGACATAGAG	2280
59	CTGTTCAAGG	GTTCCTATGT	CATAGGTAAG	TACAACTTCC	TTGGCAAGAA	CTATGCAGGA	2340
60	TTCAACCCCG	CAACGCGTAA	TGCACAGCAG	TACGAAGCGG	ATGGCAAAGA	AATCGTGGAA	2400
61	TCATGGAAGT	TGCCCGATGT	AGGTCTGTTC	GATCTGTCTG	CATCCTACAA	TTTCAAGCTT	2460
62	GGTTCACTCA	GCACCACTAT	CTATTTCAAC	ATGGACAACG	TAGCCGACAA	GCGATATGTG	2520
63	AGCGATCCCG	ACGACAATAT	CATCGGTAAG	AAACACGATG	AGGCTTCGGC	TCTCGTATGG	2580
64	TACGTTTTCG	GCCGCACTTG	GTCTACCCGT	ATTGCTGTAA	ACTTC		2625

(2) INFORMATION FOR SEQ ID NO:65

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

70 (ii) MOLECULE TYPE: DNA (genomic)

WO 99/29870

PCT/AU98/01023

45 / 490

5 TTAATACTT CTCTGCTCC GGATGCGGGC ACAGGTTATA CATTGGATGC AAATGGCAAG 840
GTAACGGCAC TACGGATTGT TACCTATCTG AATGAGCGCG ATAGCAAAGG GGCTACGGTA 900
GAGGTGCGCAT TGCCTCGTGT GGATGATGGC ACCCTTCCTC CTCGGAATT CGGTCCGGAG 960
CTTTATCGTT TGCCTTTGCC GGACAAGATC CTGCGCAATC ATTGGTACAA GTATGAAGTC 1020
GAGATT 1026

(2) INFORMATION FOR SEQ ID NO:67

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 987 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 15 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 20 (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 25 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION: 1...987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67

30 AACCTTAGGA CACAGCCTTT CTTTTGGTA GATTGCAAT CTATGATCAG AACGATACTT 60
TCAGGATATG TATCCTCGAA CTTTGGAGT CCGGGAGCTA CCTTTTTTTT CACGATTTTC 120
CCGSCCTTCA TCCTCGCCGC TACTGCTTGG CCGGCTTGTG GAGGGGGTAC TGCTTCAGGC 180
TCCGATCGTA CGCTGGCTGT GACCATCGAG CCACAGAAAT ACTTCATCGA GTCCATTGCG 240
GATAAGTCGG TGCAGGTGGT GGCATTGGTA CCGGCCGSCA GCAATCCGGA GGAATACGAC 300
CCTTCGCCTA CGGTGATGAA GCGTTGTGCC GAAGCAGATG CCTACTCTA TATAGGAGGA 360
CTGGGGTTCG AGCAAAGAAA TCTCGCTGCC ATTCGGGACA ATAACCTTAA GCTCCCTCTT 420
TTCGAAATGG GCAAAGCCTT GCGGATGCC GGAAGTGCAG ATCTCCACGG CTCCTGCACA 480
GATCATTCTC ATACAGACCT GCATGCCCAT GATCCGCACT ATTGGAGCAG TGTGGTAGGG 540
GCAAGGCGAC TCAGTCGTGC TGCATACGAC GCGCTTGTGG AGCTTTATCC GAACGAGAAA 600
GACAAATGGG ACAAAAGGCA CGACCGTCTC AACGGACGTA TCGACAGCGT GAAGAGACTC 660
GTGATACCCA TGTTTGCCAA TGGCAAAGCA GACAAAGCCT TCGTCATATA TCACCCATCG 720
CTCAGCTTTT TCGCCCAAGA GTTCGGCCTG CCGCAGATCG TCATAGAGGA AGATGGGAAA 780
GAGCCTACGG CTGCCACCT TCGTCGTGTG ATCGATCAGG CACGTGCCGA TGGTCTCAGA 840
45 ATCGATTTTA TCCAACCCGA ATTTGAAACG CSTCAGGCGG AGGACATCGC ACGCGAGATC 900
GGTGCTCGTC CGGTAAGGAT CAATCCTCTG CGCAGCTCGT GGGAGGAGGA AATTTTACAT 960
ATTGCTCGCG CTTTGGCTCA TGAACGG 987

(2) INFORMATION FOR SEQ ID NO:68

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2634 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- 60 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 65 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION: 1...2634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68

75 GCAGATTCTA TTCGATATCC TCTTTACTTT TTTGGGCGGA ATCGGAAGAA ATGCTTTAGG 60
GAACCTATTC CCACCTTATA CAATAAAMAC ATGATCGGAA AAAAAATCTT TTTTATCCTG 120
CTGGCGCTCA TTGCGTTTCA TGGGCTGAAC GCAGCGACAG ACCTGAGTT CAAGTACCCG 180

WO 99/29870

PCT/AU98/01023

46 / 490

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5  ACCGATGCCA ATATCATCGG TCACGTCAAA GACAGCAAGA CGGGTGAACA CCTTGTGCGT 240
   ATCACTATTG CTATCAAAGG CACTACCTTT GGTACATCTA CAGATGCAAC CGGGCACTAC 300
   TATCTTCGTA ACTTGCCTCC GGGTGAGATC ACTTTGATTA TGGGTGGCAT GGGCTATAAG 360
   AGCCAGGAGC GCGTAGTCCG CGTAGAAAAG GACAAGACTA TCGAGGTGAA TTTCGAAGCA 420
   GAAGAGGATG CCATCAATCT GGACGAAGTC GTGATTTCCG CCAACCGCGA ACTGACCGTT 480
   CGCCGTCTTG CTCTACTCT GGTAAATGTA TTGAACGAAA AAGTCTTCTC GCAAGTCAAT 540
   GCTTCTAACG TGGCTCAAGG CTTGTCTATC CAGCCGGGAG TTGCTGTAGA GAACAACCTGT 600
   CAGAAGCTGT GTTTCATCA AGTTCGTATC AATGGACTGG ATGGTCTGTA TGCACAGATC 660
   CTCTATGACA GCCGTCCCAT CATGAGTGCC CTTGCCGGTG TTTACGGTCT GGAGCAGATC 720
   CCTGCCAATA TGATCGAAGC TGTGGAGGTA GTACGTGGTG GAGGATCGGC CTTGTACGGT 780
   TCTTCTGCTA TTGCCGGAGT GGTGAATATC ATCAGCAAGG AACCTTCTCA CAATCTCTTC 840
   ACATTCAATG AATCTCTGAG CTTTACCGGT TTCAGCAAGC TGGATAACAA CACGAACCTC 900
   AATGCCJCCA TCGTCAGCGA TGACAACCGT GCCGGTGCCA TGGTATTCGG GCAGCCTCGT 960
   TACCGCAACC ATTGGGATGC TAACAATGAC GGTATTTCGG AATGGGTAA AATAGATGCC 1020
   CGCTCGCTGG GAGCGCATTC TTATTTCGCG TTGAGCGACT ACAGCAAATG GACGGGAGAG 1080
   TTTCACACGA TCAGTGAATT CCGCCGTGGT GCGGATCGTA TCGATTTCGC TCCTCACGTA 1140
   GTGGGTGTAG CTGAACAAC TGACCATAGC GTATTTAGCG GAAACTTGAA ATACGATCTC 1200
   TTCTCTTCCA ACTATAACA CCACTTCCAG GCTTATACTT CCGGACAGAT CGTAAATCGC 1260
   AAGAGCTGTG ACGGAGGTAT CGGAGAGATT GACGTCAATG GCCACCCCGG TGGTACGGAA 1320
   GGCTACCCCTA TCCCTCAAGA TCAATACGGC AATAATTATG GCGTGACCAA AGGCAAGACA 1380
   TATATGGGCG GTATCCAGTA CAGCTACGAC TTGGACAAAT TCCTCTCAT GCCTTCGCAA 1440
   CTTTGTTCGG GAGCGAATA TACGCGTGTG GAATCAATG AATGATGCC CATCCTTTCA 1500
   TGGCAGACCG GCGAGGATGC CAATGGGAAT ACCATTCCCC TCTATCCCGA ATTGGATCAG 1560
   AATATCAACA ACTACAGCCT ATTGCGTCAG AACGAATGGA AAAATGACAG ATGGAGCATC 1620
   CTGTGTGGCG CTCGCTTGGG CAAGCATAGC GAAGTCAAGG ATATGATTCT GAGTCCCTCGT 1680
   ACCACACTCG GTTTCACGCT GAATCCGGAC ATCAACCTGC GCGCTACATA TGCAAAAGGG 1740
   TTCGCGCAC CGCAGGTATT CGATGAAGAC TTGCACGTAG CGGTTGTAGG CGGTGAGGCA 1800
   CAGAAATAT TCAACGATCC GAACCTCAAG CCTGAAATTT CTCATGCATT CAGTTTGAGT 1860
   GCCGATATGT ATCATCGTTT CCGTAACGTC CAGACCAACT TCCTTGTTGA AGGCTTCTAT 1920
   ACTCGTTTGC TGATGTATTT CACCAACGAG GAGCAGCGTG ATCAGCACGA TGGATCAAAA 1980
   CGCTACACGG GTATCAACGG TAGCGGAGCC AAAGTATTGG GTCTCAATCT GGAAGGTAAAG 2040
   TCGCATACA AGTCTTCCA GCTCCAAGCC GGTCTTACCC TGGCCAGCAA CAAATACGAC 2100
   GAAGCACAGG AGTGGGGTCT GAATACGGTG AAAGACACCA ACGGAGCTTT TGTACCGAG 2160
   GCGAATGCAA ATGGACAACA GGAATACVAG AACGAATCCA TGACGGATAC GCAGATCACC 2220
   CGTACCCCA CCGTATACGG TTATTTTACT TTGGCTACA ATCTGTCTCA CTCATGGAAC 2280
   ATAGCCCTTA CCGGAGCATA TACCGGTGAG ATGTATGTAC CCCACGCTAT CGAATATGGT 2340
   GTGAAGTCTG CCGAATCGGA TATTATGCAG AACAACTCTG AGATTACCGA CGAATCCGGA 2400
   AAGGCTCCCG GTATTGATGA GCTGAAGAAG ACACCTGCAT TCTTCGATTG GGGCTTGAAA 2460
   GTGGGTATG ACTTCCAGGT ATTCCAGGCT ACTGAGGTTT AACTCTATGT AGGTATGAAC 2520
   AATATCTTCA ACTCTTTCCA GAAGGACTTC GATCGTGAGG CTCGACGTGA CAGCGGATAT 2580
   ATCTATGGTC CTACGACGCC GCGTACAGGC TACATGGGCT TGGTAGTGAA GTTC 2634

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(2) INFORMATION FOR SEQ ID NO:69

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 618 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
- (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...618
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69

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70 AAACAGATAG TTATGACAGT AAAGCGCGCA GTGCGAATAG CACTTCTCAC GCTGATAGGC 60
   ATTCTTTTTT CTTACCTTTC TCTTGTTCGG GCGCAAAGTC TTTTCAGCAC CGAATATGTC 120
   TTGCAACTAT ACAACAAGAT ACTCTATGGA GAGTCGGCGG CGGATACCGT CGCAGAGAAA 180
   ACGGCAGGTG AGTCGGCAAT TCCTTTTATA GACAAACTCA TCAATCTCGG CCGCACTTTC 240
   CTCGGCAAAAC CATATCGCTA TCGCGGTCCCT TCCCCTATGC CGATGGACTG CTCGGGCTAT 300
   GTGTCTTACC TCTACTCCAA ATTGACATC AAACCTCCAC GTGGTGGCGG AGCAGAGAGC 360
   CAATATACGA ATCCTATCGA GCGCGAGGAT GTTCGTCCGG CCGACCTCCT TTTTTCAAA 420
   GGCCGCAATG CAGCGAGCAA CCGTATCGGG CATGTAGCTT TGGTGGTATC TGTGATGAA 480
   GATGATATTA CCATGATGCA CAGCCGCAAT TCGCGAGGGA TCGTGATCGA AAACTCAAT 540

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WO 99/29870

PCT/AU98/01023

47 / 490

CGCAGTGCAT ACTTCTCCCG TCGCTTGGTG AGCTATGGCA GGGTACCCGG AGCCAAGAGA 600
GTGATCCAC GAAAAAGT 618

5 (2) INFORMATION FOR SEQ ID NO:70

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1401 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70

AAAGGTACGT	GGATAGAAA	AAACCGAAGA	GAAGAAATGA	AACGGACAAT	CCTCCTGACG	60
GCACTGACCG	TCCTATCTTC	GCTCTCCTTG	CTTCGTGCAC	AAATGAATC	CGAAGCATCA	120
ACCAATCCGA	TGTCAGGCCT	CTCCCTGGAA	GACTGTATCC	GGATAGCCAA	GGAGCGCAAC	180
CTGAATCTGC	GCAGACAGGA	GATCGAACAA	GAAACCGGAA	TCATTAGTCT	CGATGCAGCA	240
CGACACAGTT	TCCTGCCCTC	GGTCAATGCA	GGCATCGGAC	ACAACTATAG	CTTCGGACGT	300
TCGAAAGACA	AAACGGGAST	AACCGTAGAT	CGCTCCTCGA	TGAATACCAA	TCTCAGCATC	360
GGAGCTTCGG	TGGAAGTATT	CAGCGGCACA	CGTCGTCTGC	ACGACCTCAA	GCAGCAAAAG	420
TACAACGTGG	AGGATGGTAT	AGCCCGACTT	CAAAAAGCGC	GTGAAGACCT	CAGCCTGCAA	480
ATCGCGGCTC	TCTATATCAA	TTTGCTCTTC	CGTCAGGAAA	TGACTCGTAC	GGCAGAAACA	540
CAGTTGGCAC	TGATTCGCGA	GCAACGCAAT	CGCACGGCCG	AAATGGTTCC	CGTAGGTAAG	600
TGGGCAGAGG	GTAAGCTCCT	CGACATAAAT	GCCCAGATGG	CCAAGGACGA	ACAACTTCTC	660
GTACAATATC	GTTCGGAGGA	GGAGCTGGCT	CGTCTGGACT	TGGGGCAAGC	CCTCGAACTG	720
GAGCACCCCG	AAAGCATTCG	AGTCAAGGCT	CCCGACACAG	ACGTTCTCGT	AGCAGAAAGG	780
TTGGGATCTC	TCCTTGCTCC	CGAAGAGATC	TATCGCACGG	CTCTCGGCTT	GAAACCGGCA	840
CTGCATTGCA	CGCAGCTGCA	AATAGCTTCG	GCACGCGAAG	GTCTGGCCTC	GGCTCGTGCG	900
GCATACITCC	CGACGCTCAG	CCTCTCTGCC	GGATACAGCA	ACGGTTACTT	CCGCGACCTC	960
GGCAAGGAGT	ATGCGGCCAT	CAACCCCTCC	TTCTCGGAAC	AGTGAAGAA	CAACGGCAGC	1020
TACAGTATCG	GACTCTCTTT	GAATATCCCC	ATCTTCTCTG	CCATGCAAA	GCAAGATCGC	1080
GTTCGGAGCA	GTGCGCTGCA	AATACGCTCA	AGCGAGCTTC	GACTCGTCTG	AGAGAAAAAA	1140
GCCCTCTATA	AAGAGATCAG	GCAAGCATAC	AGCAATGCCG	TGGCAGCCGA	TAAGGCCATC	1200
GCAGCAGCCG	AAAACAGCAA	GGCCGCTACG	CTCAAGGCAT	ACGAATACCG	TCCGCGACAGC	1260
TTCCAGGCAG	GGCGCTTGTC	TGCCACAGAA	TATGCCGAGG	CAAAAACAAA	ATACGCCCTC	1320
AGCCAAGTGG	AAGAACTTCG	TGCCAAGTAT	GACTTCATAT	ACAAAGCCAA	AGTTTGGAT	1380
TTCTATCAGG	GCAAGACTT C					1401

55 (2) INFORMATION FOR SEQ ID NO:71

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1353 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1353

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71

WO 99/29870

PCT/AU98/01023

50 / 490

5 AACAAATACCT ATCCGATACT ATGGTCTGAC ACAAATACGA CAAAACAGGA CCTTGAGACA 1680
TCAAGAATGA TTTCACCTTC CTTTGAGTTA GCCTCCCAAC TTGGGGCTAC TCTCCCGATG 1740
CCCTATCTCG AGTATTGGCC AGGGACATCA TATCTCCTTG ACTATTCGGG AAATAATAAT 1800
AATAAGAGAT ACCGCTTGTT TAATTGCGCT TTTTACTGG AGAAAAGAAA AGTAAATAAC 1860
GAAGAAATTA AATTCGATGA CTGGCGTTTG CCGACAGAAG CTGAGATCAA ATTGATAGAT 1920
AAGCTGCAAC ATAATGAGCA GAGTGTCTGC CAAGCTATCA TGACAGGGAA TTATTATTGG 1980
GATAGTTACT CTGCAAAATGG GTCTTATAAA ATGCAAGGAG GAGGGGGCCA AGGAAATTC 2040
TCCAAAGCCT ATGTTCTGTT CGTGCGGGAT GTGAAAAGC CGATTCTGTA CAAGAAGTCA 2100
GGTAAG 2106

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(2) INFORMATION FOR SEQ ID NO:74

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3936 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
20 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
25 (v) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...3936
30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74

35 AAGAGGGTAG ATAGCTATGA ATGCAGACAA AAAGCTTGCA AATGTGCAAT TTGTGTGATA 60
CAAAAATTTA CTAATGTAAA ACTAAATGAT ATGCGAAAAA TTTTGAGCTT TTTGATGATG 120
TGCCTCTCTG ATTTAGGTCT ACAATCTCAG ACTTGGCATG GAGATCCGGA CTCAGTGGCA 180
GCCCTACCTT CTATCGGTAT TCAAGAGTCA AGTTGTACCC GAATCACGTT CGAGGTTGTT 240
TTCCCGGAT TTTATAGTGT GGAATAACGA GAAGGCAACC AAGTCTTTCA CGCGATTTC 300
ATGCCGGTGT GTGGCTCGTT TGGGAATCTG GCGGAAGCTG AATTGCTCTT TTTGAAAAAG 360
ATGATAGCCG TTCCGGAATT TTCAACAGCT AACGTTGCTG TAAAAATCAA AGAGACGGAG 420
ACATTGACAA ATTATAATAT CTATCCTAAT CCTACCTATG TCGTAGAGGA GTTGCTGAG 480
GGGGGGACTT ATCTGGTAGA GGCTTTCGCG ATAACAATG ACTATTATAG CCAAAATGTA 540
AGCCTCCCTT CTACTACTA TGTCTATTCT CAAGACGGGT ATTTGCTC ACAAGATTT 600
45 ATGAAAGTTA CCCTGTATCC TTTTCGATAC AACCTGTCC GACAGAAAT TCTATTGCA 660
AAAAAATCG AGGTTACAAT AACTTCGAT AATCTCAGC CACCTTTACA AAAAAACACC 720
GGCATATTTA ACAAGTAGC CTCTCTGCA TTTATTAAAT ATGAAGCTGA TGGCAATCG 780
GCGATAGAAA ATGATATGGT GTTCAGTCTG GGTACAACAA CGTACATAAG CGGAAATGTT 840
GCCAGCAACC TCCCTCAGAA CTGTGACTAC TTGGTTATTT ACGATGATAT GTTCAACGTA 900
50 AATCAACAAC CACACGACGA AATCAAAACGG CTGTGCSAAC ATAGAGCCTT CTACAACGGC 960
TTTGATGTAG CTGCTGTAAG TATAAAGGAC GTATTGAATA GCTTCCATC AATGCCCACC 1020
TCATACATCA ACGAAACTAA ACTGAAATAT TTCATTGCT CAGTTTACAA CCAAGCAAT 1080
GCCAAGAGGA CTTTAGATGG CAAACTGGGA TACGTGCTAC TGATCGGAAA ACCATTGAGC 1140
AATATTTGG CTGACACTGA TAATACAAAA GTCCCAACCT CTTTTATTCA TAATGTCTCC 1200
55 TTAATTCCAA GTACCCAAC TTTTGGTCC ATATGCGCCT CCGACTATT TTTTAGTTCT 1260
GTTTCGCCCC TTGATCTGT CGGCGATTG TTTATCGGTC GATTAGCGT CACCAATGCT 1320
CATGAATTGC ACAATCTGAT TGAAGAAGCT ATCAACAAAG AAATCTCTA TAATCCTATT 1380
GCACACAAAA ATATTCTTA CGCAGAAGGG AAAGGCTGCG ATGCTCCAAT CTTACGTTTA 1440
TTCTTAAAG AAATCGCCTC TGGTTACACA GTCAACTCTA TCTTAAATC TAATCAGGTC 1500
60 TCTGCAATAG ACTCGATATT TGACTGCTTG AATAATGGTT CCAATCATT TATTTTAAC 1560
ACTCATGGAA TGCCGACTGT TTGGGGGATA GGGCAGGGAC TCGACGTCAA TACTCTAACA 1620
GCCCGATTGA ACAATACATC TTCCAGGGA TTATGTACGA GTCTATCATG TAGTTCGGCT 1680
GTAGCAGATT CAATATTAG ATCGCTTGA GAAGTCTGA CCACATACGC ACCTAACCAAG 1740
GGATTCTCGG CTTTCTTAGG AGGAAGCAGA GCCACCCAAAT ATGCGGTTA TTTACAGGC 1800
65 CCTGTCTCT CGTCAGAATT TTATGAATAT TTACCTTATT CTTTATATCA CAATCTCTCG 1860
ACTGTTGTTG GCGAAATGTT GTATCATCC ATTATCAATA CTAATTCTGT TGATACGTAT 1920
TGGAAATTC AACTCAATTT GCTTGGCGAC CCGCACTAA ACATTATGGC TCATGGCATG 1980
GAGGTTAGTA ATTGTATTAC ACTACCAAC AACACCAITA TAAGCAGTCC GATAACATA 2040
AANAATGGTG GCTGCCTAAA AATACCGGAA AAAGGAGTTT TGCTTTTAC TAATATGGC 2100
70 TCCATACAG TCATGTCCG AGGAACCTCT GAAATAGGCA ATCAGGCTAA AATATCCGA 2160
GAGACCGGTG CTACCCCCAC CTTTATTACC GTTTACGGCG ATGGCTTGC GATTAAACAAG 2220
CAGGTAGAGA TAGACAATAT AGACCGACIT AACTTGTITT CTACGCATTG GGTATGCC 2280
AATTTTCATT TTGACAGTGT GAAATCAAC AGTGCCCGCG TGTATACAC GAATGTATT 2340
GTGGAGATAA GCAATTGCGA ATTTACCAAT CGAAGTGACA TTATTTCAAA GAATTGTGAC 2400
75 CTAGCGTTG AAAACAGTAT GTTAGCAGT TCGGGGATAA CGGTATTCAA GCCTATGGCT 2460

WO 99/29870

PCT/AU98/01023

51 / 490

5 ACAAGCTCCA TCACCGGATT ATCTACAAAA GCAAAGAITA CCGACAATAC TTTTGTGCG 2520
 ACAGGAAACT TCGCCTACCA TATCACAAC ACGCCAGGCT TAACAGCAAC CTCCAATGCT 2580
 GCCATCAAGT TAGACAATAT TCCTGAGTAT TACATTTCGG GTAATAAAAT AGTCAATTGC 2640
 GATGAGGCTC TTGTACTAAA TAATAGTGGC AACAGAACGA ACAGACTCCA CAATATCACA 2700
 CGGAATGTGA TAAAAAATG TAGGATTGGG AGCAGGCTTT ATAATTCCCTA TGGTATTAC 2760
 AACCGAAATA AGATCAGTAA CAATCATATA GGAGTACGTC TCCTCAACAA CAGTTGTTTT 2820
 TATTTTCGATA ATGCTCCTGT AATCAATGAA GAAGATAAGC AGACGTTTAT TTCTAATAGG 2880
 ACTTGGCAGC TCTATTATC AAACGGTACA TTCCCTCTCA ACTTCCATTA CAACAGCTTG 2940
 CAGGCGGAG ATACAGATAC ATGGATTAC AACGACAGT ATACGAATCG CTATATTGAC 3000
 10 GTTTCAAATA ATCACTGGGG CAACATGAT TTGTTTGATC CGAATCAGGT TTTCAATACG 3060
 CCAGACTTGT TCATTTGGAT ACCTTTTGG GATGGATTGC CAAATGGGAG ATCGGGCAAT 3120
 AGCTCTGCTG AAGCAGTAGA ATTCCAAACA GCATTGGACT GTATTGGCA TAGCCATTAT 3180
 CTTTCGGCAA AAGTGGCTCT CAAGATGATG GTTGAACCT ACCCGGAATC CGACTTTGCA 3240
 ATAGCTGCTT TGAAGGAAT GTTCAGGATA GAGAAAATGT CAGGCAACGA TTACGAAGGC 3300
 15 TTGAAGATT ATTTAGATC CAATCCAACC ATCATCTCTT CCCAGAACTT GTTCCCGACA 3360
 GCTGATTTC TGCTCGCGG ATCGGATATT GTGTGTGAAA ACTATCAGTC TGCCATCGAT 3420
 TGGTACGAAA ATCGCTTGA TAGTGAAATC TCCTATCAGG ACAGTGTITT TGCACTCAT 3480
 GACCTTGTGT ACATTTATG GAATATGCAG TTAGACTCAC TCAGAGGGAC TGGTATAGAT 3540
 TGAACATAC TTTCTGTGA ACAAGGAAA TCGCTCGAAA GCCATCAAAA TGTAAAAAAT 3600
 20 TATTTGTGT CAACCTCTCC CGAATCAACA GGTACTCTCC TGCCTCCATT AGAATGCAAC 3660
 AAATCAAGCC TTGATAAATC CAAGATAATC TCTATTTCGC CCAATCCGGC GAAAGCTGTT 3720
 GTAACAAATA TCTACTATAC CGATAACCTT TCCTGTTCTG TAATAAAAAT ATATGGAATA 3780
 AATGACCTT CCGCTGATAT AACCGGGTTG CCCAACATC TATCCGAAGG TTATTACAGC 3840
 ATACAGTTCA ATACATCCAA CTTTGATCCC GGTTCATACC TGGTAACGCT AAATGTTGAT 3900
 25 CAGAAAATTA TAGATACGGA AAAATTACGA ATCAA 3936

(2) INFORMATION FOR SEQ ID NO:75

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2814 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
 35 (ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
 40 (iv) ANTI-SENSE: NO
 (v) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 45 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...2814
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75

50 TCAGAAAATT ATAGATACGG AAAAATTACG AATCAAATAA TGGCTATCAT GATGAAVAGT 60
 ATTGTTTTTA GAGCATTCTT AACGATTTTG CTCTCGTGGG CAGCGATCAC GAATCCGACT 120
 GCTCAAGAGA TCTCAGGCAT GAATGCATCC TGCTGGGCTG CTCCGGCTCA ACCGGATACT 180
 55 ATCTTATATG AAAGTTTTGA GAATGGACCT GTTCCCAATG GCTGGCTTGA GATAGATGCT 240
 GATGCTGATG GTGCCACTTG GGGGAAGCCA TCAGGCTCTT TCTCTGTACC TTACGGACAC 300
 AATGGCTTT GCACCTACTC CCATATACGT TCCGGTATCT CAACAGCGGG CAACTATCTG 360
 ATTACACCCA ATATAGAAGG AGCCAAACGG GTCAAGTACT GGGTATGCAA TCAGTATAGT 420
 ACCAATCCGG AACATTACGC AGTAATGGA TCGACAACGG GGACTGCCAT TGAAGACTTT 480
 60 GTTTGTTGTT TTAGATATTC CATAACAGGG AAACCGACTC CTCTGTATG GCGTAGACGA 540
 ATCGTGGACT TACCGGAAGG GACCAATAT ATTGCATGGC GACATTACAA AGTACCCGAC 600
 TCACACACAG AATCTTTGAA ATTGGATGAT GTCACTGTGT ATAGGTCGAT CGAAGGGCCC 660
 GAACCTGCTA CCGACTTCAC AGTAATCAAT ATTGGTCAGA ATGTGGGACG ATTGACTTGG 720
 AACTATCCGG AGGATTATCA ACCGGGAAGGA AAGGGGAATG AAGAGTTGCA CCTTAGCGGC 780
 TACAACATCT ATCGGAACGG TACACTACTG GCACAAATAA AAGATGTCTC CATACTGGAG 840
 65 TATGTGGACA GCCTTACTC TTTGCGAGAC AATCCCTTSC AAGTGGAGTA CTGCGTTACA 900
 GCCGTTTACC ATGAAAGCAT AGAATCTTCG ACCGTATGTG CCAAGCTGTC TTACGCCACG 960
 GATGCTACCG TTTATGAAA TTTTGAGAA GTGACCTGTT CCAATGGTTG GCTTGTGATA 1020
 GACGCTGATG GAGATGGATT TAGCTGGGGA CACTATTTGA ATGCATACGA CGCTTTTCCC 1080
 70 GGCCATATAG GAGGCCATTG CTCTTGTCTG GCTTCTTATG TTCCGGGTAT AGGCCCGGTG 1140
 ACTCCCGACA ACTATCTGAT TACCCCAAG GTTGAAGGAG CCAACCTGT CAAGTACTGG 1200
 GTAAAGCAGC AGGATGCCAA TTGGGAGCGG GAACATTACG CGGTGATGGC TTCGACAACG 1260
 GGGACTGCTG TCGGAGATTT CGTCATATTG TTCGAAGAAA CCAATGACAGC GAAGCCGACC 1320
 GCGCATGGT ATGAAAGAAC CATCAACTTA CCTGAAGGGA CTAATACAT CGCATGGCGG 1380
 75 CATTAACCT GTACCGATAT ATATTTCTTG AAGTTGGACG ATATCACTGT ATTCGGGACT 1440
 CCTGCATCAG AGCCCGAACC TGTACCGAT TCCGTTGTCT CGCTTATTGA AAACAACAG 1500

WO 99/29870

PCT/AU98/01023

52 / 490

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GGACCATTAAGTGGGAATTA TCCTAACGGC TACGAACCGG ATAAGACTGA TGATAAAGAC 1560
CCATTGCAGC TTGCCGGCTA CAATATCTAT GCAAACGGCT CGCTCCTTGT TCACATACAA 1620
GACCCGACTG TTTTGGAGTA TATCGATGAG ACTTATCTT CACGAGACGA TCAGGTGGAA 1680
GTGGAAATAT GTGTCACTGC CGTTTATAAC GACAATATCG AGTCCCAATC GGTTTGCGAT 1740
AACCTGATT ATGATTCTCA ATCGGACATT ATCTTATATG AAGGCTTGA GGCCGGAAGT 1800
ATTCTGAAG GCTGGTTGTT GATTGATGCT GATGGCGACA ATGTTAATTG GGAATATTAT 1860
CCTTGGACTA TGTATGGACA TGACAGTGAG AAGTGTATTG CATCCCTTC GACTTACCG 1920
ATGATTGGCG TTTTAACTCC GGATAACTAT TTGGTTACAC CCAGACTCGA AGGAGCCAAG 1980
CTTGCAAGT ATTGGGTAAG TGCGCAAGAT GCTGTTTATT CGGCTGAGCA TTATGCTGTG 2040
ATGGTTTCTA CTACGGGAAC TGCTGTTGAA GATTTGTGCC TCTTGTTGCA AGAGACAATG 2100
ACCGCTAAGG CTACCGGTGC ATGGTATGAG CGAATATTA CATTGCTGCG AGGAACAAA 2160
TATATTGCTT GGCGGCATTA TGATTGCACC GATATGTTT TCTTGCTCTT GGATGACATT 2220
ACGGTTTATC GTTCTACTGA GACTGTTCCT GAGCCTGTTA CTGATTTCGT TGTCTCCTT 2280
ATTGAGAATA ACRAGGGTCG CCTGAAATGG AATTATCCTA ACGGCTACGA ACCCGATAAG 2340
ACTGATGATA AAAAACCATT GCAGCTTACC GGCTACAACA TCTATGCAAA TGGCTCGCTC 2400
CTTGTCACA TACAAGACCC GACTGTTTGG GAGTATATCG ATGAGACTTA TTCTTCACGA 2460
GACCGTCAGG TGGAAATGGA ATATTGTGTC ACTGCCGTTT ATAACGACAA TATCGAGTCC 2520
CAATCGSTTT GCGATAAGCT GAATATGACT ATCAGATCCT TGGATAATAT TCAATCTGAT 2580
ACAAGCTTGA AATATATCC TAATCGGCA TCGTATGTGG TAAGGATAGA GGGATGAGT 2640
CGGAGCAAGT CGACAATCGA GTTGATTAAT GCGCTGGGAA TTTGCATATT AAGGGAAGAG 2700
ACTCATTGAG AGAAAACGGA AATCGATGTT TCAGCTCTCA ATGACGGAGT CTACTTGATT 2760
AAAGTAGTCG GTGGAAATAA AACAACAACC GAAAGGTTAG AGATAAAGAG GCCG 2814

(2) INFORMATION FOR SEQ ID NO:76

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1818 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76

ATAATCTTCT GTACGATTCA TCACTCTGAG TTGGAAATAA TGAACAGCAT CATGAAATAT 60
CAATTATATA CGGCGCTCAT AATGGCTCTC TCTGTATCAT CCGTTTGGG TCAAAACCCCA 120
CGAAATACAG AAACCAACAG CCCCGACAGG CTGCGCAGGG AGCTTACTAT CGTTAATGAC 180
CAGACTGTGG AGATGGAGCA TGCGGATCCG CTTCGGCTG CATACAAGGC CATCGAACCT 240
CGATTAAAC CTTCCGTCCT GGAATATAAC AAGCGTACAT TCGGATTGTT CCTGAAGTT 300
TCCTCTTCA GACAGGAACAA TCTTCCGAAT ATCCTGCCGA CGGAAGGTCA TATGAAGCAC 360
CGGGGGTACC TGAATATCGG TATCGGCCAT ACGCTAAACC AGCGAATGGA TGCCGGCTAT 420
CGTCTGATAG ATGAGAGGCA GGAGAGACTG AATCTTTTCC TCTCCTATCG TGGGATGAAA 480
TCGGCTTTCA ATACCGGTGA CTTCGACGGC GACAGAAAGG ATAGACGAAT GATGGCAGGA 540
GTGGACTACG AGCAGCGCAG GCCTTCTCTT GTGCTTGCTA CCGGCTTGTA TTATTCGAAC 600
CATTATTCCA ATAACACGG ACGGGGAGCT ACCACCAATG TGGGCAGCAT CCTCAGCTA 660
TCGACACCTG TTAATCTCTA GATGGACAAC GGGACCCACA ACGTCCGTGT ATACTTGGGT 720
GCAAAATAAT ATGTGATCGA TGCCAGGATC GACTATCGTT TCTTCCGTTC TATTCCTAT 780
CTGGGTACCG ATCCGATGAA GGCTCTCACA GAACATACGC CTGAAGTGA CGTGACGATG 840
AGTAATGAGT TGTCCGATGA TATTAAAGCTC GGTGTGCAAG TTCTGACGGG AGGATTGTTT 900
TTTGCCAAAA ACAGCGAAAT GATTCAAAAG GCGGTTCTGT CCGAAACCGA CCGCAACCTG 960
TATTATGTTG AGGGCGCGCC CACAATCGGA TTGTGCGGAG ACTCGGACAA TATGCAATGG 1020
AACATACAGA CCGGAGTAGG GATTTCCTCC CATTTCGGAG CCAAGGGAG GTTGTTTTTC 1080
TGGCCTAAAC TGGATGCTTC GCTTAGTATC TTCCCTTCAT GCGCTGTGTA TCGGAAAGCC 1140
TTCCGCGGTG TGATTGGAAT TGSTCTCGCC GATGTTATG AAGAGGAGAT GCCTACCTG 1200
ATGCCCAATA CGATTGTACT CCTTCGCGC AATGCTTTGA CCGCCCAATT AGGGGTGAAG 1260
GGGAATATAG CCGATGTGCT ACGTATGGAG GTTATGCGG ACTTCTCCAA GCTGACAGGT 1320
GTGCTTTTCT ATACTCCGAC TCTACCCTTA TATAATCCAT CCGACTTGTA TCAGTATAAT 1380
TGAGGTTTCT TGCCGATATA TGCCGACGGC ACGCGCTGGC GCGCAGGTGG TAAGCTGGAA 1440
TACTCTTATC GCGATATGCT CCGCTTCTG GTAGACGCAT CCTATGGCAA GTGGAATTG 1500
GATGGAGGAC TTGTCGCTC CATGCAGCCC GATCTTATAT TGAAGGCAGA AGTAGGTGTT 1560
CATCCCATTT CCCCATTTGA TGTGAGACTC CGGTATACAC AGCTGAACGG ACGGTATCGG 1620
TATTCTTTG GCTCGGCTG CTGGAAGGCC TTGGGTATCG GTAATGTACA TCTTCTTAGT 1680

WO 99/29870

PCT/AU98/01023

54 / 490

5 GCGATCGATA TAGACGAGTT CGACACCATG CCCGGGAGCT ACAACAGCT GATCGTATGG 300
 GATCCGCGAA ACAAGGCTAT ACTCGGAGGC TACCGCTTTA TCTATGGGCG GGACGTTGCT 360
 TTCGATACCG ATGGCAAGCC TTTGCTGGCA ACGGCAGAGA TGTTCGCTT CAGTGATGCT 420
 TTTTTCGACG ATTATCTCCC CTACACAGTC GAATTGGGAC GTTCGTTCTG GTCCGCTCCAG 480
 TACCAATCGA CACGGATGGG CACAAAGGUC ATTTTGTGCG TGGACAATCT TTGGGACGGT 540
 ATCGGAGCAC TCACTGTAGT CAATCCAGAG GCACCTCTAT TCTATGGCAA GGTGACCATG 600
 TACAAAGACT ATGATCGGCG AGCTCGCAAT CTGATCCTGT ATTTTCTTCG CAAGCACTTC 660
 TCCGATCCGG AAGGCTTGGT CAAGCCTATT CATCCCTAC CGATAGAGAT CAGTGCGGAG 720
 GACGAAGCCT TGTCTCTCTC ATCCGACTTT GACACCAATT ACAAGACTCT CAATATAGAA 780
 10 GTGCGCAAGC TGGGTATCAA TATCCCTCCT CTCGTGAGTG CATATATAGC TTTGTCTCCG 840
 GAGATGCGTG TTTTCGGCAC TGCAGTGAAT GAGTCTTTCG GAGAGGTGGA GGAAACCGGC 900
 ATATTCTATT CTGTGGGTAA GATCCTGGAA GAGAAAAAC AACGGCACAT AGAGAGCTTC 960
 ATCTCAGCC GGAACGAAA AAAAGGTCTC GACAGTAGCA ATGCCCGATC A 1011

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(2) INFORMATION FOR SEQ ID NO:79

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1698 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

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(ii) MOLECULE TYPE: DNA (genomic)

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

40

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...1698

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79

40 TACGACGGAG CGAGACTGGT CTATACCTTA TTTCCGAATA GAAACGACAT TCACCCTATG 60
 AAAACCATTT TAAGATACAG CGGCTTCCG GTCCGCTCTCT TCTTTTGCTT TTTGGGAGCT 120
 GTGCACTTGT CTGTCGAGGC GCAGATGCTC AATACTCCTT TCGAGCTGTC GGATCAGATC 180
 GTCTGTCTCT CCACCGAAAG GCAATACAGG GAGATTGTG TGCAACGAA AGAAAAAAGG 240
 GGGGCCGATC TTTCCCGTT GAGCGATAAG CTGCGCGATT CGGCCATGT TCGTTTCGGC 300
 TCGGCCATG GCGATATTGC GGGCGACTAT CTTCGCTACA ACGGCAATAA CTAATCCTCG 360
 45 CTCTCGCTCG AATCGGGTGG TCGCATCAGT GTCCGTAACT ATGGCACATT GCAGGGCAGT 420
 GCTTCCTACT CACGTGGCAT GCACAACGC ATCGGCTGSA ATGCTCTGCG CAACGCCGAA 480
 GCCTACTATC CCTATTGGT GTCCGATTTC AGCGCGGAG ACTATCATTT CGAAGACTAT 540
 CGGCTTCCCG GCTACTATT TTTTCGGGCC GGCCTGCTTC CCCTCGGTAT AGGCTTCTCA 600
 TACAGGGGCG AAGTTGCTTA TCGGCTGACC GATCCGCTGA CGACCAATAC GACCGCTGCA 660
 50 TTGGAGCTTT CTGTGTCTAC CTCTTTGACG CTGCCCTCGA AGAACAGGCT ATCGCTTTCG 720
 GCTGCGTATC TCTATCATAG ACAACACCTC ACACAGTACA ACTGGCGTCC CGGGCAGCAG 780
 GACAAATCT TCGTCAGCTA CGGTTTCGGT CAGGTGGATG TCAGCAACAG CCTATCTCG 840
 TTCGGTATCT CCAGAAAGAA CTACGTCAAC GGATGGAAGC TTAGCTCCCG TCTGGATACC 900
 CGTAGGGGCG ATGCCATCGG TCTCGACTAC AGCGGCTACT TCCTCGATAC CGAAGAGAGG 960
 55 TCGTCCATCA ATCTCTTTCG TTTGCTTTAC AATCGGCTGC GACTCTATGG TAGCTGGCAT 1020
 CTGTCCGACT TCGATTTTTC ATTTTCAGCC GACTATGCTC TGGGCCAAGG GATAGAGCGG 1080
 ATATACGAAG ACTACAAGCC GGATGATAAT TATCATATCT ACGACCTCCG TATCTTGGCC 1140
 ATTCCGCGCT GGTATATGCT CAATGAGTTT TCTGCCCAAG CCCAAGCCTC CTACCGTATT 1200
 CGCACGGATA GAGGTTGTGC CCTGAGAGTG AGTCCCGSTA GTGATTCTTA CGGCTATGAT 1260
 60 GAGACGTATC GCAAGCATGG ACATCATACC ATGAGCGGAA TGCTACGTCC TTTTGCCGGT 1320
 ATAGCTATG ACCATGCCGG ATCCAAATTG GATTTTGGAC TTTGCTTTC GGCTGCTTAT 1380
 CGAATGGTGC TGACGCAATC GTATAAGATT CGTACCATCC AGAAAGAGCA GCTCCACTAT 1440
 CAGCTGCGCT ATTTGCCCTA TGCTATCGT AATAGAGAAG GCGTGGAGGT GCGTCTCTCT 1500
 CTGTACGTCT CGATTCCGAT GCAGAAATACC CACCGCTGA TGACAGAGCT GCGGTTGTAT 1560
 65 GGGACCTGA TGAAAAGAAA GGACGGTATA GCCTATGGCA AAACGCCCGG TGTCATCTCA 1620
 CATATCTCTG CCGATCCGCA AGCCGAACGA ACCTCCGCGC ATACCATCGG GGCATCTCTG 1680
 AATATCTCTT ACCTCTTC

70

(2) INFORMATION FOR SEQ ID NO:80

75

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2457 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

WO 99/29870

PCT/AU98/01023

55 / 490

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

5 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

10 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2457

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80

20	AGGACGAAACG	TTTTCTTATC	TTTGTCCCAT	AAAAATGGGA	GAAGGGGTGC	TTCTGTAGC	60
	AATCGGAATG	CGTGGATGGC	TGAGAACAAA	CCCTCATCAC	CTGAACCGGA	TAATACCGGC	120
	GTAGGAAACT	CTCCGTCTGA	CTATCTTCAC	GGCGAAGCAA	TCATTCCCCC	TCCTCTTCT	180
	TTGTCCAAC	TCAATGATAA	GAGATTATG	AAAAAATTC	ACATGATTGC	CGCCTTAGCC	240
	GTCTGTGCTT	TCTGCTGAC	GGCACAAGCA	CCCGTCTCCA	ACAGCGAGAT	AGATAGTCTT	300
	AGCAATGTGC	AGCTCCAGAC	CGTACAGGTC	GTAGCTACTC	GCGCCACGGC	GAAAACCCCT	360
	GTCTGTACAC	CGAAGCTTCG	CAAGGCGGAA	CTTTCCAACT	CCAAATTATG	TGCTGACATC	420
25	CCCTATCTGC	TGATGCTGAC	TCCCTCCGTG	GTAGCCACCA	GCGATGCCGG	TACGGGTATC	480
	GGATATTCCG	CGTTTCGGCT	GCGTGGCACC	GATGCCATC	GCAATCAACAT	AACCTACCAAT	540
	GGAGTACCCC	TCAACGACTC	CGAATCTCAG	TCCGTCTTTT	GGGTGAATAT	GCCCGACTTC	600
	GCCTCTTCCA	TGCAAGACCT	TCAAGTGCCG	CGAGGTGTGG	GTACTTCCAC	CAATGCTGCC	660
	GGAGCTTTTG	GGCAAGTGT	CAATATGCGT	ACGGATAATT	TGGGACTGGC	TGCTTATGGC	720
30	CGTGTGATT	TGAGCGGAGG	TTGGTTCCGC	ACATTCGCCC	GATCGGTCAA	ACTCGGTAGC	780
	GGACGCATCG	GTGCGCATTC	GGCAGTGGAT	GCCCGCCTGT	CCAAATCCGG	TTCCGACGGC	840
	TACGTGGATA	GAGGAAGCGT	GGATCTGAAA	TCCTATTTCG	CACAGGTGGG	CTATTTCGGT	900
	AGCAACACGG	CTCTCAGGTT	CATCACTTTC	GGAGGAAGA	AAGTTACGGG	TATCGCATGG	960
	AACGGTCTTT	CGAAGGAGGA	TGAAGCCAAA	TATGGCCGCC	GATACACAG	TGCCGGTCTT	1020
35	ATGTACGTGG	ACGCGCAAGG	AGTACCGCAC	TACTACCACA	ATACCGACAA	TTACGAGCAG	1080
	CGTCACTACG	ATGCCATCAT	GACGCACAGC	TTCTCTCCTT	CGGTTATCCT	CAACCTCAGC	1140
	GCACACTACA	CGGCCGGATA	TGGCTATACG	GACGAATATC	GTACCGGACG	TAAACTAAAG	1200
	GAATATGCAC	TGCAGCCCTA	TGTGGAAAAC	AGTGTGACCG	TGAAGAAAAC	GGATCTCATC	1260
	CGTCAGAACT	ATCTGGACAA	TGACTTCGGA	GGACTCATCG	GTTCCGTTAA	CTGGCACACC	1320
40	GGTGATGGG	ATTTCAGTTC	CGGGGCGCTC	GGCAATATCT	ATAAAGGAGA	CCACTTCGGC	1380
	CGTATCACTT	ACATCAAAAA	GTACAATCAG	CCCTTAGCTC	CCGACTTCGA	ATATTATCGG	1440
	AACAGGGCAG	ACAAAAGAGA	AGGTGCAGCC	TTTGCCAAAG	CCAACTGGCA	GATCACTCCG	1500
	GAACGTAACA	TCTATGCCGA	CCTCCAGTAT	CGTACCATCG	GCTACAGAT	AAACGGCATC	1560
45	ACGGACGAAT	ATGATGAGGT	ACAGGGAAGT	ATGCAGCACA	TCGATTGGGA	CAAGACCTTC	1620
	CGCTTCCTTC	ATCCGAAGGC	CGGTCTTACC	TATAGTTTCG	ACGATGCTCA	TACTGCCTAT	1680
	GCCTCTGTTG	CGGTAGCACA	CCGCGAGCCT	AACAGAACCA	ATTACACCGA	AGCCCGAATA	1740
	GGACAGTATC	CTACGCTGTA	GCGACTGATC	GACTATGAGC	TGGGCTACCG	CTATGCTTCG	1800
	CCCCCTCTGT	CGGCCGGAGT	AGGTCTCTAT	TATATGCAAT	ACAAGGACCA	ACTCGTGCTG	1860
	GATGGCCGTT	TGAGCGATGT	GGGACAGATG	CTCACAAAGCA	ACGTCCCCGA	CAGCTACCGT	1920
50	ATGGGACTGG	AGCIGACTCT	CGGTTGGCAG	ATCCTTCCTC	GTTTGCTGCG	TTGGGATGCT	1980
	TCTTTCACTA	TGAGTCGCAA	CAAAATCGAC	CGCTACGTAC	AATATACATC	CGTATATGAT	2040
	GCGGACTACA	ACTGGGCTCGA	ACTCAAGGAG	GAGACCCCTG	AAAGCACGGA	TATAGCTTAC	2100
	TGCGCCAATG	TCATTGCOGG	CAGCATGCTT	ACCCCTCTCT	ATGCCCGTTT	CGAAATGGCT	2160
	TGGACGAGCC	GCCTCGTCAG	CAAGCAATAT	CTGGACAATA	CACAGCGCAG	CGATCGCATG	2220
55	CTTTCCTCCT	ATTGGGTGAA	CGACCTCGCG	CTCGGCTATG	TGCTGCGCGT	TCACTTCGTT	2280
	AAGAGAGTGG	CACTGGGCGT	ACAGCTCAAT	AATCTCTTCA	ACCTCATGTA	TGCGTCCCAT	2340
	GCCTACATCT	ACGATGCCGG	TTACGTACAG	GCATCCGGAG	AACTAAGTGC	ATATGCCGAT	2400
	CTGCGTTATT	ATCCTCAGGC	CGGATTTAAT	GCATCGGGTA	GTCTGACAAAT	CGATTTC	2457

60 (2) INFORMATION FOR SEQ ID NO:81

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1596 base pairs

65 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

70 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

75 (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature
(B) LOCATION 1...1596

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81

10 TACAGGCGAT CGGGAAGGGT TTGTCTCGT ATCTCCGGG ACAACGGTTC CTACGCAGAT 60
ACTCGGTTAC AGCCGAGAAG AGCGGTTTGA CTACGAGCCG GCACCGAGAC AAAGATGAAA 120
AGAAGGTTTC TATCGCTGTT ACTGCTGTAC ATACTCTCTT CCATCAGCCT TTCTGCTCAG 180
CGGTTTCCGA TGGTGCAGGG AATCGAGTTG GATACCGATT CGCTTTTCTC TCTGCCCAAG 240
CGTCTTGGC GCGCCATCGG TAAACGATA GCGGTCAATC TGGCGTATG GGGCTTCGAT 300
15 CATTTCATCA TGAACGAGGA CTTTGCAGAC ATCAGTTGGC AGACTATCAA GAGCAATTC 360
CAAACAGGCT TTGGCTGGGA CAATGACAAG TTTGTACCA ACCTCTTCGC ACATCCTTAT 420
CACGGATCGC TCTATTTCAA TGCAGCGAGG TCGAACGGTT TGAGCTTCAG GCACTCTGCT 480
CCGTTTGGCT TCTTTGGCAG TCTCATGTGG GAGCTGCTTA TGGAAAACGA GCCACCGAGT 540
ATCAACGACC TCTGTGCCAC CACCATAGGC GGTATAGCTT TGGGGGAGAT GGGGCACAGG 600
CTGTGCGACC TGCTCATCGA CAATCGTACC ACAGGGTGGG AACGTATGGG GCGCGAGGTG 660
20 GCTATCGCTC TGATCAATCC GATGCGCTTT CTCAACCGTC TGACAGCAGG AGAGGTGACT 720
TCTGTCCGGA GTCCGAGCGG ACAGATATTT CAGTCTGTCC CCATAACAT AGTCGTTCGAT 780
GCCGGCTTTC GCTTTTGGC AGACAAGCGG CATGCCGAA CCGGTGCCAC GGCTCTGACC 840
CTGAATCGA GATTCGACTA CGGCGATCCA TTCCGAAGCG AGACTTTCTC TCCATACGAT 900
25 TTCTTCCAAT TCAAGCCGG ATTGAGTTTC TCGAATCGC AACCTCTGCT GAGCCAGATC 960
AATCTGATCG GAATCCTAAG CGGATGCCAA CTGCTCGCAC ACGAACGAAC GGTTTGGTG 1020
GGAGGTCTCT TTCAGCACTT CGACTACTAC AATTCCGAAA AACGAATAAG CAAAATTCG 1080
GAGGAGGTAC TCGTCACCCC ATACCGTATC TCGCAAGTGG CAGCTCTGGG AGGCGGTCTT 1140
ATCTTCAGC ACCACGGAAT ATTTCGACGA CGTCTCTGG AGCTATATGC CGAGACCTAC 1200
CTGAATGTGG TCCCGATGGG AGCCAGTCTG TCGGATCACT ACAACGTGGA CAATCGGGAC 1260
30 TATAACCTCG GCAGCGGATT GAGCGGCAAG CTATACCTTG GTGCTACGTA CAATGATCTG 1320
TGGAGCTGGC TCTTGGGAGT CGAAGCTAT CGGCTCTACA CATGGATCGG GTATGAAGAG 1380
CCGCACCAGA AAAATACCGA TGTCAGCTCT TTTATGGTGC AGGGGGACGA AAGCAAGGCG 1440
CGCTACTCG TGACGAGTTC CGAGTTCGCA TTTCATCTTG GCCCTGGCA TGTAGCCATC 1500
35 GTCGCTCGCC GTTTCATCGG CAAAACAGCC TATCAATTCT ACCCTAACGT ATCATTGAT 1560
ACCGGCGACA TACAGCTGCG TGTCGGATT CACTTC 1596

(2) INFORMATION FOR SEQ ID NO:82

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 900 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
45 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
50 (iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
55 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82

60 AAAAGAAGAA AAAACAGAT GAAACGACTG ATTGT'TTTC TGGCAATGGG TGGCTTGCTG 60
TTCACCCCTT CGAAGCGACA AGAAGCAAAC ACTGCATCTG ACACCTCCAA AAAGGACTGG 120
ACTATAAAG GTGTGACCGG ACTAAATGCC TCTCAGACTT CTCTGACCAA CTGGGCTGCC 180
GGTGGAGAAA ACACGGTGGC AGGTAACCTC TATTTGAACA TAGATGCCAA CTACCTGAAA 240
65 GATAAATGGA GTTGGGACAA CGGTTTGCCT ACAGACTTCG GTCTGACCTA CACAACAGCC 300
AACAAATGGA ACAAAAGTGT AGACAAGATC GAACCTCTCA CGAAGGCCGG CTATGAGATC 360
GGCAACATT GGTACGGAAG TGGCTTTC ACTTTCCTCT CACAGTATGC CAAAGGATAT 420
GAGAAGCCCT CGGATCACTT GACAGGAGTC AAGCATATCT CTAATTTCTT CGCTCCTGCA 480
TATCTCACTC TCGGTATTGG TCGGACTAT AAGCCCAATG AGAAGTTCTC TCTCTACCTC 540
70 TCTCTACAA CGGCAAGCT GACTGTAGTA GCAGACGACT ACCTCTCAAG TTTGGGAGCC 600
TTCGGGGTGA AAGTTGGTGA AAAGACAATG TTGGAAGTGG GTGCTTTGGT AGTGGGTTCG 660
GCCAATATAA ATCTGATGGA GAATGTCAAT TTGATAACCA AGGCTTCATT CTCTCGGCT 720
TATACGCCAC ACTTTGGCAA CATTGACATC AATGGGAGG CTATGCTGGC CATGAAGATC 780
AACAAATGTC TCACGGCTAC GATAGCCACC AATCTATCT ACGACGATGA TGTGAAGATC 840
75 AACGATGGCC CGAAAATCCA GTTCAAAGAA GTTGTGGGCG TGGGTGTTGC GTACACTTTC 900

(2) INFORMATION FOR SEQ ID NO:83

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 663 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

10 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

15 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

20 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83

ACGAGAGAGA	GTGTCTTACA	TTGTAGAACA	AAACTCAAAA	AAGAACGAAA	AATGAAGAAA	60
ATGATTTTGG	CAGCTACTAT	GCTGCTCGCA	ACAATCGGTT	TTGCAATGTC	TCAGAGTCGT	120
CCTGCTCTTA	GACTGGATGC	TAACTTTGTC	GGTAGTAACT	TAATGCAAAA	AGTCGCAAAC	180
ACGAGCGTGA	ACAATAAGAT	GATCGTAGGC	TTACGTGTTG	GTGCTGCTGC	TGAGTTGCGT	240
30 CTTAGCAATG	ATGGATTCTA	TCTCGCCCCC	GGATTGGCCT	ATACGATGAG	AGGTGCTAAG	300
ATGGAAATCAC	TAAAGTAAAC	GACAACTCGC	TTGCATTATC	TGCAAAATACC	GGTGAATGCC	360
GGTATGAGAT	TTAGCTTTGC	TGACAACATG	GCTATTTCAT	TGGAAGCAGG	TCCCTATTTT	420
GCATATGGTG	TCGCCGGGAA	GATTAAGACT	AAAGTTGCAG	GCCTTACGGC	TTCTGTAGAT	480
GCCTTTGGTG	ATAACGGATA	TAACCGTTTC	GACTTGGGCT	TGGGCTTGTC	TGCTGCCTTG	540
35 AGCTACGACC	GTTATTACGT	ACAATTTGGA	TATGAGCATG	GATTGCTTAA	TATGTTGAAG	600
GATGCTCCGG	ATAAGACTTC	TTTGCCTAAT	CATGACTTCT	TTGTGGGTCT	CGGTGTTTCG	660
TTC						663

40 (2) INFORMATION FOR SEQ ID NO:84

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 744 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

45 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

50 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

55 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...744

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84

ATCAAACGAA	TAGAAATGAA	AAGGATTTTT	ACTGTAGCCC	TTGTGCTACT	TGCTTCGGTC	60
ACTATGGCCA	TCGGACAAAG	CCGCCCGGCA	CTTCGCGTAG	ATGCCAACTT	CGTAGGCAGC	120
65 AATCAGAGCA	TGAAAAGAGA	CGGATATGTG	TGGGACACCA	AAATGAATGT	CGGCCGTGGG	180
GTCCGTGCCC	CTGCCGAATT	CATGATCGGA	TCAAGAGGAT	TCTACTTGGC	TCCGGGTCTG	240
AACATATACG	TGAAGGGCTC	CAAAACCGAA	TGGGATATAC	CCGAATGGT	TCCTGGTACC	300
TATATTACGA	TGGTTTCCAC	TGCTTGCAC	TATCTGCAAC	TGCCGATCAA	TGCCGGCATG	360
CGGTTCCGAC	TGATGAATGA	CATGGCGGTT	TCGATCGAAG	CGGGTCCTTT	CCTTGACATC	420
70 GGTATATATG	GTACATATCG	GCAGAAGTTG	GAAGGATGGA	AGCCGAACAA	CTACAGCACA	480
GAGTTTTTTG	GCCCAACGCT	TGGTGGCCCA	ACAATATATC	GCTGGGACAT	CGGGGCAAAAC	540
ATAATAGCCG	CATTCCACTA	TAAGCGTTAT	TATATACAGA	TAGGCTATGA	ACATGGATTT	600
GTGGATATTG	TGTCAGGTGG	AGGTTCTGAT	ATTCCCGGAC	TGAACGACAA	TAGGCAATCC	660
TCTTCGACGA	CCGCTCTAAG	AGAAAAGGGA	AATAACGAAT	ACGCTTATAA	TCGTGACTTC	720
75 TTCGTGGGCA	TAGGTTACCG	CTTT				744

WO 99/29870

PCT/AU98/01023

58 / 490

(2) INFORMATION FOR SEQ ID NO:85

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 633 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- 10 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 15 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 20 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION: 1...633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85

AAAAGAAAGA	GTATGAAAG	AATGCTGCTG	CTTCTCGTTG	TATTATTATA	TGGAATTGCA	60
GGCCGATTGG	CTGCACAAGA	CGTTATCAGA	CCATGGTCAT	TGCAGGTCGG	AGCGGGATAC	120
TCCGATACGG	AGAACATCCC	GGGAGGATTC	ACCTATGGTT	TCTATTGGG	AAAGCGTATG	180
GGGAGCTTTC	TGGAAGTGGG	GCTGTCCATG	TACAACCTCA	CACGTCAAAAC	AGCCAACAAT	240
GCAGACTCCT	TTGCATCGAA	CSAAGGAGAC	GGATCTTTTC	AGGTAAATAT	GTCTTCTCCG	300
AATGAGAAGT	GGTCATTCTT	CGATGCAGGC	AGTGCCAACT	GCTATATGAT	CGTCGTCCGA	360
GTCAATCCTC	TCCATCTGTT	TTGGCAGAAT	AGCCGGCACA	ATTTGTTTCT	GGCAGTACAA	420
GCCGGCCTGT	CCAATAAGCA	CAATATTCAT	TTCATCTATG	GAGACAAGGG	AGCCAAAGTC	480
AGTATCTACA	CCAATTCGAA	TACCTACATC	GGTTACGGAG	CACGTGTAGC	CTACGAATAT	540
CAAAATCATA	AAAACGTGGG	GGCGGGTGCC	GCTGTAATGT	ACGACCACGG	CAATAAGATG	600
CTTACGGCCA	TGGCCACGCT	CTCCACTCAT	TTT			633

(2) INFORMATION FOR SEQ ID NO:86

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2859 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- 45 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 50 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 55 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION: 1...2859

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86

ATCCGAATGA	GAGTATCCGA	TCTCTGTTCC	AGACTTTTCA	GGTTATTACC	CGTAATCCTT	60
GTCCGATTGC	TCTGTGCTAC	TTTGGTGGCT	GCGGAACGTC	CTATGGCCGG	AGCAGTCGGA	120
TTGCACCAAC	GTCCGGCATG	TGCGCTGTCT	GATTCTACAG	CGAAAGACAC	GGTGCCCTCT	180
GCAAAACCTA	TTCTGTACAG	TGCTTTTCGA	GATTCCCTTC	CTGCCGATTC	CACCGGATCG	240
ATGCCGCAAG	ATAGCGTGTA	TGACGATGAA	TTGGAATTGG	AAGATATAGT	GGAGTACGAA	300
GCTGCCGATT	CCATCGTTTT	GCTCGGACAG	AATCGTGCCT	ATCTTTTCGG	CAAGAGCTAT	360
GTGAGCTATC	AAAAGAGTCG	CTTGGAGGCA	AACTTCATGT	ATCTCAATAC	CGACAGCAGT	420
ACGGTTTATA	CTCGCTATGT	CCTCGATACG	GCGGGTTATC	CGATGGCCIT	TCCTGTTTTT	480
AAGGATGGAG	AGCAGTCGTT	CGAAGCCAAG	AACTTTACCT	ACAACCTCCG	CACGGAGAAG	540
GGGATTATCA	GCGGAGTGAT	CACGCAGCAG	GGCGAAGGCT	ATCTGACTGC	CGGTAAGACC	600
AAGAAGATGC	CCGACAATAT	CATGTTTATG	CAAGGAGGGC	GTATACGAC	CTGCGACAAT	660
CACGATCATC	CTCACTCTTA	TATCAATCTT	TCCAAGGCAA	AGGTGCATCC	GGAGAAAGAC	720
ATCGTCACAG	GTCCGGTCAA	TCTGGTTATC	GCGGATATGC	CGCTGCGGAT	AGGTCTTCCT	780
TTCCGCTATT	TTCCCTTTTC	CAACAAATAC	TCTTCCGGTA	TATTGATGCC	CACGTACGGA	840

WO 99/29870

PCT/AU98/01023

59 / 490

5 GAGGACAATC GCTATGGATT TTATTGAGG AATGGTGGAT ATTATTTTGC CTTGAGCGAC 900
TATATCGATT TGGCATTGCG TGGGGAGATC TTTTCCAAAG GGTTCATGGGG CATTTCAGCC 960
CAATCGAAT ATAAGAAGAG GTATAAGTAC AACGGCTCGT TCGAAGCCAA TTATCTGGTA 1020
TCGAAGTCCG GCGACAAATA CGTGCCCGGA GACTACAGCA AGACCACCAAG TCTGAATATC 1080
CGATGGACAC ACAGTCAGGA TCCGAAGGCC AATCCTTTGC AAACGTTGTC GGCCAATGTC 1140
AATTTTGCCA CCGGGAGCTA TTCCAGAAT TCGCTGAATA CCACCTATGA TGTCATGCCC 1200
CGTACTGCTA CGACACGAAG TTCGGCCGTG AGCTATTCCG GCAAGTTTCC GGGTACTCCT 1260
TTTTCGATTA CCGGTAGCAT GGAATATCAG CAGAACATGC CTTTCAAGCG GAAGACCCGT 1320
ACCTTGCCGA ATCTTTTCGAT TAATATGTCC ACGCGTTATC CTTTCAAGCG GAAGACCCGT 1380
10 GTAGGACCCG AGCGATGGTA CGAGAAGTTG AGTGTGGGCT ATTCCGGTCA GCTTCGCAAT 1440
AGTATCTTGA CAAAAGAGAA AGATTGTGTC CAGAGCAATC TCGTCCGCGA TTGGAAGAA 1500
GGTATCGCTC ATTCGCTACC GATCAGTTTG ACTGTCCCTT TGTTGGATTA TATCAATCTG 1560
ACTATGGGGG TTAACATCAA TGATGGTGG TACACGAAG GCATACGGA GTCTGGAA 1620
GAGGATAAGA AAACATTCCT GCCITCGGAC ACSACCTATA AATTCGCGAG ACTGTACGAT 1680
15 TACAGTCTGT CCGCAGGCTT ATCTACCACA TTGTACGGTA TGTTCAGGCC TTGGAACCT 1740
TTTTCTTCG GAGGCAATCT CATTATGATC CGTCATCGCT TCACGCCAC TGTCAGTTTC 1800
TCCATATCG CGSACTTCAC GAAACGCCGA TATGGCTTTT GGGAGCTTCT TGAGCATACG 1860
GATCAGACG GCAAGCTGCA TACGCTGCTC TACTCTCCTT ATTCGAGCA GATATTCGGT 1920
GCTCCCTCCA TGGGCAATGC AGGATCTGTC AATTCTCTT TTGACAACAA CTTAGAGGCC 1980
20 AAGATCAAT CCMATCCGA TTCGACAGG ATCAAGAAGA TCAGCCTGAT AGATCAGTTC 2040
ACATGGTCTA CATCTATAA TATGTTTGCC GATTCGATCC GATGGAGCAA TATCTCGGCT 2100
TCGCTGGCAC TTCGCTCTC CAAGAGCTTT ACCTTGCCTT TGTCCGCTCT GTTCGATCCC 2160
TATTTGACGA AGTATTATGA GGGAGAAGAT GGGAGAATCA TTCCCTATAA GAGCAACGAC 2220
25 CTGCGCATTT TTAACGGCAA GGGATTGGCA CGCCTGATCA GTACGGGTAC TTCTTTCAGC 2280
TATACGCTCA ACAAAGAGTC GCTCAGCGGA TTGATAGCTC TTTTCAGTGG CAAAAGGAG 2340
CGGAGAGATG AAAAGAAAAA CACAGGGGCT ACTCCTCATG AAGGAGACGA TGCTGCCCAT 2400
ATACTTGAGG GAGGAAGACC GCAAATGAA AGTCGGGGGT CCGTCTCCGA GCGCAACCGT 2460
CAGGGCGGAG CAGTGGATCA GGTGGTTAC TTCGATATT CGATCCCATG GAGCCTGTCC 2520
30 TTCGACTATA GTTGAATAT TGCTACCGAC TACAATAGGT ACATATGTC TAAGATGGAG 2580
CACTACTACC GGGTAACGCA GAATCTGAGC TTTCGCGGCA ATATCCAGCC TACACCGAAC 2640
TGGAGCTTGG GATTCAATGC GAATCAAT TTGACATGTA AGAAAATAAC ATCGCTTACC 2700
TGCAACGCTA CTCGCGACAT GCACTGTGCG GCTATCTCG CCAATTTTCA CCTATAGGA 2760
GCATACAAGT CCTATAATT CGTCATATCG GTGAAGAGTT CACTCTTGCA GGATCTGAAG 2820
35 TATCAGCAGA GCAATCGTCC CATCAGCAAT ACTTGGTAT 2859

(2) INFORMATION FOR SEQ ID NO:87

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3753 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
45 (ii) MOLECULE TYPE: DNA (genomic)
(ii) HYPOTHETICAL: NO
50 (iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
55 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...3753
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87

60 AAATGGAAAT TGGCATGCGC TTTTGATTGC GCGTGTGTGT TCGATCCATT TGTAATACT 60
AACGAGGTAA TAATAATGAT GAAACGATAT ACAATAATTC TTGCAGTTT TCTTTTATTC 120
TGACCGGTAT TTACCTTTCA AATAAAGCT CGCCCTTATG AAAGATTTC AGATGTAGAG 180
AAGCCTTGGA TTCAGAAACA TTCAATGGAT TCTAAATTGG TGCCCTGCAA TAAGGGTAAC 240
65 TTAATTCAAG CTGAAATTGT ATACCAATCT GTTTCTGAAC ATAGTGACTT AGTTATTTC 300
CCTGTGAACG AAATAAGGCC TGCAATCGT TTCCTTCCG ATAGGAAGTC TTTTTCGCA 360
GAAAATCTAC GGGCATCTCC CCGGTAGTT CCGGTTCGG TCGACAAGTA TGCGGTACCG 420
GTTGCCAATC CAATGGATCC TGAAATCCC AATGCCTGCG ATGTGACGCT AAAAATCACT 480
70 ACTAAAGCGG TAACAGTACC TGTCGATGFG GTGATGGTTA TCGACCAATC TTCTGCAATG 540
GAGGGCAAAA ACATTGCCAG ATTTAAAGCT GCCATTGCA TCGGACAGCG TTTTGTGAAA 600
AAAATGTTG CTAAGGGGAC GGCTACAGAA GGGGTGCGTA TCGCTCTTGT GAGTTATGAC 660
CATGAGCCTC ATCGCTTATC TGATTTTACC AAAGACACTG CTTTCTCTG TCAAAAATC 720
CGGGCTTTGA CTCCTATTG GGAACACAT ACCCAGGGGG GGCTTAAAT GCGGAGAAC 780
ATTATGGCCA CTTCTACTGC TGTGGATAAG CATATCATAT TGATGTCTGA CCGGTTAGCG 840
75 ACGGAGCAGT ATCCTGTTAA AAATGTAAT ACTGCAGACT TCATTGGCAA AACTGGAAT 900
GCGAATGATC CCATTGATT GGTATACAA GGAGCAATTA ATTCCTTAC AAATTATGTT 960

WO 99/29870

PCT/AU98/01023

60 / 490

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TCCACAATC CATCTACACC TCTTACCCCA AATTATCCAA CTCATTCTTC TAAAGTTGGA 1020
CGGAGAAATC TGCCGGAATC CAAATTCGAT TATAGTAATC TGAGTGCAAG GATTACTTTT 1080
GATGGTGTG CTGGCGCATT GGTCTATGAA CCGAGGTTTC CTCATCCCTA TTATTATTAT 1140
TTCCCTTGTA ACGCTGCTAT CAATGAGGCT CAGTTTGCGA AAAACTCTGG TTATACAATC 1200
CATACTATTG GCTATGACCT GGGAGATTTT GCCTTGGCCA ACATTCGTT GAAACTAACC 1260
GCTACAGAGC AGAATCACTT CTTTACGGCG ACACCGGCCA ATTTAGCTGC AGCGTTTGAT 1320
AATATTGCCC AAATATTAA TATAGGTATA CAGAGGGGGG AGGTGACCGA CTTTGTAGCT 1380
CCTGGTTTCA TCGTTAAAAA TCTGACGCAA TCGGGAGATG TTACTCATT GCTAAATGTT 1440
TCAAATGGAA CGGTGCACTA TGATGTCTCT ACTAAAAAAC TGACATGGAC TACTGGTACT 1500
ATCCTGAGCT CATCAGAAGC TACCATAACT TATCGTATT ATGCCGATT GGATTATATA 1560
CAGAACAATG ATATTCCGGT AAATACTACT TCTGCTATCG GCCCGGATCT TGGTGGATTG 1620
GATACCAATA CCGAGGCCAA ATTGACCTAT ACCAATTCOA ATGGCGAAC GAATCAGCAG 1680
TTAATTTTCC CACGTCCGAC GGTAAAGTTA GGTATGGTG TTATTAGCG GCACATATGA 1740
TTGGTAAATA AAGAGGTCA ACCCATACAG GCAAAATGGA CAGTTGTAG TCCCTAAGC 1800
GAGGCTCATG TTCTACAGTC ACRAAGTTTC TTTTTCCTT CAGGTGGAGG TCATATTGTT 1860
CCCAATGGA TAAAGTTGGA CAAAGCAGC GAAGCATTAC AGTACTATT CGTACCCCGG 1920
ACTAACACCG TCATCACTAC TGCCGATGGT AAACGTTATC GTTTTGTGA AGTCCACAGC 1980
TCCACGCCGA ATCCGGGCCA AATCGGTATC AGTTGGAAAA AACCGGCAGG AAACGCTTAC 2040
TTGCTTACA AGCTCCTCAA TTATTGGATG GGAGGAACAA CAGACCAACA GAGTGAATGG 2100
GATGTGACGT CCAATTGGAC AGGAGCCCAA GTACCGCTCA CAGGAGAAGA TGTAAGTTT 2160
GCAACGACAG AAAATTTCGG TTCTCCGGCG GTAGCCGATT TGCAATGTCC GACAAACCAAC 2220
CCCAAAATTA TCGGTAACTT TATCAATAAT TCCGACAAGG ATTTAGTTGT TACCACAAGC 2280
AGTCAATGGA CGATCAACGG CGTGGTTGAG GATAACAATC CGAATGTCCG TACGATCGTC 2340
GTGAAGTCGT CGAAGACAA TCCTACGGGG ACATTGCTTT TTGCCAATCC GGGCTATAAT 2400
CAAAATGTAG GGGGACCGT CGAGTTTAC AATCAGGCAT ATGATTGTGC CGATTGTGGT 2460
ATGTATGCGA GGAJCTGGCA GTATTTCGGT ATCCCTGTCA ATGAATCAGG TTTTCCAATT 2520
AATGATGTGG GCGGAACGA GACCGTCAAC CAATGGGTG AGCCTTTCAA TGGCGATAAG 2580
TGGCGGCCAG CACCTTATGC ACCTGATACA GAGCTTCAAA AATTCAAGGG CTACCAGATC 2640
ACGAATGAG TGCAAGCACA GCCTACGGGA GTTTACAGCT TCAAGGTAT GATTGTGTG 2700
TGGATGCGCT TCCTGAATCT GACACGCAGG TCCGCTGTCA ACTACTCGGG CGCCAACCTG 2760
ATCGGCAACT CATACACTGG AGCCATCGAC ATCAAGCAGG GTATTGTCTT CCCGCCGSA 2820
GTGAGCAGA CGGTGTATCT GTTCAACAGG GGAACACCGG ACCAGTGGCG TAAGCTTAAT 2880
GGAAGCACCG TTTCAAGGTA TCGAGCCGGT CAGTACCTCT CTGTACCTAA GAATACAGCG 2940
GGTCAGGACA ATCTCCGGA TCGTATTCCA TCGATGCATT CCTTCTGGT GAAGATGCAG 3000
AACCGAGCGT CTGTACGTT GCAATCTTG TACGATAAGC TGCTCAAGAA CACGACTGTA 3060
AACCAACGGA ATGGTACGCA GATCAGATGG CGATCCGGCA ACTCCGGATC GCGCAATATG 3120
CCGTCACTTG TGATGGATGT TCTTGGTAAC GAGTCCGGCG ACCGTTTGTG GATCTTTACC 3180
GATGGGGGCT TTTCTTTCGG ATTCGACAAC GGCTGGGATG GTGCAAGCT GACTGAAAAA 3240
GGTTTGTAC AACTTTATGC GATGTCTGAC ATCGGTAATG ATAAATTCOA GGTTCAGGGG 3300
GTTCGGGAGT TGAATAACCT GCTGATCGGC TTCGATCGCG ATAGGATGG TCAATACAGC 3360
TTGAGTTTGG CTCTTTCGGA TCATTTTGGG AAAGGGGGTG TTTACCTGCA CGATCTTCAG 3420
TACGAGGACA AACACCGTAT TACGAATCT ACCTCGTATT CATTCGATGC CAAGCGGGGA 3480
GATTCGGGG CTGCTTTCGG CTTGTATAT GGATGTGATG AGAACGTAGA TGATTCCGAT 3540
TCGTGAGTA CAAATGGCGG TGAATATATA ATTCTGAATC AAGATGCTCT TGACTGCACT 3600
GTAACTTAT TCACAATAGA AGGTAAGCTT CTTCGCCGCT TGAAGTATT AGCTGGTAT 3660
AGAGAGTCA TGAAGTGCA GACCGGAGGG GCCTATATTG TGATCTTCA AATGCTTTC 3720
ACTAATGATG TGCATAAGGT GCTTGTGAG TAT 3753

50 (2) INFORMATION FOR SEQ ID NO:88
55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1278 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
60 (ii) MOLECULE TYPE: DNA (genomic)
65 (iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(v) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
70 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1278
75 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88

ACTATGGAAG TGAAGAAAAA CACAGTGGTG CTACGCCTTC TGATTGGGTT CGTGGCCATT 60
CTTCTCTTCC ACTCCTCAGG GCTGTGGGGA CAGGAAGGGG AGGGGAGTGC CCGATACAGA 120
TTCAAAGGAT TCGTGGATAC CTACCATGCC GTACGCAGCT CTTCTCCTTT TGATTTCATG 180

WO 99/29870

PCT/AU98/01023

62 / 490

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(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

5 (ii) MOLECULE TYPE: DNA (genomic)
(ii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
10 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
(ix) FEATURE:
15 (A) NAME/KEY: misc feature
(B) LOCATION 1...798
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90

20 ATAATTTATA GATCAACAAT GAAACTATTA CTTTATCTCC TATTGGTCTT GTCGACTCTA 60
TCCCCGATGT ATTGCGAAAT GCTCTTCTCA GAGAATCTCA CAATGAATAT AGACAGCACC 120
AAAACCATAC AAGGAACGAT ATTGCCCGTA CTGGATTICA AAACCGAAAA GGAAAATGTG 180
TTCACCTTCA AAAAATCTGC CAATCTCAAT CTGGTGATAA AGCAGCGTCA AGTAATCAAC 240
TTAATTAATA AGCTTGAGTT TTCTACCTAT GGCAATAAAG TAACCGTAAG TGGAGGATAT 300
GTACACACCG AATACCGCTA TTTGTTGCAT CATGTTTTTG AGGTTTATCC TTATGTCGAG 360
25 TCGCAATGGG CAGAAAGTAG AGGAATGAAA TATAAGGTTT CTACGGGATT ACAGTCGCGT 420
TATCGGCTGG TAAATAGTGA TAACTGTCTC ATGTTTGCAA CATTGGGGGT ATTTTTCGAA 480
TTCGAAAAGT GGGAACAGCC AGCCACTAGC CTCTTTGCAG GAACGTATGC ATACAGCCGA 540
AGTATCAAAA GCCACCTGTC TATCAGTTTC AGACATCGGT TGGGTGAACA TTGGGAATTT 600
ACAATACGG CTATTCACCA GGGAAAGCCT GACAGTTATT TTAAGAAAGC ACGTTTTCGA 660
30 GGAGCTATCG ACCTCAATA CCAATACACA CCTACGATAG GAATACGGG GGCCTATCGG 720
ATCATCTACG ATACTGCCCC TATTGTACCT GTGCGGAAAG ATTACAACAC CGTIGATGTT 780
GGTATCGATA TTTGTTTT 798

35 (2) INFORMATION FOR SEQ ID NO:91
(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2721 base pairs
40 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
(ii) MOLECULE TYPE: DNA (genomic)
45 (iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
50 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
(ix) FEATURE:
(A) NAME/KEY: misc feature
55 (B) LOCATION 1...2721
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91

ACTATATGCG TTGCCTTCTT ATCCGCTCCC GTTGGGGCAT TGCGCGAGTC GCCGCCAATG 60
GGGGCGGAGC GGAAGACTCC CTCTCTCCTA CCCCTTCTTT TCGAGCATTG TGATAAAGGA 120
AAGGGGTTTC ACTACAGACT ATTCACAAGC AATAAACTTA AAGTGTGTC CACAGGTAAC 180
AGCCGATACA TACACAATAA ACCAACAATC ATCCAAGCAA TGAACCGAAT CGTTTATCA 240
TCTTTCTGT TCGTTCTGTC CATACTTCT TTAGTGGCAC AGAACATAC CCTCGATGTA 300
CACATATCCG GTACGATCAA GGATGCCCTC TCGGCGGAAC CAGTGCCCTA TGCCACTGTA 360
AGCATCCGCG TGACAGGAGC AGATACCACA CAGGTGTTC GACAAGTGAC TGACGGCAAC 420
GGCTACTTCG TCATAGGCTT GCGGGCAGCT CCTCTCTATC ACCTGACAGC TTCGTTTCGTA 480
GGTATGAAAA CCCATACCAT GCAGATTAGT CGGGGAAATG GACAGCAGCA CATCAATCC 540
ATCGACATTT CTCTCGAATC CGAGGACAAA CAACTCTCCA CCGTCACCGT ATCGGCAGCA 600
CGACCACTGG TGAAGATGGA GATAGACCGC CTGTCTCTATA ATATGAAGA TGACCCCGCA 660
GCCAAGACGA ACAACCTGCT CGAAATGCTG CGCAACGTTT CTTTGTAAC GGTGGATGGT 720
70 CAGGGCAATA TCCAGGTGAA AGGATCTTCC AACTTCAAAA TCCACCTCAA TGGCAGGCC 780
TGAGCATATG TGAGCAGCAA CCGAAGGAG GTCTTTCGCT CCATTCTCTC CCATACGATC 840
AAACGGGTGG AGGTCATCAC CGATCCGGGT GTAAAGTACG ATGCGGAAGG CACAAGTGCC 900
ATCCTGACCA TCGTCACGGA AGAAGGTAAG AAGCTGGAAG GATATTACAG TTCCATCAGC 960
GCCAGTGTCA GCAACAATCC CACAGCCAAC GGTAGTATCT TTCTGACGGC AAAGTCCGGC 1020
75 AAAGTCGGGC TGACTACCAA CTATACTAC TACGGTGGCA AAAACAAGGG CTCTCGCTAC 1080

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WO 99/29870

PCT/AU98/01023

63 / 490

5 TTTACCGAAC GTACTACATC CATGCTCCAA ACGATAGAAG AAGGCAAAGG GCAAGAAACC 1140
 TTTGCGGGAC ACTTCGGCAA TGCCCTCCTC TCATTGAGAG TAGATTGCGT CAATCTCTTT 1200
 ACGGTGGGGC GCAATGTACG CCTTTGGGAG ATGACCACCG ACCGGAACAG CGTAGAAAAA 1260
 AGCTTTGGCG GCAGCAACCT CATGTCTTAC ATAGACAGAA AACTCAAAAC ACAGATGGAT 1320
 GCCGGATCAT ACGAGCTCAA TGCCGACTAT CAGCACAGCA CTCGCCCTGCC GGGCGAATTG 1380
 CTACCGGTTT CCTACCGCTT CACTCACAAAT CCTAATAATA GCGAGACCTT CATTGACCAA 1440
 TGGAAGCGCG ATCCGCTCAA CACAGCTAAT ACGATCCAGT ACGCCGGCCA GCACTCCAAA 1500
 TCCGATGCGG GCATGGACGA ACATACGGCA CAAGTGGACT ATACACGTCC CTTAGGACAA 1560
 GCACATCTCT TGGGAAGCAGG GCTGAAGTAC ATCTATCGTC ATGCCACGAG CGATCCTCTC 1620
 10 TATGAGATAC GACCATCCGA AGATGCTCCG TGGCAGCCCG GCTCTCTATA TGCACAGAAT 1680
 CCGTCGAACG GAAAGTCCCG CCACGATCAA TACATCGGAG CAGCCTATGC CGGTACAAAC 1740
 TATCGTAAGG ATCAGTATTC TTTGCAAACC GGCCTCCGAG TGGAAAGCAG CAGGCTGAAA 1800
 GCACTCTTTC CCGAAAACGC AGCAGCAGAT TTCTCCACA ACTCGTTCGA CTGGGTGCCA 1860
 CAGCTCAGCG TCGGCTATAC CCCCTCGCCC ATGAAGCAGC TTAAGCTGGC CTATAACTTC 1920
 15 CGAATCCAAC GTCCTGCAAT CGGCCAACTG AATCCCTACC GGCTACAGAC CAACGATTAT 1980
 CAAGTACAGT ATGGTAAATCC CGACCTAAAG TCGGAGAAGC GTCACCAAGT CGGTCTCTCC 2040
 TATAATCAAT ACGGAGCCAA GGTATGCTT ACAGCATUGC TCGACTACGA CTTCTGCAAC 2100
 AACGCCATCC AGAATTACAC CTTCTCCGAC CCGGCCAATC CCAATCTGTT CCACAGACC 2160
 TATGGCAATA TCGGACGAGA GCATTCTTTC AGCTTGAATA CTTATGCCAT GTACACGCCG 2220
 20 GCGGTATGGG TCAGGATTAT GCTCAACGGA AATATCGATC GCACATTCCA AAAGAGCGAA 2280
 GCACTCGGCA TTGATGTCAA TTCATGGTCC GGCATGGTAT ACTCAGGCCT GATGTTCAAC 2340
 CTGCCGAAGG ATTTGGACTGT GAATCTCTTC GGAGGTTATT ATCATGGGGG AAGAAGCTAC 2400
 CAGACGAAT ATGATGGCAA TGTATTCAAC AATATCGGTA TAGCCAAACA GCTTTTCGAC 2460
 25 AAAAATTTGA GAGTCTCGCT GAGCGCAAAC AACATTCATG CGAAGTATTC GACATGGAAG 2520
 AGCCCGACCA TCGGCATATG ATTTACTATT TATTCGGAAA ATGCCGGTAT ACAACGGAGT 2580
 GTTTCCTCTA GCCTCACCTA CAGCTTCGGT AAGATGAATA CACAAGTGCG CAAGGTAGAG 2640
 GGTACGATCG TCACGACGGA CCTCAAGCAA ACCTCATCCC AAGGACAGCA GGGTGGCGGA 2700
 CAAGGAAATC CTACCGGCAA T 2721

(2) INFORMATION FOR SEQ ID NO:92

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1350 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
 (ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (v) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1350
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92

55 TGGTGCCAAT CCGACCCAAT ACCTCATTGC CATGCAGTAT ATCGAAACGC TCAAGGACAT 60
 CAACAAGGGC GATCAGACCA AGACCGTTTA CCTCCGTTT GAGGCTACCG GTATGCTCGG 120
 TGCCCTGGGC GGTATGAAGG ATTTGGTGAA AGGATGAGAC TCTCTGCCAT TCTTATCGCT 180
 TTGATTGTGA TGCTGCCTGC TGTGCTTAGC GGGCAGCATT ATTATTCCAT GCGGGGAGAG 240
 CGACTGGAGA CCGACAGCAT TCGTCCGAAC GAATCTCTCG CATCGATCCG AAGTGCAGCT 300
 60 TTCTTTCGGA ACAAATGAATA CAATGCCAGT TCGGTCAAAG GTTATACGTT GCGGGGTGCA 360
 GGGGTTTCGG CTTTTGCCCT TTAATCGCTG CCGGCAGCAC ATGGGTGTAA GCTTTCGCTC 420
 GGAGTATCTA CCTGAACCTA CTGGGGGGCA AGTCGCTATC CGGCCGGTAT CGCTTATTC 480
 GATTTACCTT ATTGGACGGA CTATAACGAC TATGTACGCT TGGGTATCCT GCCTTATGTA 540
 CAGGCCATGC TGAAGCCGAC GGGCAGGACT GCTCTCATGC TGGGCAATAT AGCCGGTGCT 600
 65 ACGGCTCAGC GACTGATCGA ACCGATCTAC AATCCTGAGT TGGATTGAC GGCTGATCCT 660
 GAAGCCGGTG TGCAATTTCG GGGTGATTGG ACAGGTTTCC GAATGGATGT TTGGGTCAAT 720
 TGGATGAGCA TGATTTTCAA AAATGACAAT CATCAGGAGT CGTTTGCTTT TGGCTTGCTC 780
 ACTACTTCGA AATTGTTATC GGGTGAAGGC AAATGGCGAC TCGAACTGCC CTTGCGAGCT 840
 ATTGCCAGCG ATCCGCGCGG GGAATACAAV TGGGCGCAGC AGGATACCGT GCATACATGG 900
 70 GTCAATGGAG GTGTCGGACT TAAGCTTTCG TATCGCCCTC GTACCGACAA ACCCATGCG 960
 ATTTGGGGAT CTGCTTATGG TGTGGCAGCC TTGTCAAGCG GAGGATACCT CTTTACGAA 1020
 AGAGGGTGGG GCGGTTATCT TTCTCTCGGA ATGGAAGTGG AGCACTTCGC TTTTCGTACC 1080
 GACTATTGGT ACGGCGAGCA TTACGTTTCT CCCTTTGCTG CACCTTTTCG CAATCCCTG 1140
 ACGTATGACA AACAGCCTCT TACGAACGGT TGGGGCGATT ATATTGCTCT CTATGCCGAC 1200
 TATTCGTGGC GGATGGCAGC AAGTGTTCG TTGGCGGCTG TTGCTGGGT ATGGTTCCAG 1260
 75 CCTTCGGATC GTTTTGGCAT GAGCCACGCC TTGGAAGTGA CGATCGGTAT CGATCCCAAA 1320

WO 99/29870

PCT/AU98/01023

64 / 490

TTCCCAATAG CTTTTCTGAA AGGCAATCAT

1350

5 (2) INFORMATION FOR SEQ ID NO:93

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1341 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

15 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...1341

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93

CCGTTTTCAC	CGCCATGGGT	ATGTGCTGGA	GCGGCTTCCT	CAGTACGCAC	ACGGCCATGC	60
TCCACAGTCT	CAAGTACCGC	CGCCTCATCA	CACAGGCGAT	CGGAGCACAT	GCGATCGGCG	120
GACTCGTGGC	CGGCATATTC	GCCCATTGGC	TCTTTGTCTT	CATCTCACTC	ATTTGATTTCG	180
ATACCCGACC	AACGTATGAA	CAATCGCTA	TTATCATTGG	CATGGCTCAT	CCTGTGCGGT	240
ATGCCGGCCA	TCGCCCAACA	GACAGGACCG	GCCGAACGCA	GCGGCGAGCC	TTCTCTGGCC	300
GAACGTGTAT	TCGGTCTGGA	GCAGAAGCAG	AAAAAGCTGA	AGGTGTACTT	AGGCATACAG	360
TCGTCTACG	ACCAGCGGCT	TGTCGATGAC	GAATCCCAT	TCGGACACTT	CAAGGTACAG	420
GAGCTGCGGA	TGCTGTCTCA	TGGCGAATCG	AACCGCCACC	TCAGCTTCGA	CTGGCGACAA	480
CGTCTCAACC	GTGCCGCCGA	CGGCCTTCG	TTTGCCGACA	ATCTCTCCAA	TGCCATCGAC	540
ATCGCAGGTG	TGGACTGGCA	CCCGAACGAC	AAGGTGTCTT	TCTCTTCGG	ACGTCACTAC	600
GCGCGTTTCG	GAGGGATAGA	ATACGACATG	AACCCCGTAG	AGATCTACCA	GTACAGCGAC	660
CTTGTGGATT	ACATGACCTG	CTATACTTCG	GGCGTGAAGT	TCGCATGGAA	CTTCCACCCC	720
GAACAGCAGC	TGCAGCTACA	GGTACTCAAT	GCTTACAACA	ACCGCTTCGC	CGACCGCTAC	780
CACGTGACAC	CCGATGTCCG	TACCGCCACG	AGCTACCCGC	TCCTCTACTC	GGCACAGTGG	840
AACGGTACCC	TCCTCGGAGG	AGCACTGCAT	ATGCGTTACG	CCGTGTGAT	GGCTCATCAG	900
GCCCAAGAGC	GTAATATGTG	GTACTTCACT	GCGGGCAACC	TGTTCAATCC	GGGCAACCGG	960
ATCAACGGAT	ACCTCGACCT	CACCTACTCG	ATCGAGGGAT	TGGACGACAA	AGGCATTATG	1020
ACTGTCTCGT	ACGGCAAGGG	CAAGACCCCTC	ACGGACGTCA	AGTACTATGC	TCTGGTATCG	1080
AAGTGGAACT	TCCGCAATTT	CGATCAGGTC	AATCTCTTCC	TCAAAGGCAT	GTACGAGAAC	1140
GGCTATGOGC	CTGCCCAATA	CGGCGAGAGC	AGCCACACGC	GCCACTCCTA	CGGCTATATG	1200
GGAGGGGTGG	AATATTACCC	TACGGAGACC	AACTTCCGTC	TGTTCTGTAC	CTACATAGGA	1260
CGGCATTACC	GGTACAGTGC	GACCGAGACG	GAAAGCACCA	ATGCTCTTCG	CGCCGGTCTG	1320
ATCTATCAGA	TACCTTTCTT	A				1341

55 (2) INFORMATION FOR SEQ ID NO:94

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 681 base pairs

(B) TYPE: nucleic acid

60 (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

65 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

70 (A) NAME/KEY: misc feature

(B) LOCATION 1...681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94

75 TATAAGCAAG CTATAATGAA ACATTTGTTT AAGTCGACAT TAGTACTTCT TTGTGCTCTT

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WO 99/29870

PCT/AU98/01023

65 / 490

5 TCTTTTTCGG GTACCTATAC CTTTGCACAA GAAAATAATA CAGAAAAGTC ACGATTGAT 120
TTTTCTGTGA GGCCTGGGACA GGGATATATT GCAGGTTCAA CTACCAACCT GATGTATGGG 180
TATACATCTG CTAACGATAG ACTTTTGCTT GGTGCAATTT ATCTGGGCTT GACACCAAGT 240
AAGAAAGAAA ATGCAACCGG CGTAGCATTT CGTTTCTTAT CCCCCCTCC GGGTTATTAT 300
GTCGATATAT CCGGCRAAGA AAATACCTTG AATTATGCGT TTACGTTGT CGGAGCATAT 360
AATAGAATAG CCATTCTTAT ACGCCCTATC AAAAATTTTA ATTCTACTT CTCTACAGAA 420
GTCGCAATGG CTTGGATGAG TCGTCATGAG CAAATTTACA ATTCTACTT GCAGACTTGG 480
GATAAGCAGC GCAAGTCGAG GTCGGGACTG GATTTTGGTC TCGGGATGCA TCTGCAATHC 540
CACATTAATA AGACCGTTTA CTTTATGGCA GGAACCGATC TTACGTTCTG CATGTTGGGA 600
10 AAAAGGATCA ATGACTACCA GCAAAAGGAT CGAACCTTCA TTGCACITAT CGACACAGT 660
ATTGGCATAG GATTAAACCT C 681

15 (2) INFORMATION FOR SEQ ID NO:95
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1218 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: circular
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
25 (iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
30 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...1218
35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95

ATATTTCATAG ACCCGGATAA GAATACAAAA CAAAACGAAC GAAATATGAT TATCAAGAAA 60
ATCGTGAAAA ATAAATGGGC CCCCTTGGCC ATACTGTTC TTTTGTCTCC AAAGGCTATG 120
AAGGCTCAGG AGCAACTGAA TGTGGTACAC ACCTCTGTGC CATCGCTGAA TATCAGTCCG 180
40 GATGCACGTG CCGCCGGTAT GGGGGATATA GGTGTGGCAA CGACGCCGGA TCGGTATTCA 240
CAGTATTGGA ATCCGAGTAA ATATGCTTTC ATGGATACGA AAGCCGGTAT TAGCTTCTCA 300
TATACACCCCT GGCTGTCCAA GCTGGTCAAT GATATTGCC TGTATGAGAT GACCGGTTTC 360
TACAAATTGG GAACAGACGA GAATCAGGCT ATTAGTGCTT CTCTGCGTTA TTTCACATTA 420
GGAAAGTTGG AGACTTTTGA CGAATTGGGC GAATCCATCG GAGAGGCCCA TCCCAATGAA 480
45 TTTGCTGTG ATTTGGGCTA TAGCCGCCAG TTGTGGAGA ACTTCTCCAT GGCTGTGCA 540
CTGGCTTACA TCGGCTCAGA CCAAAGCACT CACAACACCG GAGAGATCA GGCCGGAAAT 600
GCCTTTGCGG CGGATATAGC CGGTATTTC CAGAAGTATG TGCTACTGGG TAATGCGGAG 660
AGCTTGTGGT CGTTGGGTTT CAACGTAAAG AATATCGGAA CGAAGATCTC CTATGACGGA 720
GGTGTACGCA CTTTTTCTAT CCTTACTTCG TTGAATCTCG GGACGGGGCT GTTGATCCG 780
50 ATCGATGACT ATAACAGCAT CAATTTC AACCTTGAAC GCAAGCTGCT GTTACCCACT 840
CCTOCTATCA TGGATCAAAA CGATCAGGCC GGGTATGAGG CTGCACTCAA GAAATATCAG 900
GAAACTTCTT CGATCAGCGG TATATTCTCT TCTTTCCGGT ATGCGCCGGG AGGACTCAAG 960
GAAGAATTCC GTGAGATTAC ATGGGGACTT GGGGCTGAAT ATAGCTATGA CGATAAAATT 1020
TTTGTCTGTG CCGGATATTC ATACCTGCAC CCCACCAVAG GCAATTTCGA GTACTTCAG 1080
55 GCCGGTGGCG GCTTCAAAAT GAACATATTC CGTATCGATG CTTCCTACCT GTTGTCTACG 1140
ATCCAGAGTA ATCCGTTGGA TCAGACTCTG CCGTTTACGC TTGCTTTCGA TATGGATGGA 1200
TTGCCAATT TGTCCAC 1218

60 (2) INFORMATION FOR SEQ ID NO:96
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1356 base pairs
65 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
(ii) MOLECULE TYPE: DNA (genomic)
70 (iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
75 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

WO 99/29870

PCT/AU98/01023

66 / 490

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...1356

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96

CTAATAATCG	AAAAGGAAAT	GAAAACAACA	GTTCACACAA	TTATTCTGTG	CCTGGGCTTTA	60
ATGATGTCAG	GTGTATTGGG	CGGAAACGCA	CAGACCTTTT	GGGAAGAAAT	AGCTCCTCCT	120
TTTATCAGTA	ATGAGCCTAA	CGTCAAGTAT	ATAATTCCCA	ATATGGGCAT	TGATTCAAAAG	180
GGACAATCT	ATGTAACCGT	GACAAAAAGG	ATTCAGCAGG	GAGCAAAATTA	TACTTCTGAG	240
CAATTGGGTA	TGTACTATCG	ACCAATTAGG	GATAATGAAC	AGTGGTGGAA	ACATGATCCG	300
TATTTTGATG	ACAAGATAGT	TGCGGATATT	CAGACAGATG	CATATGGCAG	AGTTTATGTA	360
TGTACGACTT	CTTCTCGACA	TCAAGAGTAT	CAACTTTATA	TAAACGAGCA	GAACGAATGG	420
AGGTGTATAT	TCAAACTTTC	TGTGTCTACA	TATGAGCATG	GTATGGCTGT	TTTTCGCTCT	480
TCGACAGGGG	TGACTTATAT	AGGTACCAGG	CATCAGATCT	TCGCATCAGG	TGTAAATGAT	540
TTCGAGTTCA	ACACTATCTA	TGAAGACTCT	ACACCTATGA	GCTGTGCTTT	TGCAGAGGCT	600
ACGAATAGTG	GCACCATCTA	TCTGGCATTG	ATGCATGAAA	CCACAATGTC	TACGACTATC	660
CTTACTTATC	AAAACGGTGA	GTTTCGTGAT	ATCTCGGAAA	GTGAATTGAG	TAACTCGATT	720
ATTGCATCCA	TGTGCTCTAA	TAAAGAAGGT	GATATAATAG	CTCTTGTTC	TTCATATACA	780
GGATTATGA	GTGGAACCTT	TGCGATCACA	AAAGCAGATG	AAGGCAAAAT	GCAACTTGTT	840
GGCGGAGATA	TACAGAATGC	GATCGTTCAA	AATATATGCA	TGATGGACGA	CAACAAGATT	900
GCTTGTGAAG	TCTTCGGGAC	TCCTAACCGA	GTAGATGGTC	GGACAAGGGT	TTGTGTTTCT	960
GACGCATCTG	TCTTTGATTT	TGAGTGGTAT	GAAGATGAAA	TATACGGAGG	CCTGATATTT	1020
GACACTTTCT	TCTATAGCCC	TTGGGACAAA	CTTCTTTATG	CGAAATTTGG	TGGGATTATG	1080
CTCAGAGTGA	AAGAGTCTTT	TATAACCTCT	TTCAATTTCT	CGACAGTTGT	ACAAGGAGTG	1140
GATGCTATA	CTTTGGCCGG	GAAGATAAAG	ATCGAAAGTG	AAACTCGGGT	GTCTGAGGTG	1200
TTGCTTTTCG	ACCTGGCTGG	CAGGATGGTA	CTTCGGGCAA	CCATTGATAA	TAAATCTAT	1260
TCGGACATAG	ATACTAACGG	ACTAAAGCGA	AGCGGTATTT	ACGTAGTCTC	GGTGCGGCTC	1320
TCTTCCGGAC	AGGTATTTCG	TCTAAGGTG	CAGGTA			1356

(2) INFORMATION FOR SEQ ID NO:97

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 993 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

40

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

45

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

50

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...993

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97

GGCCTGTACG	GTATGTCGTG	TGTACCTATA	ATTAATTTATC	TTTGGGGTAT	ATCAAATTAT	60
GCAAGACTCA	TGATAATCCG	GTGCTTTATC	CGTCGTCGGA	GAACCGTCCT	GTTCGGGTTG	120
ATATTCGTGG	TAGGTCTTTT	CTCTGCGATG	GCGCAAGAGA	AAAAGGATAG	TCTCTCTACG	180
GTTCAGCCAG	TGCGGAATAG	CAGCATGGTG	GAGCAGACCC	CTCTCTCTCT	CATTGATCAC	240
CCCGTCCTGC	CCGCTTCTTT	TCAGAATACC	CGTACACTGA	AAAGGTTTAG	AGACAAACAT	300
CTTTCGATG	CTTTGCTCAA	TGGATTGAAG	CCTCATCGCT	CATCTTTGCA	ATTGAATGAG	360
GAACCTCACT	TGCGGGCAGA	GCGTCGGGAT	TTCTTTTCTC	CCCTCTTGCA	AACTCGCCAC	420
GCTGCCGGTG	TCCTTTTATG	GCGACCGACC	GATAGGATGC	ATTTTATATC	ATCGGGCAAT	480
ATCGGCTCTG	GCCATGATTT	ATTGACCGGT	GTGCGCAAGG	ACTTCGGATG	GAATGCTGGT	540
GCCGACTTCT	TGCTGAGTCA	AAATCTTACG	GCACATGTCC	AAGGCGGTTG	GCAGCAGAAAT	600
TTGCGGCTTA	TACCTATGAC	GGCTGTCAAT	GGCCAACTGC	GTTCGGCAAGC	CACCGAGAGA	660
TTGAGTTTGA	CCACCGGTAT	CGATTATCGA	CAGGTACAGT	GGAAATGCTTT	CGATAATAGA	720
ACGTTCTCGC	TTAAAGGAAG	TGCTCGATAC	GAAATGATGG	ACAAATGCTT	TGTCAATGGA	780
TTTGGGACGT	ATCCTCTCTA	CAGCAGTACG	CGCTCAGGAC	TCAATATGGC	TGTTCCGATG	840
CATGGATTCC	GCCCTCAGTA	CGGTGGATCG	CTTGAGCTGA	AAGTCTCCGA	CGGATTCGGC	900
TTTGGCGTCG	GTATGGAGCG	CGAATACAA	ATCTGGACTC	GTCGGTGGGA	AACGCATTAC	960
TTTGCTTATC	CTGTATTCTA	TGGCGATAAG	AAG			993

75

(2) INFORMATION FOR SEQ ID NO:98

WO 99/29870

PCT/AU98/01023

67 / 490

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 987 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98

GAGACGAACT	CTTGGGTATC	CACGATTGC	AATTGACGA	CGATGAAAC	GAATAGACGA	60
TACGCAATTT	TTTGGCCGCT	TCTGCTACTC	ACCGGATTGT	TGGCATGGGG	GCAGGATTCT	120
TCCCACGGTA	GCAATACAGC	GTTTGCAACT	GATTCTTCGA	GTAGAGAGTT	GCCCACGGAG	180
CAGTCCGCCT	ACCGCATTCA	TTCTGCCTAT	ATGGTCGGTG	GTGGCGGAAG	CATAACGGCG	240
GACCACTATT	TGTCACCCCT	TCGTTATGGA	GGATGGACAC	TCAATTTGTT	GGGAGAGAAG	300
ACGTTCCCTC	TCAAAGCCTC	CGATTCCCGT	TGGATGATCC	GTACCGGGCA	TGAGCTGGAT	360
TTTGGCCCTGA	TGGACAATCC	GGCCAATAAT	GCTCATTCT	ATTCCCTGCT	GTATAACGGT	420
TCCGCTGCGG	CTCTTTACCG	CCTTGGCGCT	AAGCATCTGC	GAGCCGCGTG	GATGGACAAT	480
CTGCGCTTGG	CATTGCGCCC	GGGCTTGGAA	ATCGGGCTTG	GAGGAATTTA	TAGTACACGC	540
AACGGCAATA	ATCCTGCGAC	ATTGAAGCTC	TACACCAATG	CCATCGCCCA	AGCCTCGATA	600
GGATACTACG	TCCCTCCCGA	AACTTTTCCC	CTGTATTTTC	GGTTGCTCTC	CCAGATCAAT	660
CTCTTCGGTA	TAGCCTATGG	AAATGGTTTT	GGTGAGAGCT	ATTACGAGAA	TTTTTTGCTC	720
AAATACGGCA	TTCGAGGCTC	CCTGCATTTC	ACTTATCCGG	GCAAGTTTAC	TCGGTTACAG	780
ACACTCATAA	CGGCGGATAT	TCCCATTCCG	AACTTCTGTA	CGCTTCGGTG	CGGTTATCGC	840
TATTCCCAAT	TGGGCTCTTC	GCTTAACGCA	TGGGATACTC	GAATCCACAG	TCATACGGCT	900
TTTATCGGTT	TCGTACGGGA	GTTTACCGA	TTCGCTGGGC	GCAAGCCAT	GAATACCGGT	960
CGGAGAACCA	GTCTTTACTA	TCATGAT				987

(2) INFORMATION FOR SEQ ID NO:99

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 957 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99

TTTACGTCCG	GTACGATATT	CGTCCGTATA	GCCATATCCG	GCCGTGTAGT	GTGCCGTGAG	60
GTTACGGATA	ACGGAAGGAG	AGAAGCTGTG	CGTCATGATG	GCATGGTAGT	GACGCTGCTC	120
GTAATTGTGC	GTATTGTGGT	AGTAGTGCGG	TACTCCTTGC	GCGTCCACGT	ACATAAGACC	180
GGCACTGTGT	TATCGGCGGC	CATATTTGGC	TTCATCTCC	TTGGAAAGAC	CGTTCCATGC	240
GATACCGATA	ACTTCTTTTC	CTCCGAAAGT	GATGAACCTG	AGAGCCGTGT	TGCTACCGAA	300
ATAGCCCAAC	TGTGCGAAAT	AGGATTTTCA	ATCCACGCTT	CCTCTATCCA	CGTAGCCGTC	360
CGAACCGATT	TTGGACAGGC	GGGCATCCAC	TGCCCAATGG	CGACCGATGC	GTCCGCTACC	420
GAGTTTGACC	GATCGGCGGA	ATGTGCCGAA	CGAACCTCCG	CTCAATCGA	CACGGCCATA	480
AGGAGCCACT	CCCAAAATTAT	CCGTACGCAT	ATTGACACTT	GCCCCAAAG	CTCCGGCACC	540
ATTGGTGAA	GTACCCACAC	CTCGCTGCAC	CTGAAGGTCT	TCGATGGAAG	AGGCGAAGTC	600
GGGCATATTC	ACCCAAAAGA	CGGACTGAGA	TTCGGAGTCG	TTGAGGGGTA	CTCCATTGGT	660

WO 99/29870

PCT/AU98/01023

68 / 490

AGTTATGTTG ATGCGATTGG CATCGGTGCC ACGCACGCGA AAGCCGGAAT ATCCGATACC 720
CGTACCGGCA TCGCTGGTGG CTACCAACGGA GGGAGTCAGC ATCAGCAGAT AGGGGATGTC 780
ACGACCATAA TTGGACTTGG AAAGTTCGGC CTTGCGAAGC TTGGTGTAAG CGACAGGGGT 840
TTTCGCCGTG GCGCGAGTAG CTACGACCTG TACGGTCTGG AGCTGCACAT TGCTAAGACT 900
5 ATCTATCTCG CTGTTGGAGA CGGGTCTTC TGCCGTCAGG CAGAAAGGCA GGACGGC 957

(2) INFORMATION FOR SEQ ID NO:100

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1842 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 15 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 20 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 25 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION: 1...1842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100

30 CCATATAATG TCCAATCTAT TAGCAACAAG ACGATTAAAA AACAAATGGA AAACCTTAAAG 60
AACATTGAGC CCAGAGAGGA TTTCAACTGG GAAGAGTTTG AGGCCGGTGG CGTCCATGCT 120
GCCGTGAGTC GTCAGGAGCA GGAAGCTGCT TATGACAAAA CGCTCAATAC CATCAAGGAA 180
AAGGAACTGG TAATGGGTAG GGTAACTGCT ATCAACAAGC GTGAAGTGGT TATCAATGTA 240
GGGTACAAAT CGGAAGGTGT GGTACCTGCA ACAGAATTCC GCTACAATCC CGAACTCAAA 300
GTGGGAGACG AAGTGAAGT TTATATCGAG AATCAGGAAG ATAAGAAGGG CCAGCTCGTC 360
TTGTCTCACC GCAAGGGTCG TGCCGCTGGC TCTTGGGAGC GCGTGAAACGA GGCCTCTGAA 420
AAGACGAAAA TCGTAAAGGG CTATGTGAAG TGTCGTACCA AGGGTGGTAT GATCGTCGAT 480
GTATTCTGGT TCGAGGCTTT CTTCCCGGGA TCACAGATCG ACGTGCGCCC CATTCGCGAC 540
40 TACGATGCAT TCGTTGAGAA GACGATGGAG TTCAAGATTG TGAAGATCAA TCAAGATAT 600
AAGAATGTAG TTGTTCCCA CAAGGTGCTC ATCGAAGCAG AGCTCGAACA ACAGAAGAAA 660
GAAATCATCG GCAAGCTCGA AAAAGGGCAG GTACTCGAAG GTATCGTCAA GAATATTACT 720
TCCTACGGAG TATTTATCGA CCTCGGTGGA GTGGATGGTC TTATCCATAT CACTGACCTT 780
TCATGGGGTC GTGTGGCTCA TCCGGAAGAA ATCGTACAGC TGGATCAGAA GATCAATGTC 840
45 GTTATCCTCG ACTTTGATGA AGATCGCAAG CGTATCGCTC TCGGACTCAA ACAGCTGATG 900
CCTCATCCTT GGGATGCTCT CGACAGCGAG CTTAAGGTAG GCGATAAGGT GAAGGGTAAA 960
GTTGTGGTGA TGGCAGATTA CGGTGCTTTC GTTGAGATTG CACAGGGCGT TGAGGGTCTT 1020
ATCCACGTAA GCGAAATGTC ATGGACACAG CACTTGGCTT CTGCTCAGGA CTTCTTGCAT 1080
GTAGGCGAGC AAGTGAAGC CGTGATCCTG ACGCTCGACC GCGAAGAACG CAAATGTGCG 1140
50 CTCGTCCTGA AGCAACTCAA CCGGATCCTT TGGGCTGATA TCGAACTCG TTTCCCTGTA 1200
GGCTCTCTCG ACCATGCTCG TGTTCCGAAC TTCACCAATT TCGGTGTATT CGTTGAGATC 1260
GAAGAGGGCG TACATGSCCT TATCCATATT TCCGACCTTT CTTGGACGAA GAAGATCAAA 1320
CAGCCAGCGG AGTTTACGGA AGTAGGTGCT GATATCGAAG TTCAGGTAAT CGAGATCGAC 1380
AAGGAAACCC GTCGTCTCAG CTTGGGTGAC AAACAGTTGG AAGAGAATCC TTGGGATGTA 1440
55 TTCGAGACGG TATTCATGTT AGGATCTATC CACGAAGGAA CGGTAATCGA AGTGATGAC 1500
AAGGGTCTG TCGTTTCTCT GCCTTACGGT GTGGAGGTT TTGCCACTCC GAAGCAGATG 1560
GTGAAGGAAG ATGGCTCACA GGCTGTACTC GAAGAGAAGT TACCTTTCAA GGTATTGAG 1620
TTCAATAAGG ATGCCAAGCG AATCATGTA TCTCATAGCC GTGTATTGTA AGATGAGCAG 1680
AAAATGGCTC AGCGTGAAGC CAATGCAGAG CGTAAGGCTG AAGCCAAAGC GGCTCAGAAA 1740
60 GAAGCTGCTG CGAAGCTGCG CAATCCTGCA CAGGCTGTAG AGAAAGCCAC TCTCGGAGAC 1800
CTCGGCGAGC TGGCGCTTT GAAAGAAAAG CTTTCAGAAA AC 1842

(2) INFORMATION FOR SEQ ID NO:101

- 65 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 729 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 75

WO 99/29870

PCT/AU98/01023

69 / 490

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

5 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...729

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101

TCGACAATAA	TGAAAAAAGC	TATTCTTTCC	GGAGCGGCCT	TGCTCCTCGG	CCTATGTGCC	60
AACGCACAAA	ACGTGCAGTT	GCACTACGAT	TTCGGTCATT	CCATCTACGA	CGAACTAGAT	120
GGACGTCCCA	AACTGACTAC	CACAGTGGAA	AACTTCACAC	CCGACAAATG	GGGAAGCACC	180
TTCTTCTTCA	TCGACATGGA	TTACACGGGC	AAGGGTATCC	AGTCGGCCTA	TTGGGAGATT	240
TCGCGCGAAC	TGAAGTTTIG	GCAAGCTCCC	GTTTCCATTG	ATTTGGAGTA	CAACGGAGGC	300
CTCTCCACAA	GCTTTACTTT	CGGACACGAT	GCTCTAATCG	GTGCCACCTA	CACCTACAAC	360
AACCCCTCCT	TTACACGTGG	ATTACGATC	ACGCCCATGT	ACAAGCATCT	GGGTGCGCAC	420
GACTTCCACA	CCTATCAGAT	CACCGGCACT	TGGTACATGC	ACTTTCGTGA	CGGTCTGCTT	480
ACCTTCAACG	GCTTCCCTGA	TCTTTGGGGT	TTCCCCAAG	AGAACCAAT	CGGGGGCCCT	540
GTGCTCAAAG	AAGGGCATAA	GTTCGTATTC	CTGTCCGAAC	CGCAGTTCTG	GATCAACCTC	600
AAFCGCATCA	AAGGCATCGA	CAAGGATTTC	AATCTCAGCA	TAGGGACAGA	GATGGAAATC	660
AGCAGGAAC	TGCTCGCAT	GGACAAATTC	TCCTGCATCC	CTACTCTTGC	GGTCAAATGG	720
ACTTTCAAC						729

(2) INFORMATION FOR SEQ ID NO:102

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 705 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102

ATGAAAACAA	TTAGTAAGAA	CCATGCGGCA	CGGATCTGTG	CGGCCATTGC	TTTGTTTGCA	60
GTGTGTAACG	GCCGGATAGC	TGCTCAGGAT	TTTCTCTATG	AAATAGGAGG	AGGTTTGGGT	120
GCTGCTCAGT	ATTTTGGCGA	TGCNAACAGA	GGCTTGTTCG	GTTTATCCGG	AGTAGGTTTG	180
GAGTTGGTCG	GACGTTACAA	TTATAATTTT	CGCTGGGCTT	TCAGTACCAT	GTTGGATTGG	240
CGTACATTGA	GAGGCGATAC	CGATAAGTCC	GGGAATGTCT	TCCCCGATT	TGCTCAAGCG	300
GATTTTAAGG	TCGGCTTGAC	TCAGCTCCAC	GTTAGAAGCG	AATTTAACTT	TCTCCCTTAT	360
AGCGATGSGT	ATAAGTATCT	TGGTACAGCT	CGGCTGTCTC	CTTATGTAGC	GGCCGGGTTG	420
TCTTTGGGTT	TTGCTTCGGG	TGCTAAGGCT	TCGGCTTTTG	CTCCCGGGAT	TACTGCGGGA	480
ATGGGAGTGA	AGTATAAGCT	TAAACCGCGG	ATCAATGTCT	GTATCGAGTA	TTCTTTCACG	540
GGGTACTTGA	CGGATGCTTT	GCATGCGCTG	ACGATAAAAA	GTGTTTGGCT	CGAGGATCCA	600
TATAAGATCA	ATGACTCCTG	GGTCAAAAAC	AAGGATGCTA	CAGGGGCCCT	AGTGCTTAGG	660
ATTACGTATG	ACTTCGGCCT	GCGTAAGACT	TTTTGTAATA	AACAA		705

(2) INFORMATION FOR SEQ ID NO:103

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1308 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

WO 99/29870

PCT/AU98/01023

70 / 490

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103

AATATAATGT	ATAAAGACTA	TAAGGGTTTG	TATGCGTCGC	TTCCGGTGGTA	TGCCCTGATC	60
ATTGGGTTGC	TATTTCGAGC	ACACGGTATA	CAGGCTCAGA	ACAACAACCT	TACCGAGTCG	120
CCTTACACIC	GCTTCGGCCT	TGGCCGTCTC	GGAGAACGGA	CGACTATTAG	TGGGCATTCC	180
ATGGGAGGAC	TGGGCGTCGG	TCTGCGTCAG	GGCACATACG	TCAATGCCGT	CAATCCTGCT	240
TCATACTCGG	CTGTGGATTC	GATGACGTTT	ATCTTCGATT	TGGGTGCATC	TACCGGAATT	300
ACGTGGTATG	CCGAGAACGG	GAAAAAGGAC	AATAGGAAAA	TGGGAAACAT	TGAGTATTTC	360
GCCATGCTTT	TTCCTATTTC	CAAAATCCATT	GCTATGAGTG	CGGGAGTGCT	TCCTTACTCC	420
GCATCCGGGT	ACCAGTTCGG	ATCCGTGAT	CAAGTGGAG	GAGGAGCGT	CCAGTACACC	480
CGTAAATACT	TGGGGACAGG	CAATCTGAAC	GATCTCTATG	TGGGTATAGG	TGCACCCCGC	540
TTCAAAAAC	TCTCAATAGG	AGCCAATGCT	TCATCCCTTT	TTGGGCGATT	CACACACAGC	600
AGGCAGGTAA	TCTTCTCCAC	GGAGGCTCCT	TACAATCCCG	TACATCTCTC	GACGCTGTAC	660
TTGAAGGCTG	CCAAGTTCGA	CTTCGGTATG	CAGTATCACC	TTCTTCTCAA	ATCAGATCGT	720
TGGTCTGTTA	TGGTGCCCGT	CTATCTCTCG	CGGGTGAAGA	TGCATAGCGA	GCTGACTCAG	780
ATAAAGATC	AGGTTCAAG	CGGTGTAGTA	GTGGAGAGCG	AAACCCAAGA	ATATATCAAG	840
GGAATGGACT	ATTATACCTT	GCCTCATACA	TTGGGGATAG	GTTTCTTTTA	TGAAAGGAAA	900
GATAACTTC	TCTTAGGAGC	AGAGCTCCAA	TATAGTAAAT	GGAAGGCGA	GAAATTTTAT	960
AAATCCGATT	GCAAAATCCA	GSACAGAATA	CGGGTATCTC	TGGGCGGAGA	GATCATACCG	1020
GATATAAATG	CCGTGGGGAT	GTCGCTTAAA	GTTTCGGTATC	GCTTCGGTTT	ACATGGTGAA	1080
AATCTCTACC	TGAAAGTGCC	GACTAAAGGC	GGTGTATATC	AAGGATACCA	TATCGTAGGT	1140
GCTGTATTCC	GTATAGGAAT	CCCGCTCAAT	GACAGACGTT	CGTTCGTAAA	TGCTCTCTTT	1200
GAATATGACC	GATTGATCCC	GAAGGAGGGT	ATGATCAAG	AAATGCTCT	GAAATTGACC	1260
TTCCGGCTCA	CGTTCAACGA	GTCATGGTTT	AAAAAGCTGA	AACTGAAC		1308

(2) INFORMATION FOR SEQ ID NO:104

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2835 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...2835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104

AATACCATT	CGGAGAATGG	GAACGATAGC	ACCTATTTT	CTTTTCAAAC	TTTTCTTATG	60
CGATCGATTT	ATCAATTACT	GTTGTCAATA	CTCCTTGCTT	CTCTTGGTTT	CGTCGGGCTG	120
GAAGCCCAAC	AAGCCGGAGT	AGCAGGTAGA	GTATTGGACG	AAGAAGGCAA	CCCCATGATT	180
CAAGCCCAAC	TACAGCTTGT	ACAGAGTACC	GGCCAAGTAG	CCGTTGCCGC	AGGTGCCACT	240
AATGAAAAAG	GGTTGTTCAG	CCTGAAAAAG	TCACAGGAGG	GTGACTACAT	TCTGCGCGTT	300
TCATATGTAG	GTTACACTAG	CCAGGACGAA	AAAATATCTC	TTAGAAACGG	GCAAAACATT	360
ACGCTCAAAG	ATATATCCAT	GAACGAAGAT	GCCCGTCTTC	TACAGAGTGT	GACGGTGCAG	420
CGTAAAGCGG	CACAGGTCTG	GGTACGCAAC	GATACGCTCG	NATTCAATGC	CGGATCCCTAT	480
ACCGTAGCAC	AGGGAGCTTC	TATCGAGGAA	CTGATCAAGA	AGCTACCCGG	AGCAGAGATC	540
GGATCCGATG	GGAAGATCAC	CATCAACGGC	AAGGACATTA	GCAAGATCCT	TGTCGATGCC	600
AAAGAGTTTT	TCTCCAAAGA	TCCACAGGTG	GCAATAAAGA	ATCTTCGGGC	CGATATGGTC	660
AATAAATGAC	AGGTACTGAA	CAAACTGAGC	GAGCTCTCGC	GGATGAGCGG	TTTCGATGAT	720
GGAGAAGAGG	AGACCGTAAT	CAACCTGACG	GTGAAGCCCG	AAVAAAAGAA	AGGCCCTCTC	780
GGAAACGCTT	AGGCCGGCTA	CGGTACCGAC	CAACGCTATA	TGGCCGGAGG	GAACGTCAAT	840
CGGTTCGATG	GAATAAGCA	ATGGACATTG	ATCGGTAGTG	CGAACAATAC	GAACAATATG	900
GGCTTTAGCG	AGATGGACAG	CGAGATGGGA	TCCATGACCT	TCTTCTCTCC	CCAGGCGGCT	960
GGTCGACGCG	GCTTCGGCAA	TAGTGGAGGT	GTTACGTCTT	CGTCGATGCT	GGGCGGCAAC	1020

WO 99/29870

PCT/AU98/01023

71 / 490

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TTCAGTGTCTG AATTCTCTCTC TGCCCTTAAT ACAGGAGGCG ATGCACGCTA CGGATACAC 1080
GACAAGGCCA TAGAGACGAC CAAACGCGTG GAAAATATCC TCGCCGAAGG GAATACTTAT 1140
ATGACGAGAA ATATATTGGA ACGCTCTTTC TCTCACAATG GTGAGGCGCG ATTTAGGATG 1200
CAATGGAAAC CGTCCGAACG TACCGAAGTG GTATTGAGC CGGATCTTTC GATATCCAAG 1260
ATCGATGGGT TCTTTAACGA CACATACGAG ACGAAAGATG CCACCGGAAT CTCTATCAAC 1320
AAAGGTTCTA TCCACCAAAC TACACAAGGA AACAACTTCA GACTGAACGG AGAATTGGAT 1380
ATCAGTCACA AGCTCAACGA CGAAGGCGGT ACGATCAGTG CCTCCGTCTG TGGCGGTCTG 1440
ACCGACGAAG ACGGAGATGG CATATATCAG GCTGTGCTCC AAGCGGTGGA GACGAATCAA 1500
AAGCAATTC ACGACAATC CAACCTGCAA TATCGGCTTC GCCTCTCGTA TGTGGAACCG 1560
TTGGGTAAAA ACTACTTCGC ACAAGCGATT CTGAACGAGC GTTCTCTCCG TCGCAATTCTG 1620
GATCGTGAGG TGTACCGACT GGGCGATGAC GGGCAATACT CCATATTAGA CAGTCAGTAC 1680
GGACTCTCCT ACAGTAACGA GTTCACCCAG TATCGCATCG GACTCAACCT CAAGAAGATT 1740
GCCAAAACGT GGGACTACAC CGTAGGATTG AATGTGGATC CCAACAGAAC TCTCAGCTAT 1800
CGGAGCGTAG CCGAGTAGA GCAGGACAAA CTGGCTTTCA ATCGTGTCAA TCTCTCCCG 1860
ATGCTCCGAA TCAACTACAA ACCGAGCAGG ACTACCAACC TCCGAGTGGG CTACCGAGGA 1920
CGCACGACAC AACCATCCAT CAATCAGATG GCTCCCGTTC AGGACATCAC GAATCCGCTA 1980
TTCTGAGCGG AAGGCAATCC CGGTCTGAAG CCGAGCTATT CCAACAAATG GATGGCCATG 2040
TTCTCGGACT TCGATGCCAA AAGTCAGCGA GCTTTCAACA TTGTTTCTT CGGCAACTAT 2100
ACATTCGAGC ACATCGTCCC CAATACGAC TACGATCCGT CTACAGGGAT CCGTACCACT 2160
CGTTACGAGG AAGCCCTCCG TACGTGGCAA GCGAATCTTC ATGGGACACT ATCGCTTCCA 2220
CTCAAGAACT GGGCATTTTC TTTCAGGATG TCCTTGTTC AAGGTTGGC CGAAGGACAA 2280
AGCTTCATCA ATGACGATAA GAACAAAGCT CTCTCTTTCC GAACGAGGGA ACGCTGAGC 2340
CTGACCTATC GCAACAATTG GATCGATACG AGTATCGGTG GCAATATCGG ATTCTATATG 2400
GCGAATATA GTCTGAGCGG ACAGAAAGAT TCTCGCACAT ACGATTTTGG CGGCAATTAT 2460
CAAGTTGCCG TAACGCTTCC CTATGGATTG CGTATCGACA GCGATGTTGA ATACAATACG 2520
AATCTCGGTT ACAGCGGAGG ATTCAGTCTG GACGAATGSC TTTGGAATGC TTCGCTTTCA 2580
TACAGCTTCC TCCGTGACAA GGCCGGTACA CTGCGTGTCA ATGGCTATGA CATCTCGGT 2640
CAGCGGTCAA GTATCAGCGG TTCTGCTTCG GCCATCAATA TAGAAGAGAG CATGTCCAAT 2700
ACGATCGGAC GCTACGTGAT GGTGGACTTT ATCTACCGAT TCAACGCCCT CAGTGGTGGT 2760
GGATCTCGCA CGGATCATCA GCGTGGCAAT ATGAATCGTC CGGGCCACC TTTGCGCGGT 2820
GGCAGACGAC CGTCC 2835

35 (2) INFORMATION FOR SEQ ID NO:105
40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1236 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
45 (ii) MOLECULE TYPE: DNA (genomic)
50 (iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
55 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1236
60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105

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GGAGAGTATC CTGCAAAACG TAACGACAAA AAAGAGATGG TTATGAAGCT GATTAAAAGA 60
AGTTTGTCTC TGCTTGGAGC GGTACTGTCT ATTACGCTTC CTGCGTACTC GCAGAATGAT 120
GACATCTTCG AAGATGACAT CTATACATCG CGAAAGAAA TACGTAAACA AAACCAAGTT 180
AAAGACTGGC AAAACCAAGA GGACGGATAC GGCGACGATA CGGAATATAC AGTGGCTTCC 240
GATCGGGACA TTGAGCGCTA CAATCGTAGA GATGGCCAST CCTACGATGG GAAAAAGTTG 300
TCCAAAGACA AGAAAAGAGA CTCCACTCGT TCTTCTGTTC CCGGTGCTA TAGTCGCCGC 360
TTGCTCGAT TCTATAAGCC GAATACGATC GTCTTTTCAG GTGCCGACA TGTATATGTA 420
ACTGATGATG GTGAGTATTT CGTCTATGGA GACGAATACT ATGATGACGC GTCGTCTGTA 480
AACATTTACA TCAACAGTCC TTGGTGGGAT CCGTCCCTT ATACGTCATG GTATCCATCT 540
TTCTCCGGCT GGTACAACAT TACGTGGAAC TATCCATGGT TCTACTACGG TAGCCATATC 600
GGATGGGGCG GTTATTACCC CGGATATAAT TGGTATTGGA GCTACTACTA TGATCCTTTC 660
TACATTCCTT ATGGNAATCG TATGGGTTGG GGATATCCCT ATGGCTGGGG CAGCTATTAC 720
GCTTGGGGTG GGTATCCGGG AGTGATACAT CACTACCACC ACTACCCCAA GAAGACCTAT 780
TCCAAATGGT AGCATTCGGG AGCTTACTAT TCTATGSCC GACCGAATCG TATCAAAGGT 840
GGAAAGCTCG GTGCCAAACT TGGGACAGGA CGCTACGATA GAATTCAAAA TTCCTCTTCG 900
CAAAAAATA AGTTCGGATT GCAGTCGAAC AAACCCATA ATATCTGCA AAATGTCAAG 960
TCGGGACGTA CCGGCCGAGC CAATAGAGAC CGAAATATAG AAACGGTAAC TCCAAACAC 1020
GGGCAAAAGC AAGATCGTCC CGTATTCAG CAGATACAST CCGCAATGA CCGACCGACC 1080
GGACGGAATA TCCGCAGCGA GAGACAGGGG GAAAATAACG ATAGACATT TTCGACTCCT 1140

WO 99/29870

PCT/AU98/01023

73 / 490

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature
(B) LOCATION 1...756

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(x1) SEQUENCE DESCRIPTION: SEQ ID NO:107

10	AGGGGGTCGA GTTCGGGCAT TTCAGCCCGT GGACGCGACA TGGGTTCTTT ATTTTGTAGC	60
	GCGTTTGGCA GCTCCTCTCT CCATGGTTCA GAGCGACGCA GTCCGATAAG TTCTTCTGTA	120
	GTCATGTCAA TAAGGCAGAA AATAAGGTTA TTCCATCTCT CGGTATGCGC CCAAACGCAT	180
	GATCATCTCA TCGAAATCCA CTGGGTGTGC ATCGAATTCG GGGCCATCGA CACAGACGAA	240
	TTTCGTCTGT COTCCACGCG TTATACGACA AGCCCCACAC ATACCGGTGC CATCCACCAT	300
	AATTGTATTG AGAGAAGCTA TGGTCGGTAT CTCGTAACGT TTGGTCAGGA GAGAAACGAA	360
15	CTTCATCATC ACAGCCGGCC CGATCGTAAC GCAGAGGTCT ACCGTTTCCC GTTTGATAAC	420
	GCTTTCCACT CCATCGGTTA CGAGGCCCTT CGTCCCATAA GACCCATCGT CTGTCATGAT	480
	GATCACTTCA TCGCTATTGG CTCGCATTGG TTCTTCAGG ATAACAGAT CTTTAGTTCT	540
	GGCAGCCAAT ACGACAATTA CACGCTTGGC TGCTTTGTGG AAAGCCTCCA CGATCGGGAG	600
	CAAAGGAGCC ACACCCACAC CGCCTCCGGC ACAAACTACT GTGCCGACCT TTTCGATATG	660
20	CGTACTCTGT CCCAGCGGAC CTACCACATC CGTGATATAG TCGCCGACTT CGAGTTCGGC	720
	CAATTTCTTG SAAGATTTGC CCACGGCCTG AACCAC	756

(2) INFORMATION FOR SEQ ID NO:108

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2370 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

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(ix) FEATURE:

(A) NAME/KEY: misc feature
(B) LOCATION 1...2370

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(x1) SEQUENCE DESCRIPTION: SEQ ID NO:108

50	CTCTTGTTTT TTCTCCTTT ACCCGGAATG GATCGTCTTA AGCCTTCATA TATTGTTGCA	60
	ATAGCAGCCA TTCTCTGCTT GTTTGTGCGC AGGCCCTTGT TTGCGCAGAG CTATGTGGAC	120
	TACGTGATCG CGCTGATCGG GACGCTAAGT TCTTTTGAGC TGAGTGCGGG CAATACCTAT	180
	CCGGTGATCG GTTTACCGTG GGGAAATGAAT AGCTGGACAC CGATGACCGG TGTACCGGT	240
	GACGGCTGGC AATATACCTA CTCGGCACAC AAGATTCGCG GATTCAACA GACCCACCA	300
	CCAGTCTCTT GGATCAACGA CTACGGCCAA TTCTCCCTTC TTCCCTTAC GGCACCGCAG	360
	AAGCCATCAT CGAACGACTC CATAGCTCTG ACTAAATGGT GCAAGCACT CTTTTCGGAC	420
	GAACAGACCT CGTGGTTCTC GCACAAAGCG GAGACGGCGA CGCCATCTA TTATAGTGTC	480
55	TATTTGGCCG ATTACGACAC ACGCGTGGAG ATGGCTCCGA CCGAGCGTGC AGCTATCTTT	540
	CGCATACGTT ATTCGGGCAA TACCGAAAGT GGCTCCGGTC GATGGCTTCG TCTTGATGCC	600
	TTTACCGGTG GTTCGGAGAT TAGCATCGTG GATCCTCACA CCGTAGTGGG CATATCTCGC	660
	GAAGATAGCG GAGGTGTGCC GGCTAACTTC GCCTGTTATT TCATCTGCA GTCCGATACT	720
60	CCTATGGCCG ATGTCTGTCT TGAGACAGAT ACCGGCPAGT CAGACGAAGG CACAAGGGCA	780
	TGGGCAGCCT GTCGCTTCGA TTCGCAAGAA GTTACCGTCC GGGTGGCATC TTCTTTTATC	840
	AGTGTGAGCG AGGCCGAAAG AAATCTTGCG GAAGTCAAAG GGCAGAGTT CGACCGGATC	900
	AGACTTGCCG GTCGCGAAGC TTGGAATAAG GTGCTCGGAC GCATACATGT GGAAGGAGGA	960
	ACGAAGGATG AGCGCACTAC ATTCTATTCC GCACTCTATC GCTGTCTGCT TTTTCCCGCT	1020
	CGCTTCTATG AGGAGGATGC TPCCGCAAT TTTGTGCATT ACAGCCCTTA CAATGGAGAG	1080
65	GTACTTCCCG GTTATCTCTA TACCGATACC GGATTTTGGG ACACITTTTC AGCCCTTTTC	1140
	CCCTGTCTCA ATCTGCTGTA TCCCGATGAA AACATTAAAA TTCAGGAAGG TCTGCTGAAT	1200
	GTATATCGCG ASAGTGGCTT TTTCCCGGAA TGGGCCACTC CGGGCCATCG GGATTTGATG	1260
	ATAGGCAACA ACTCTGCTTC TGTTCTGGCG GATGCCTACC TCAAGGGTGT TCGGGTAGAA	1320
	GATACCCGTA CACTGATGAA CGGACTCTTG CATGCTACGA AAGCCGTCCA TCCGAAATC	1380
70	TCCTCCACGG GTCGCAAGG TTGGGAGTGG TACAACCTCT TAGGTATATG TCCGGCTGAT	1440
	GCAGGCATAG ACGAAAGTGC TGCCCGTACG CTCGAATATG CTTATAACGA TTGGTGCATC	1500
	CTCCGACTGG GGGCCACATT GGGTTGGGAT AGAGCTGCAT TGGACACGTT GGCTCATCGT	1560
	TGATGAACAT ATGCTCATCT GTTCGATCCG GAAACCAAC TCATGCGCGG TAGAAATCAG	1620
75	GATGGTAGTT TCCGGACACC TTTTCCCTT TTTCAATGGG GAGATGTATT CACGGAGGGC	1680
	AATGCCGCGC ACTACACTTG GTCGCTCTTT CATGATGTGC AGGGGCTTAT CGACCTGATG	1740

SUBSTITUTE SHEET (Rule 26) (RO/AU)

WO 99/29870

PCT/AU98/01023

74 / 490

5 GGAGGAGATC GCCCGTTCGT GTCTATGCTC GATTCGGTAT TCAATACTCC TCCTATGTTT 1800
GATGAGAGCT ATTACGGATT TGTATCCAC GAAATCAGAG AGATGCAAAAT AGCGGATATG 1860
GGCAATTATG CTCATGGCAA TCAACCCATA CAGCATAIGA TATATCTGTA TAATCATGCC 1920
GGTCATCCAT GGAAGCTCA GGAGAGACTA CGCGAAGTGA TGGGGCGGCT CTATCGTCCT 1980
ACTCCGGATG GGTATTGCGG CGATGAAGAC AACGGACAGA CTTCGGCTTG GTACGTTTTC 2040
TCTGCTTTAG GCTTCTATCC TGTACACCC GCTACGGATC AGTATGTGCT CGGTCGCGG 2100
ATTTTTCCTA AGGTAATACT CTCTTTCCC GACGGACACA AAACGGTGTT GCATGCTCCG 2160
GCCACAGTG CCGATACGCC TTACATCCCG TCGATCAGCG TAGAAGGAAA AGAATGGAGC 2220
10 TGCAATTACC TGACTCAGC ACAGCTTCGC TCTTCTGCAT CCAATTCAATG GATGATGGAC 2280
ACGAACCCA ATTATAATCG TGGTATGAAG GAAAGTGACA GACCTTATTC CTCTCCAGC 2340
GAGCAACAGC GTCGCGCTAA TCACAGTAAT 2370

15 (2) INFORMATION FOR SEQ ID NO:109
(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 858 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...858
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109
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180
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ATTGTGGCA GTAAATGAA TCTATCGGGA TTACAATCTT TCACTATGAT GAAATCCATG
CGCAGCGTGC TGTGCTACT CTTTCCATTG TCTTTGATCA CTGCTTTGGG CTGTAGCAAT
AACAAAGCTG CCGAATCGAA GTCTGYCTCT TCGATTCCGG CCTATCTCGA ACCTACATC
CCTCTGCGGG CAGACATAGA TACGCCATCG CTGCATGTGA TGATCAGCTA CGTCTATCCT
TCGGGAGATG ATATGCTCAC AGAGATTTTC AACGGTTTGC TCTTCGGCGA CAGCCTGATG
GATTCTCTT CCGCGGAGAA TGCCATGGAA GGCTATGCAC AGATGCTGGG AGAAGACTAT
CGCTCTAACA ATGCCGAACC CAATCTGCAA GGGCTTCCTT CTGACCTTTT GGAATATATC
TACAAGCAGG AAAATACCAT CGCTTATTGC GATACGGGAT TGATCTCCAC GCGCATCAAT
ACATATACTT ACGAAGGCGG TGACATACG GAGAATACAG TCCGGTTTGC CAACATCCTT
CGCACCCCG GCAAGGTGCT CGAAGAGCGA GATATATCA AGATCGACTA TCGGSAAGG
CTGTCCGCAC TCATCATAGG ACAATTGGTG CACGATTTCG GCAAGACCAC ACCTGCCGAA
TTGGATGCAA TAGGTTTCTT CAACGCAGAA GAAATACAGC CCAATGGCAA TTTTATGATC
GATGACAAAG GTCTCACATA CTGTTTCAAT GAGTATCAGA TAGCTGCTTA TGCCAGAGGT
GCTGTCTATG TCCGTCTCGG ATATGACGTA TTGGCTCCTT TGCTAAGGGA TGATTCGCCA
CTAAGCGTT ACTTGCCG

55 (2) INFORMATION FOR SEQ ID NO:110
(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1134 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1134
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110
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WO 99/29870

PCT/AU98/01023

75 / 490

5 GGGATAATAT CTGTTCTTTC ACATGTGGTT GACCGTCCAC AATGGGGTGC TTCTCCCGAA 60
 GCTGCTGGCA CGCATAGTGT GTATTTCGATT CTACATCCCT CGCCCGGTAT TATCCGGATC 120
 AGGTCTATGG GTATTATCTC AGCCTGCCGT ATCGCAATTC TTGCCGGCAA GCACCCCGGT 180
 10 AGCGGTCTGT CGAGGGCAAA TGTAGGTATT CTTTCGTACA ATCCAGAAA CACGCCCGAG 240
 AAAAAGAGAA AACTGCAAGA AAAAATGTT TTCCTCCAAA TCCGGCTCCG TCAATCATT 300
 AATAATTTGA TACCTTCGCT CCCATTAGA ATCGATAACA CAAAAAAAT CACTGAAATG 360
 AAAAAAATA CTTTGACAGG ATCGATATGT GCTTTACTCC TGTTTTGGG TCTCTCGGCC 420
 AATGCCCAAT CGAAGTTAAA GATCAAGAGC ATTGAGGCAG CTACCACTT CAGTTCGGCC 480
 15 ACGGCCGAA ATGGTTTGG TGGCAATATC TTCGGCATGG ACATGAGCAT ACGGATGAGG 540
 GTACACCACA GCATTCTGCC CGAAGGGTTG GATTTTTCGG TAGGAATACA TGAAGAAGA 600
 GCACACTGGG AAGAGGCCGG AAGTCCGAAG CTCATGTATA CGAATGTCCC AAGTATCATT 660
 GGTATTGTTG AAAAGGTAAT AGTCTTCGAA GACGCAGAA ACTTTTGA CAAAAAGCT 720
 CTGGCCGCT TCCTCATCAG TTTGGGGATA TCCTATACCA AGCATCTGG AGCGTATTGG 780
 20 GGATGGACCA ATGACGCCCA TATCTTTTC TCACCGATAC CCAAGAGCAA GGTCCACTAT 840
 GACACCTACA CAAGAGCTGG CAGTGACCTT GTACTTCAGT CCGAAGATGT TGCCACAGTG 900
 AGCAATGGT TTTACCGGG GATCGGACTC AAAAGTTCTA TTTGGTGGAA AATGCCCATC 960
 AAGAGCAAT ATGATTTTCG CCTCGGTTTC AGCCTGGGCT ATGAGTATCT GAACCTGCTA 1020
 TATCCGTATC GTAAATTTCAA GCTGGATGGA AATAAGCCGC TTTCAGCACT ATCTCTCGC 1080
 25 ATGAACCACA TCGCCATGT GGCCTTCAAC TTTACCGTGG GTCTTTGGAC TAAT 1134

(2) INFORMATION FOR SEQ ID NO:111

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3807 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
 30 (ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
 35 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS
 40 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...3807
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111

45 GTAAATGTA TGGGCAAGTA TAAAGAGCT AAGTACCGCT ATTGGCTTTT TCCTTTCTGT 60
 TCGGATTATT ATACCTTTGA GGGAGTTACT TTTTATGCG CATCTGACGA TATGACAACC 120
 AAGAAACCCC AAGCCATTTT AGACTTAGAG AAGGCCTATA ACATTGAAAT TCCTGATCTC 180
 50 TCCTCACAAG AAGGGATAAG CTGCTCGGTA AATAGATATT TCAAGCAAGA TTCCTCCGGT 240
 GCAGTCCGTT AGCTTTGCTT GCGAGAATGT CAGATAGAAA GCATGACTTG GCTTATTGAT 300
 TTTCTGCTC TAAAAAGCT TGATCTATCG TATAACCAAA TCAGTAAGCT AGAGGGTCTA 360
 GAACGTCTTA CTGTTTAAAC AAAACTTCGT CTAAGTAGTA ACCAAATCCG TAACTAGAG 420
 55 GGCTTGGATA GTCTCACCTC GCTAACAAA CTTTCTCTCT CCGATAACCA AATCAGTAAG 480
 CTAGAGGGTC TGGAACTGCT CACCTCGTTA GCGGAGCTTT ATCTTTTGGG TAACCAATC 540
 AGTAATCTAG AGGGTCTGGA ACGTCTCAGC TCCTTAGCAA CGCTTGAAC ATCGGGTAAC 600
 CAAATCCGTA AGCTGGAGGG TCTGGAACGT CTCACGTCTC TAGCAACGCT TGAACATCG 660
 GGTAAACCAA TCCGTAGCT AGAGGGTCTG GAACGTCTCA CTTCTTTAAC AAAGCTTCGT 720
 CTAAGAAGTA ACCAAATCAG TAAGCTAGAG GGTCTGGAAC GTCTCAGTC CTTAGCAACG 780
 60 CTTGAACTAT CCGGTAACCA AATCCGTAG CTGGAAGGTC TGGAACTGCT CACCTCCTTA 840
 GCAACGCTTG AACTGTGCGG TAACCAATC AGTAAGCTAG AGGGTCTGGA ACGTCTCTCT 900
 TCGTTAACAA AGCTTCCTCT AAGAAGTAAC CAGATCAGTA AACTAGAGGG CTTGGAACGT 960
 CTCACCTGCG TAACAAAATC TTTCTCTCTC GATAACCAA TCAGTAAGCT AGAGGGTCTG 1020
 GAACGTCTCA CTTCTTAGC GGAGCTTTAT CTTTGGATA ACCAAATCCG TAAGCTGGAG 1080
 65 GGCCTGGAAC GTCTCACCTC GTTAACAAAG CTTCTCTAA GAAGTAACCA AATCAGTAA 1140
 CTAGAGGGCC TGGATAGTCT CACCTCGCTA ACAAACCTT CTCTCTCGA TAACCAATC 1200
 AGTAATCTAG AGGGCCTGGA ACGTCTCAGC TCCTTAGCGG AGCTTTATCT TTTGGATAAC 1260
 CAAATCCGTA AGCTGGAGGG TCTTGTGGT CTTGCTTCT TAACAAGGCT TAGCTAAGG 1320
 70 GSCAACCAAA TCAGTAAGCT GGAAGGACTA GACAGACTAA AGGTTTGGAG AAACTTGAT 1380
 GTTTCGGGCA ATGATATCA ATCTATTGAT GATATTAAGC TATGGCTCC GATTCTGGAG 1440
 CAAACTTTAG AAAAATGAG AATCCATGAC AATCCATTG TTGCATCATC AGGCTTGATA 1500
 CTCTCTCTCT ATGATAATCA TTTGCCGGAG ATTAAGCTC TTTCTGAAA AGAAAAAGAA 1560
 AATCAGAAAA AGACTTCAGT TGAATATCAC CCAATTTGCA AAGTAATGCT ATTGGGAAAT 1620
 75 CATTCTTCGG GTAAACCAAC ATTCTTAGT CAATACGATA CAAATTATAC GTATCAGAAA 1680
 AATACACATG TGTGTGCGT ACATCGAAGC AATAACCTTA ATGCGATCTT TTACGACTTT 1740
 GGGGACAGG ACTATTATCA TGGGATTAC CAAGCTTTT TTACCACCA ATCGTTATAC 1800

WO 99/29870

PCT/AU98/01023

76 / 490

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CTTCTCTTTT GGGATGCTAA GAAGGATCGA AACTTTGTGA GCGTAGATGA TAAAGAATAT 1860
CAGACTCTTA ATTTCATCG CCCCTATTGG TTAGGACAGA TAGCCTATGC CTGCAATCGT 1920
TGTATGTCGG TTGGAGGAAA TCCTGATGGC AAGGACACAC CACAGACCAC AGACGATACA 1980
ATTATCATTC AGACTCATGC CGATGAAACG GCGGCTAAGC AGCAAACTT AGGCTGTGCA 2040
GCCGAGAAATG GAGTATTGGA AGAAATCTAT GTATCCTTAG AGCCCAAGGC GAATAGTGCC 2100
GTACATGCGC TCAACTATCT GAATGAGCGG GTGCGAGAAG TTGTCGCAAG CAGGAGTAAA 2160
TCAATTGAGA TCACAGAAAA AGATAAGGGA TTGTACGAAG CTCTTCCAC AATCGCCGGT 2220
GATATAAATC ACATCCCTAT CTCTCTCGAA GCTCTTGGG CTCMAATTGAA TAAGGGAAGA 2280
GCTGAAAATG ATCTTTACAC CATAGAGTAT CTACAGACCG AATTGAACCA GCTTAGTCTG 2340
CGAGGGGAGG TGCTTTACTA TCGTGAGAT GAGAAGCTGA ACAATTATGT CTGGTTAGAT 2400
CCGGCAGCTT TTGTCCAAAT GATTCAATGA GAAATCCTCC AAAAAGACAA CATCAATAGA 2460
GGAACAGTTC CTAAAGACAT TTTTGAATGC AAATGCATA ATCTAAGTTC CGGAAGTATA 2520
TTTGAAGAAG ATGGCCAAAA TGGTAATATG ATCTTGACGC TATTATTGGA AGAGCTGATC 2580
GTATATGAAG ATAAGGACTG CTATGTGATA CCGGGCTATC TCCCTTTGCA TTCCGATGAC 2640
GAAGCCTATA AATGGCTTAC TTTGGGATTC GAGAGGCCCA ATTTTGTCTT CAAATTGGA 2700
CGTTTTATCC CTTTTGGCCT GATCAACAG ATTATAGCCT ACTATGCGCG GGAAGAAGGT 2760
GCTCTAAGC GGTATTGGCT AGATCAGGTC ATCTTCACAG CAGGCGGTGA GATGGATAGG 2820
CAAAACGCTG AGCAAGAAGA AGAGAAGAG GGTTTGCCCA AGACGAATGC CGAGGATTAT 2880
CAGATCTGGA TCAAGCTCGA CTTTACCGAC TTGGCCATAT CCGTATTCTT CAAAGAGCAG 2940
AGAAAGACAT CAGCTAAGGA TATGCAGCGG AAAGAGGCTA CTATCCTCAG TGATATGTTG 3000
GATATGTATT GGAACAATAT CCCTCCGAGG GAGCAAAATG GAGATAAGGA TACGAGAGCA 3060
ACGAGAAGCA CTATTCTGTA AACAACACGA AAGAAGAGAC CCATCCAGGA TCTCTACCTC 3120
TCCTGTGCCC AAGCGGATAA AGATTGACG GAGTCTCATT ATATCCATT GGGCAGCCTG 3180
GACGATGAAA CCAAGACTAC GCGGAGGATT SCAGCCTATC CCGTGAAGAA CGGCGTTATC 3240
GATAAAGAGC GGGTGGGAGA AGTAACGACT CGTCCCTACA AACATCTTTC CGTCAATAAA 3300
AATCTGCTCA CTGCAAAACA GATCTTTATT TCCYATTCCA AAGAGGATCA GACTGAACTG 3360
GAGACCTGTC TGCAATTITT CAAACCCCTG GAGAAGAATG GTCAGATCGA GATCTACTAT 3420
GATAAGTTGA CTAAGTTTGA AACACCTATT CACCTGAAA TAAGAPAGCG TATGTGCGAA 3480
GCCGACTGTA TAATCGCTTT GATCAGCCAA CGCTATCTGG CCACGGATTA CATCCTGGAT 3540
CATGAGTTGC CTGTATTTCG GGAGTATAAC AAGACCATAG TGCGGATATT GATCAAGCCT 3600
TGTCATTTCC AAGACGATGA GTTCCTTCGG GAGAAATATT TTGCTCAGAA AGCTCAAATA 3660
ATCAATCTTG GAAAGAGGG AAAAACCATT AAGCTTATG ATAGTATTAC GGCATCAGCC 3720
CATCGTGATG AAAATTGGGT GGCAGTAGTC AGAGAGTTCA AAGAGAAGAT ATTAAGAATA 3780
ACAAAACAGG AGGTAAATAC AGATGAA 3807

(2) INFORMATION FOR SEQ ID NO:112

40
45
50
55

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 693 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112

60
65
70

AAGTTTATGA TGA AAAAAGC ATTGTGTTTC GTACTACTGG TTTGCCTATT CTCTCGTTTC 60
AGCAGTTCCG CCCAAACAAC GACGAACAGT AGCCGGAGTT ATTTTACAGG ACGAATCGAG 120
AAGGTGAGTT TGAACCTAGG GGTCCCCCCC GTAAGCACAG AGGTTTGGGG AATGACCCAT 180
GATGCGAAGC GTCTCCCTTT CGAAATACCT ATCTCTTTCA GTGTTTCAA CAGCCAGGGA 240
GATATAGCTA CCACTTATTA CATAGCSAAT AGCGAGGCAA CTTTGAATGA ATGGTGGGAC 300
TATGCACACC CGGGCGGCAT CGTGAGGGTA GAGGTCGTT TTTGAAAT GACTTACAAC 360
ATACCAACCT ACAATGCAGT CTGCCCCCGG ATTACATTCG AAAATCAAGA AATAGAAGGA 420
ACGATCGTCT TGATACCCAA GCCCAAAGTC TCGCTGCCTC ATGTGTGCGA ATCGGTGCCT 480
TGCAATCGAA CCGAAGCCGG GAGGGAATTT ATCCTTTGGG AAGAAGACGA CACCTTTGTG 540
TCTCAGATG GTAACGAAGT AACGATAGGC GGTAAALUTT TCTTGCTCAA TACCAACGTA 600
AAGATTGTGG GGGACGTATC TCAAAAGTAT GCCGTGGGGG TAGGAGAAAT TCGATTCTCTG 660
CAGATTTGTG CCCAAACAGT ATCACAACAA AAA 693

(2) INFORMATION FOR SEQ ID NO:113

75

WO 99/29870

PCT/AU98/01023

77 / 490

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1689 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...1689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113

TCGCTAATCA	ACAAATTCAG	AGACTGGAGG	GCTCCTGTCC	GATTGAGTCT	CAAAAAAAG	60
ACAAAAACTA	TGAAGACAAA	AGTTTACGC	AAATTCGTGG	TGGCGGCTTT	CGCGTCCCA	120
ACCTCTGTG	CTCTCGCCCA	AGCGCAGACG	ATGGGAGGAG	ATGATGTCAA	GGTGGTCCAG	180
TACAATCAGG	AAAAACTGGT	ACAAACGAGG	ATGAGTGTGG	CGGACACCGG	ATGGATCTAT	240
GATTAACCCC	ACAGTGGATA	CGACACCGGC	AATAGCAATG	TGAAGATCTT	CCGCTCCAAA	300
GACCAAGGTG	CCACATACCA	AAAGTTGAGG	GATTGGGATC	CATCGGATGA	TTATCAGTTT	360
CAAGACTTCG	ATATCGTGGT	AACGGGTAA	AATGAATCCG	ACATCAAGAT	TTGGTCCGTA	420
GAGCTCATGA	ATAAGCCCCG	AGGATATAAG	AGTAGAGTTG	CGGCTTTCAG	TCGCGATGCC	480
AACCGGCAGA	ATGCGAAACT	CGTGTATAAG	CAAGACTTCT	CCAATGTGCA	GTTGTACGAT	540
GTGGATATAG	CCTCCAACTA	TCGTTCCGCT	TCTTCTCTTA	ACAATGGTGG	CAACCCCTTT	600
GCTTTGGCTT	TCGCTTACAC	CGGCTTCAAC	AATACGCACA	AAATAAGTTT	TGTGGACTAT	660
GTGTTCTCTC	TGAATGGAGG	GCAAAATTTT	AATAAAAACT	TACTCTTCAG	TCAAGATGGA	720
GAGAAGAAAA	TTGACAAGGT	GGATCTCTCA	TTGGGTAGCA	CCTCTGAATC	CATGGGTCAC	780
AATGCCCTGG	CGCTAATGGG	TGTGGTATTC	GAAATGAATA	AACAAGGGGG	AAAAAGCGAT	840
ATCGGTTTCT	TGTCGAACCT	TGTGACAAAT	GATCCCGAAT	TTCAAGTGGT	AGGCCCTATA	900
AAAGTGAGTG	AAAGCGACAT	GTCGTTCCAG	CCCAAAATCC	AAATGTTGCT	GGACGAGGAT	960
AACAATACGA	TCAATGGGGA	GAGTTGCCAC	AACTTCTATG	TTACGTACAG	CGATTATGAT	1020
TCTGAATATT	CGGATTGGGA	CATTGGGTAT	GTATATCCCA	AGAAATCGTT	CAAGTATGAA	1080
AAAGGAAAAA	CTCCGACTAT	GGATGATCTG	GTGGAGGCTT	TCCTTACAGC	TTGTTACCCG	1140
AGTGAGACCA	ACTCGGGGCT	GGGGTATGAC	AAGAAGGCCA	ATCACTACCT	GATTACATAT	1200
GCCAAVAAAA	AAGAGAACGG	TACGAACACG	CTGAAATACC	GCTGGGCCAA	TTATGACAA	1260
ATTCATAACA	AAGATTGTG	GAGCGACACA	TTTACGTATA	CATCATCTGC	CAATGCTCTC	1320
TACACACCTC	AAGTAGACAT	CAATCCGACC	AAGGGTCTCG	TGTGCTGGTC	ATGGGTGGAA	1380
TATCTGCCGG	GCAACCGGAT	CGTTTGGTCT	GATACGCAGT	GGACCATATC	CAACGGTGTA	1440
GAAGACATCG	TAATGCCAAG	AGGCAGCATG	AAGCTCTACC	CGAATCCGGC	TCAAGAATAT	1500
GCTGTGATTA	GCCTGCCGAC	GGCAGCAAAC	TGCAAGGCTG	TTGTTTACGA	TATGCAGGGC	1560
AGAGTAGTCG	CTGAGGCTTC	TTTCTCGGGC	AACGAATACA	GGCTGAACGT	GCAGCACTTG	1620
GCTAAGGGTA	CGTACATACT	CAAGGTCGTA	TCCGATACGG	AGCGTTTCGT	AGAGAAGCTC	1680
ATCGTGGAA						1689

(2) INFORMATION FOR SEQ ID NO:114

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2358 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...2358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114

WO 99/29870

PCT/AU98/01023

79 / 490

5 GCGGAGCTAT TGCCTCTCTC CTCCGCGGAT TCACGACTGT ATGTGACGGA TCGTGGTCTG 660
 10 TTTATCTGTG CCGAGAATCG AATTTATTTT ATAGAAAAG GTCGCAAAAC GACACATTT 665
 15 CCTATAGCCG ACGTCTTGG TGTCCGTGCC ATGAACGAA GCAATAOCCG ATACATAGCA 1020
 20 TTTGGAGAAG AAGSTTTGGC TTCCTTTCTT CTCGCGAGG GAAGTACGCC CGAAGCCATG 1080
 25 CCTGTAGCAT TCGACGGACC GGGGGACAAT GATTTCTACG AGATGCGGTT TAGTCAGGGA 1140
 30 CGTCTGTATG CAGGCAGCGG ACTCTGGGGA ACAAACCTGA TGGGACATGC CGGTATGGTG 1200
 35 AAGCTATACG ACGGCAACCG ATGGACTAAC TTCGACAAGA AGACCGTACA GGAACAGTTG 1260
 40 GCGGCGGATG TCAGTTTCAA TGATGCTATC GATATAGCTG TTTCCAAACG AGACCCCGAT 1320
 45 CACTTTTGTG TCGGTACATG GGGAAACGGT CTGTTGGAAT TCAAGGATGG CAAAGCGATA 1380
 50 GCTCGCTATT CCGGAAACGA AACTGCTATC GCAGAATGTA ATCCCGGAGA TGCCCGTGTG 1440
 55 AAAGCGATTG CCTTTGACAA TAAGGGCAAC CTCTGGGGGA CGCTCGGTGC CGTAGGCAAG 1500
 60 AACATCTTCA TGTACGATCC GCAGAGTAGC ACATGGCAIT CTTCAGCTA TCCGATGTA 1560
 65 GGCATCTGCG CCTCTCTCGG CAATATGATT ATCCTACCCA ACGGAGACAA ATGGGTAAAT 1620
 70 ATCCTTCACC GTAGTGGCGG ATCCACGCGC AAAGGTGTCT TGATCTTCAA CGATCGGGGT 1680
 75 ACACCGGAAL CGACTTCTGA CGACAGCCAT CTTTACGTCG AGCAGTTTGT CAATCGCCTC 1740
 80 GGGGAGGCAA TAGGACATAA GACTATCTAT GCAATGGCCG TCGATCATAA CGGCTCTGTC 1800
 85 TGGATGGGAT CGGATATAGG CATTTCGGGC GTCTACAATG CAGCCGGAGT ATTCTCCTCG 1860
 90 ACTTCTACCC CTATCGCTGT TCGCCCGGTC GGAGGAGAAG AACCCAATTT GTACTATGTG 1920
 95 CTGGACAAAG TGACGGTGAC AGACATCGTC GTGGACAAAC TCAATCACAA ATGGGTTGCC 1980
 100 ACCCAAGGSA CAGGACTCTA TCTCCTTTCC GAAGATTGTA GTAAGATCCT CGCGCAATTT 2040
 105 ACCGTASAAA ACAGCCCTTT GCTTTCTAAC AACATACTAT CCCTGGCCTT AAATGACGAT 2100
 110 AACGGACTGC TGTACATCGG TACGGCGGAC GSACTGATGA CGTTCCAAAC GGSTACGGGG 2160
 115 AGTGGATCAG CTTCCGAACT GGACGGCGTC TATGTATACC CCAATCCGCT AAGGCCGGAA 2220
 120 TATCCCGATG GCGTCACCAT TGCCGGACTG CAAGCCGGCT GTAGTGTCAA AATCACCGAT 2280
 125 ACCACCCGCA GACTGCTATA CCACACTGAG AGCGTAACCA CCGAAGTCAA ATGGAATGCT 2340
 130 CGAGGTGGCG ATGSCAATAG GGTAGCTTCG GCGGTATATG CCGTTGCAGT GTACGATCCG 2400
 135 GTATCGAAAA AGTCCAAACT AATTCGCTTC GCAGTGATTC GC 2442

(2) INFORMATION FOR SEQ ID NO:116

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3486 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
 40
 (ii) MOLECULE TYPE: DNA (genomic)
 45
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 50
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1...3486
 55
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116

60 GCTATTCTC AGATGAAACG AATACTTCCA ATAGTCGGAT TCCTTTCTCT CTTCTTGCC 60
 65 CTTGCTTTGC CTGCGAAGAC GCAACGAGCT ATGGGGAAGA CGGCCGACCG TTCCGTAATG 120
 70 GCTTCGGGAC ATTGGGTCAA GATACGTGTC GATGCAAGTG GAGTGTATCG CCTTACGGAC 180
 75 GAACAGCTCC GTGCCAATGG CTTCTCCGAT CCGTCCAAAG TAGGTGTGTT CCGTTATGGT 240
 80 GGAGGGGTGC TTCCCGAAGA TCTGAGCCGG ATCAGCAGAG ACGATTTGCC TCCGGTACCG 300
 85 GTACTCCGTC AGGGCAATGC GCTGTATTTU TATGCCGTGG GCCCGGTGAC ATGGTTCTAC 360
 90 AATCCGGCCA AAACCCCATG GGAGCATACG GTGAATACAT ACAGTACGCA TGGCTACTAC 420
 95 TTCTGTGCGG ATGCTGCCGG AGCACCTTTG CAGATGTCTT AATATACGGG TGGAGGTGCG 480
 100 TCGGCCGAGG CTTTGATCGA CTACTACGAT GAGCTGATTC TCCATGAACA GGAATTGTAT 540
 105 TCGGCCAAG AATCGGGACG AGATCTGTAT GCGAGTCTT TCASTCCAGT CAATACCGGT 600
 110 ACGGTCAAGT TCCCTTTGAG GGGCAACACC CGTCTGCTCT GCGAACTCGG TACCGTATTC 660
 115 TCATACATAG CCAAGGCCAG ATCGGCCGGT GCGGCGCGTG AGATGTGCGT CTGCGCGAAT 720
 120 GGCATTCTGA TCTTACGCGA TCCTTTTTC ATGACATGSA ATGAAGTCTC CAATTCCTAT 780
 125 TTGGCGCGCA AGAAGCGTCG TCTCTATCAC AGTACGCCGA TGAACAGCTT GGTCAATGAG 840
 130 TTGCGCTTGG ACGCGAACTA TAGCATGACA GGAGATGCGG TCAATCTGGA TTTCATAGAG 900
 135 GTGGCTACAG AGAAGCACT CCGGTACGAT GGCGCACCZA TGCATATCAG GCGGTTTTC 960
 140 AATTGCCCCG TTTTGGGGGG CGAGTCTGTC CGGTTCTGTA TCAGTGAGGT GCGGGAGTCT 1020
 145 CTGGTGGTTT TGCAGGCCAA TTCTTCCCTG ACAGCATCGC TTGTTCCCGT TAAGACTGTC 1080
 150 GGGGATAAGA CCATTGAGTT CGTGGCTCCG CCGAAGGGTC AGGATCGTAG GACTATCAAT 1140

WO 99/29870

PCT/AU98/01023

81 / 490

	CCTCTCGGGC	AAGCTATCAA	CTATGCGAAC	CTCGGACGTA	TCTATCGACA	ACGCAAGAA	660
	TACGACAAGG	CICGTACCTA	CTTCCTCTTG	TCTCTGGAGC	AGAACAATAT	GGCAGAGAAT	720
	CTGATGGGTA	TCGGGACTCTG	TAGCATCAAT	CTCGGAGAAG	TAGACGAAGA	AAAAGGGGAT	780
	TATCAAAAGG	CTTTGCAAGA	GTATGCCACG	GCATACAAAC	TGATGGAACA	GTTGTCCGAT	840
5	CGATGGCACT	GGCTGAATTC	CTGTATCCCG	ATGGCACGTA	TCAATCTCAA	ACAAGGTAAC	900
	GAAAGGCTCT	ACCAGCATTT	CATTCTCTTG	GCCGAAGGGA	CTGCGAAAGA	AATTAATTCG	960
	ACTTCACATC	TGATAGAAAT	ATACAATCTT	CAATACGAGA	ATCTCGAGCG	TAAAAAAGAA	1020
	TACAAACAAG	CCCTCGAAGC	ATTCTGTCTG	AGCAAGACGT	TGAGCGACAG	CATGTCCATT	1080
	GCGCACAAGG	TCAGCAGCAT	ACAAGAAACG	CGATTCAACT	ACGAACGAJA	CAACTCCCAA	1140
10	AAAGAGCTTG	AAGAAATACA	GCAAGTAAGC	AAGGCAAAAC	AAGAGAAATC	GAAGTTTATC	1200
	CTCTTGAGCA	CTCTTTTTCG	CTTTTTCATC	TCGATTCTTT	TGATTCTGT	TCTGACATAT	1260
	GCATACCGTC	AGGGCAAGAA	GCATAACAAG	CTGATCAAAG	AGACGGATAA	ACTTCGCTCC	1320
	GGCTTTTTC	CCGGTATTAC	ACACGAATTT	CGTAGCCCTA	TCACCGTCAT	ACAAGGTTTG	1380
	AATGAGAAAA	TGAGTTCAAG	TCCTGATCTC	CAAGCATCGG	ACAGAACCAG	GCTGCACAAG	1440
15	ATAATAGACA	GACAGAGTAG	CCATATGCTG	AATTTGGTGA	ACCAGCTGTT	GGATATTTCG	1500
	AAGATCAGAA	GCGGAGTATC	CACGCCCGAA	TGGCGCAATG	GCGACATCGT	CTCCTTCGTA	1560
	CAGATTCTCA	TGCGATTGTT	TGCACCATAC	GCACAGGCTC	AAGACATAAC	CTTGGAGCTA	1620
	CAACCCGAGA	GCAAACTTAT	TGTCGTGAC	TTCTGCTCC	CCTACTTGCA	AAAAATCATA	1680
	TCCAATCTTT	TGTCCTAATG	CATCAAGTAT	TCTTTAGCCG	GAGGGAGAGT	GGTCATATCT	1740
20	CTGGCAAAAA	CCAAGAAATG	AAAAAATCTG	ATCATACGCG	TGCGAGACAA	TGGCATAGGA	1800
	ATAGATAAAA	CTGATCAGGC	TGATATCTTC	GACATCTTCT	ATCGAGGACA	GTCCGCTACC	1860
	GAAAGCATATG	GATCAGGCGT	CGGACTCTCG	TTTACCAATA	TACTGGTCGA	AAACCTTCGA	1920
	GGTACGATCA	AAGTGGAAG	CCAGCCGGGG	AAAGGAAGTG	CUITCACCAT	CAGTATTCCT	1980
	ACACAAVACC	AGTCTCTTTC	GGCAGAGATT	CTTCTTGGC	TACCTCTCTC	CGATGACATT	2040
25	GTCTATCGCT	TCCACATCGC	GCCCGATGAC	TCACCGACAT	CTCCGNTGGT	AGCAGCTCTG	2100
	AATCATCGCT	TCGAGGACGA	ACGTCCGACC	ATACTGCTCG	TCGAGGACAA	TAAGGATATC	2160
	AACCTGCTCG	TCAAACTACT	CCTTTGCGAT	CGCTACAATG	TGCTATCCGC	CGCAAAACGGA	2220
	AAAGAGGGTA	TAGCCCTCGC	TACCGAGCAT	ATTCCCGACA	TTATCATTAC	GGATATTATG	2280
	ATGCCGATAA	TGGATGGGAT	AGAAATGACA	ATCCGGATGA	AGCAATCGCC	TCTGCTCTGT	2340
30	CACATTCCCA	TGTGCTCTTT	GACGGCCNAG	AGTACCGAAC	AGGACAGATT	GGTAGGAATC	2400
	AAAAGCGGTG	TAGTCTCTTA	TCTATGCAAG	CCATTCTCTC	CGGAGGAGCT	TTTGATGCGG	2460
	ATCGAGCAGC	TCTTGAAAGA	CCGTGAGTTG	CTCAAGAAAT	TCTATATGCA	AAAACCTCAT	2520
	CTGGATCGGA	AGCCGGAGGA	GGAGCCTCAA	CCGATAGATG	ACAGCAGTAT	GCAGTTTCTC	2580
	CTTGCTGCCA	AAGATGCAAT	GTCCGGTGGA	ATCAAAACAA	ATCCGGATTT	TTCCGCTCAA	2640
35	GACTTGCCCG	AAAAAATGTG	CATGAGTCCA	TCCCAACTCA	ACAGAAAGCT	CACGAGTGTC	2700
	GTAGGTTGCT	AGCAACATCG	CTACATACAG	CAGATCAAGA	TAAATTTGGC	CTGCAAGCTC	2760
	CTTGCCGATG	CGAGCAAAAA	CATCTCCGAC	ATTAGCATTG	AGGCAGGCTT	TTCCGATCCG	2820
	GCTTACTTCT	CTCGCACCTT	CAACGCTAC	ATGAAGTCTG	CTCCCTCCCA	ATATCGGCAA	2880
40	AAACTCTCTG	CCATGCCGGG	GAGCGACAAG	GAGACAGTT			2940

(2) INFORMATION FOR SEQ ID NO:118

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1689 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
- (A) NAME/KEY: misc feature
- (B) LOCATION 1...1689
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118

65	CATCATAAAA	CATATCAAA	AATGAAAAAG	CTTTTACAGG	CTAAAGCCTT	GATTCTGGCA	60
	TTGGGACTCT	TCCAATGCG	CGCAATCGCC	CAAAACGCAA	TGCAAGCAGA	CCGAACAAAC	120
	GGTCAATTTG	CAACAGAAGA	GATGCAACGA	GCATTCCAGG	AAACGAATCC	CCCTGCAGGT	180
	CCTGTGCGTG	CTATCGCTGA	GTACGAACGC	TCTGCAGCCG	TTTTGGTACG	CTACCCGTTT	240
	GGTATCCCGA	TGGAATTGAT	CAAGAGAGCTG	GCCAAGAACG	ACAAGGTGAT	TACCTTTGTC	300
70	GCGAGTGAAA	GCCAAAAAAA	CACCGTTATA	ACCCAGTACA	CCCAAGCGGG	TGTGAATCTC	360
	TCTAATTGGG	ATTTTCATCAT	TGCGAAAACT	GACTCTTACT	GGACACGCGA	CTATACCGGT	420
	TGGTTGCGAA	TGTACGATAC	GAACAAAGTA	GGTCTCGTGG	ACTTTATTTA	TAACCGCCCT	480
	CGTCTTAACG	ATGATGAATT	CCCCAAATAC	GAAGCACAAT	ATCTGGGCAT	CGAGATGTTT	540
	GGGATGAAGC	TCAAGCAGAC	CGGTGGCAAC	TACATGACGG	ACGGATATGG	ATCCGCTGTG	600
75	CAGTCACATA	TCGCATATAC	GGAGAATCTC	TCTCTGTCTC	AAGCTCAAGT	AAATCAAAAG	660

WO 99/29870

PCT/AU98/01023

82 / 490

5 ATGAAAGACT ATCTCGGCAT CACACATCAT GATGTGGTAC AAGATCCGAA CGGCGAATAT 720
 ATCAACCATG TGGACTGTTG GGGCAAGTAT TTGGCACCAG ACAAATCCT CATCAGGAAA 780
 GTGCCTGACA ATCACCCTCA GCACCAAGCC CTGGAAGATA TGGCAGCCTA CTTCGAGCA 840
 CAGACTGCG CATGGGGAAC GAAGTACGAG GTATATCGCG CTTTGGCCAC CAATGAACAA 900
 CCGTACACGA ACTCTCTGAT TCTGAACAAC AGGGTATTGG TTCTGTCAA TGGCCCCGCC 960
 TCCGTGGACA ACGATGCTCT GAACTCTAT AAGACGGCAA TGCCCGGTTA CGAAATTATA 1020
 GGTGTCAAAG GGGCTTCAGG AACACCTTGG TTAGGAACAG ATGCCCTGCA TTGTCGTACT 1080
 CACGAGGTAG CGGATAAGGG CTATCTCTAT ATCAAGCACT ACCCGATACT GGGCGAACAG 1140
 GCAGGCCCTG ATTATAAGAT CGAAGCAGAT GTCGTCTCAT GCGCCATGTC TACTATCTCG 1200
 10 CCGGTACAAT GTTACTATCG TATCAATGGT TCCGGTAGCT TTAAGGCTGC TGATATGAGT 1260
 ATGGAATCAA CAGGTCACTA TACTTATAGC TTTACAGGTC TTAACAAGAA TGATAAGGTA 1320
 GAATACTATA TCTCTGCCGC TGACAAATAGT GGTCCGAAAG AGACTTATCC CTTTATCGGC 1380
 GAACCTGATC CTTTCAAGTT TACGTGTATG AACGAAACCA ATACATGTAC TGTGACCGGA 1440
 GCTGCCAAAG CTCTTCGTGC ATGGTTCAAC GCCGGTCGTT CAGAACTGGC TGTTCGGTA 1500
 15 AGTTTGAATA TTGCCGGCAC ATATCGGATA AAGCTTTATA ACACCGCAGG AGAAGAAGTC 1560
 GCTGCAATGA CCAAGGAATT AGTAGCAGGG ACGAGTGTCT TCAGTATGGA TGTGTATTCT 1620
 CAGGCTCCGG GCACATATGT TCTGGTTGTT GAAGGAAATG GAATCCGTGA GACAAAGAAA 1680
 ATTCTCAA

20

(2) INFORMATION FOR SEQ ID NO:119

25 (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1311 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

30 (11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

35 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

40 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119

45 ACCACAAATA GAAACCAAAA TACTAATATG AAACCTTCAT CTAAGAAAAT CTTAGCAATC 60
 ATTGCATTGC TGACGATGGG ACATGCTGTG CAGGCACAGT TTGTTCCGGC TCCCACCA 120
 GGGATTCCGA TGTCTGTAC TACAACCAAG GCCGTAGGCG AAAAAATCGA ATGTGTTGGT 180
 CATTCCTATG AGAAGAAAGG CATCTGGATC GATCTCAATG GGGATGCCAC TTACCAACA 240
 GGAGAGGAAA TAACCGTATT CGATGAGGCA TACCACGAAT ACACGATCGG GACGCAACC 300
 50 CTCATATCT ATGGTAATAC GACCCGATTG GGCTGTCGAT CTAACCGTGC AACGGCTGTC 360
 GATGTAAAGA AAAACCTTAA TCTGACCTAT CTCGCATGCC CGAAAAATAA TCTGAAATCA 420
 TTGGACTTGA CGCAAAACCC AAAGCTGCTG CGAGTTTGGT GCGACTCTAA CGAAATAGAA 480
 AGTTTGGACC TGAGTGGCAA TCCGGCTTTG ATCATCCTCG GCTGTGACAG GAATAAGCTG 540
 ACTGAGCTGA AGACCGATAA CAACCCCAAG TTGGCCTCTC TTTGGTGTTC TGATAATAAC 600
 CTGACGGAGT TGGAACTCAG TGCCAATCCT CGTCTCAATG ATCTTTGGTG CTTCGGTAAT 660
 55 CGGATCAGCA AACTCGATCT GAGTGCCAAT CCTCTATTGG TAACACTTTG GTGCAGTGAC 720
 AATGAGCTTT CGAECTTGGG TCTTTCCAAG AATTCGGACG TTGCTTACCT TTGGTGTTC 780
 TCGAACAAAC TTACATCCTT GAATCTGTGC GGGGTGAAGG GACTGAGTGT TTTGTTTGT 840
 CATTCCAATC AGATGCGCAGG TGAAGAAATG ACGAAAGTGG TGAATGCTTT GCCACACTA 900
 TCTCCCGGCG CAGGCGCTCA GAGCAAGTTC GTCGTGTAG ACCTCAAGGA CACTGATGAG 960
 60 AAGAATATCT GTACCGTAAA GGATGTGGAA AAAGCTTAAA GTAAGAACTG GCGAGTATT 1020
 GACTTCAACG GTGATTCTGA CAATATGCTT CCATACGAAG GAAGTCCGAC ATCGAACTG 1080
 GCAGTAGATG CTCCCACTGT CAGGATATAT CCAATCCGG TAGGAAGATA TGCGCTCGTC 1140
 GAGATCCCGG AGTCTCTTT AGGECAGGAA GCTGCTTTAT ACGATATGAA TGGGGTAAAA 1200
 65 GTCTATAGTT TCGCGGTAGA STCTCTTCGT CAGAACATTG ACCTGACACA TCTTCCCGAC 1260
 GGCATTATT TGTTCCTCT CGATAACTAT ACCACTAAGC TCATCAACA G 1311

(2) INFORMATION FOR SEQ ID NO:120

70 (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 954 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
 75

WO 99/29870

PCT/AU98/01023

84 / 490

5 ATGGCAACAC CTTGACAGA AGCTCAGGTA GCAGTCTATC TCAATCCGTC AACGGACGG 1200
TTAGTGATTG TGGCCAAACG CATCACACAT CTGAGCATGT ACGACTTGCA GGGTAAGCTT 1260
ATCCGTGATT GTGCCTTGAG CGGCGATAAG GTGGAATGG GTGTCGGATC TTGACCAAA 1320
GGGACATACC TGCTTAAAGT GAATACGGAT CAGGGAGCCT TTGTGAGAAA AGTCGTGATT 1380
CGA 1383

(2) INFORMATION FOR SEQ ID NO:122

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1353 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 15 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 20 (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 25 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1353
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122

30 ATGGCAAAAG TTATAAAAC AAAAAAGGC CTTGCACTTA ATCTGAAAGG AAAACCGCTG 60
CCCGAGATGC TGGCCGAACG GGGCCAAAGT CCTACTTACG CGGTGCTGCC CGACGATTTT 120
GAAGGTGTTA TCCCCAAGGT GACGGCTCGT CCGGGGGATA AGGTGCGTGC CGGCTCAGCA 180
CTGATGCACC ACAAGGCATA TCCGGAGATG AAGTTTACAA GTCCGGTTAG CGGCGAAGTG 240
ATCGCGGTGA ATCGCGGTGC CAAGCGCAAG GTGTTGAGCA TCGAGGTGAA ACCGGACGGA 300
CTGAACGAAT ACGAGTCATT CCCTGTCCGG GATCCGTCCT CCCTCTCTGC CGAACAGATC 360
AAGGAGCTTT TACTGTGAG CGGTATGTGG GGTITTATTA AGCAACGTCC TTACGACATA 420
GTGGCTACAC CGGATATAGC TCCACGCGAC ATTTATATTA CTGCCAACTT TACTGCACCA 480
TTGGCTCCGG ACTTCGATT CATCGTTCCA GGAGAAGAAC GCGCCCTGCA GACTGCCATC 540
GATGCCTTGG CCAAACTCAC GACAGGAAAG GTGTATGTGG GCCTGAAGCC GGGTTCATCT 600
CTGGGCTTGC ACAATGCAGA AATCGTAGAA GTACACGGAC CTCATCCGGC AGGTAACGTG 660
GGCGTGCTGA TCAATCATAC GAAGCCCAATC AATCGGGGCG AAACGGTGTG GACGCTCAAG 720
GCTACCGACC TGATCGTGAT CGGACGTTTC CTGCTTACGG GCAAAGCCGA TTTTACCAGA 780
ATGATTGCCA TGACCGGCTC AGACGCTGCA GCTCACGGAT ACGTCCGTAT TATGCCGGGT 840
45 TGCAATGTCT TTGCTTCCTT CCCCGGCCGA CTGACAATAA AGGAATCTCA CGAGCGTGTG 900
ATCGATGGCA ATGTGCTGAC CGGTAAGAAAG CTCTGCAGGA AGGAGCCTTT CCTGTCAGCC 960
CGGTGTGACC AGATCACGGT GATCCCCGAA GGCAGCATG TGGACGAATC CTTCCGGTGG 1020
GCTGCACCCC GTCTCGATCA GTACAGCATG AGCAGAGCTT ATTCTCTTGG GTTGCAGGGG 1080
AAAAACAAG AGTACGTACT CGATGCCCGG ATCAAGGGTG GCGAACGTGC TATGATCATG 1140
50 AGCAACAGAT ATGACCGCGT TTTCCCGATG GACATCTATC CGGAGTATTT GCTCAAGGCT 1200
ATTATAGCAT TCGACATCGA CAAGATGGAG GACTTAGGCA TATATGAAGT GGCTCCGGAG 1260
GACTTTGCCA CTTGCGAATT TGTGGATACA TCCAAGATCG AGCTGCAGCG TATCGTTCGG 1320
GAGGGCTTGG ATATGCTCTA TAAGGAAATG AAT 1353

(2) INFORMATION FOR SEQ ID NO:123

- 60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 585 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 65 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 70 (v) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...585
- 75

WO 99/29870

PCT/AU98/01023

85 / 490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123

5 ATGGATAAAG TGAGCTATGC TCTGGGATTG AGCATCGGTA ATAATTTCAA GTCTTCGGGC 60
ATCGACAGCG TCGTTATGGA TGATTTCATG CAAGGTCTGT CTGATGTACT GSAAGAAAAA 120
GCCCCCTCAGC TCTCGTATGA CGAGGCCAAG CGCGAAATAG AGGCGTATTT CATGGATTTG 180
CAGCAGAAGG CTGTCAAACCT GAACAAAGAG GCCGGAGAGS AATTCCTCAA GATAAATGCA 240
CACAAAGGAG GTGTGACGAC CTTACCSAGC GGCTTGCAAT ACGAAGTCAT TAAGATGGGA 300
GAGGGCCCGA AACCCACCTT TTCGGACACG GTAACCTGTC ATTATCACGG TACGCTCATC 360
10 AACGGTATCG TTTTGGATAG CTCTATGGAC AGGGGAGAAC CGGCCAGTTT CCCTCTAAGA 420
GGAGTTATAG CCGGCTGGAC GGAGATTCTT CAATTAATGC CTGTAGGATC CAAGTGGAAA 480
GTAACATATC CGAGCGATCT GCGGTATGGA GATCGTGTG CCGGCGAACA TATCAAACCG 540
GGTAGTACCG TCATTTTAT AATCGAATTA TTGAGTATCA ACAA 585

(2) INFORMATION FOR SEQ ID NO:124

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 819 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124

40 ATGAAAAAAG CATTACTTAT TGGTGCTGCT CTTTGGGAG CAGTCAGTTT TGCAAGTGCT 60
CAGTCTTTGA GCACAATCAA AGTACAGAAC AATTCAGTAC AGCAACCTCG TGAGGAAGCC 120
ACTATTCAGG TTTGTGGAGA ATTGGCAGAG CAAGTTGACT GCATTGGGAC AGGTAATTCT 180
GCAATCATAG CCGCTGCAGC GAAATTTGAA AGCGATGATC TCGAAAGCTA TGTGGCTGG 240
GAGATCATGA GTGTTGATTT CTTCCTGGA TATAAAGCGT GCAAGTACAC ATCTGCAGTC 300
TGGGCTGATG ATATGACCAT TTTGGGCCAA TCAGAAGATA GTGATCCCGA AATGCAGACT 360
45 ATCAACAATC TFGCTCTCAA GACTAGTGTC AAGATTGAAG CCGGCAAGAA TTACATAGTT 420
GGTTATATTG CTAATACCGC AGGTGGACAT CCTATCGGAT GTGATCAGGG CCCTGCCGTT 480
GATGTTATG GAGATTGGT TTCTATATCA GAAGATGGTG GTGCTACTTT CCCTCCGTTT 540
GAATCTCTTC ATCAAGCAGT TCCTACCTTA AATTACRACA TCTATGTCGT TGTTCATTG 600
AAGAAGGGTG AAGGTGTTGA GGCTGTTCTT ACCAACGACA AGGCTAATGC TTATGTTTCA 660
50 AATGGCGTTA TCTATGTAGC CGGAGCTAAT GGTGTCAGG TATCTCTGTT CGACATGAAC 720
GGTAAGGTTG TTTATACCGG CGTTAGCGAA ACGATTGCG CTCTCAGAA GGGCAATGAT 780
ATCCTCCGTG TAGGTGCTAA GAGCATCAAG CTGGCTATC 819

(2) INFORMATION FOR SEQ ID NO:125

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1662 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1662

WO 99/29870

PCT/AU98/01023

86 / 490

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:125

5	ATGCCAAGAA	TTATGAAATT	AAAAATTGCA	CTCAGACTGC	TGCTGGCGAC	TTTTGCCATA	60
	GTTTATTATTA	GCCTCTGGC	CAAGGCCCCAG	ATGGATATTG	GTGGAGACGA	TGTATTGATC	120
	GAGACGATGT	CCACCCTATC	AGGATATTCA	GAGGATTTTT	ATTACAAGAT	GCCTGTGGCA	180
	GACAAATGGAT	GGATCTATGT	GATGTTGGAT	TTCTCTCGTA	TTTATTTTGA	TGATGTGAGG	240
	CTGTATCGTT	CCAAAGACGG	TGGTGCCTACT	TACCAAAAGT	TAGGGTCTTT	GGGGTCTTTG	300
	GTGCCTTATG	ACTTCGATGT	CTCGCATTCG	GATTTTATTG	TACGGGAAA	GGATGAAGAT	360
	GATATCAATG	TTTGGACAGT	CATGACAGCA	TTGGAATATG	TAGGTGGTAC	TATTGGCAAT	420
10	GGCGTTTTGC	TGATGCATCG	CCATGATGCA	GATATCAATA	ATACAGAGTG	TGTGTACAAG	480
	AAGGATTTCC	CTAATAATAG	ACTGATGGGT	GTAGCCATCG	CTCCCAACTA	CCGTGCGCCC	540
	TCCTCTTAGG	TTTTGGGGGG	CGATCCCTTT	GCTCTCGCTG	TCCCGCTTAG	TGGCTCCGGA	600
	AGCGATCACA	GCTTCTTGGG	CTATAATTTT	TCGTTAGATG	GTGGAGTACA	CTTTGAGCAA	660
15	AAGCGTATT	ACACAAGACC	CCAAAACTG	ACTATCAATA	GAGTAGACCT	TTCATTAGGC	720
	AGTACATCTC	CTTCTCTTGG	ATTTAATACT	TGGCCACTAA	TGGGAGTCGT	ATTCGAAATG	780
	AATAAGAACC	TGATGGCTT	CGACATTGGT	TTCAATTTCC	ACTTTGTGGA	CTATGATCCC	840
	CGCTATCGCT	GGTCTGAACC	GATAATAATA	GAAGAAGACT	GTGGATGGAG	TGATTTTAAT	900
	CTTTTGGGAG	CACAAAGTAT	AGAGATCCAA	ATGATGTTGG	ATGACAATTC	GGATAATACC	960
20	GTGGGTGGAG	AACGCTCCCA	TAACCTCCCT	ATCACTTACC	CGGGCCATTG	CGTATATCCG	1020
	ARGCAATCTT	TCAATTAATC	TCCCGGACAT	ACACCGACAA	AGAAAGATCT	GGTCTTTAAA	1080
	CATCTGATAG	GTATTCCGGC	TTTGGCATAC	GATAAGGAAG	GCGATCGTTA	TCTGACTACT	1140
	TTTCAAGATC	ACAATCTAAT	GAGATACAGA	TGGATCAAAT	ACGATGACAT	TAATCTTTT	1200
	TATGGTTGGA	GTGGCCATA	TGTATATGCA	AAAGAAGCTA	AAGATAAAAA	GAGGCGCCGT	1260
	CCGCAAGTAG	CACCTAATCC	TACCAATGGA	AAGGCTTGT	GGGTATGGCA	TACTCGCAAG	1320
25	AGCCCATATG	ATGAAACCAA	ACCACATCCT	ACTCCTGTAA	TTATTAAACA	TTTCTATGG	1380
	TCCGATACGG	AGTGGGTACA	TGCTCTGGAC	GTGGGGGACG	TATTGCAGAA	GGAGGGTAGC	1440
	ATSAAGCTCT	ACCCCAATCC	TGCCAAGAA	TATGTTCTGA	TCAACCTACC	CAAGAAGGG	1500
	GGGCACGAGG	CAGTCGTATA	CGACATGCAG	GGCCGAATCG	TGGAGAAAGT	TTCATTTTCA	1560
	GGGAAAGAT	ATAAGCTGAA	TGTGCAGTAT	CTGTCCAAAG	GTACGTACAT	GCTGAAAGTT	1620
30	GTAGCGGATA	CGGAGTATT	CGTGGAAAA	ATCATTGTAG	AG		1662

(2) INFORMATION FOR SEQ ID NO:126

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1650 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- 40 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 45 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 50 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1650

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:126

55	ATGAAATTA	AAATTGCACT	CAGACTGCTG	CTGGCGACTT	TTGCCATAGT	TTTATTAGC	60
	CCTCTGGCCA	AGGCCAGAT	GGATATTGGT	GGAGACGATG	TATTGATCGA	GACGATGTCC	120
	ACCTATTCAG	GATATTGAGA	GGATTTTAT	TACAAGATGG	CTGTGGCAGA	CAATGGATGG	180
	ATCTATGTGA	TGTTGGATT	CTCTCGTATT	TATTTTGATG	ATGTCAGGCT	GTATCGTTCC	240
60	AAAGACGGTG	GTGCTACTTA	CCAAAAGTTA	GGGTCTTTGG	GGTCTTTGGT	GCCTTATGAC	300
	TTGATGTCT	CGCATGGCA	TTTTATTGTA	ACGGGAAAGG	ATGAAGATGA	TATCAATGTT	360
	TGGACAGTCA	TGACAGCATT	CGAATATGTA	GGTGGTACTA	TTGGCAATGG	CGTTTGTCTG	420
	ATGATCGCC	ATGATGACGA	TATCAATAAT	ACAGAGTGTG	TGTACAAGAA	GGATTTCCCT	480
	AATAATAGAC	TGATGGGTGT	AGCCATCGCC	TCCAACCTACC	GTGCGCCCTC	TCCTTACGGT	540
65	TTGGGGGGGG	ATCCITTTTGC	TCTCGCTGTG	GCCGTTAGTG	GCTCCGGAAG	CGATCAGAGC	600
	TTCTTGGACT	ATATTTTTTC	GTTAGATGGT	GGAGTACACT	TTGAGCAAAA	CGGTATTAC	660
	ACVAGACCCC	AAAACTGAC	TATCAATAGA	GTAGACCTTT	CATTAGCGAG	TACATCTCCT	720
	TCTCTTGGAT	TTAATACTTG	GCCCAATATG	GGAGTCTGAT	TGGAATGAA	TAAGAACCCT	780
	GATGGCTTGG	ACATTGGTTT	CATTTCCAAC	TTTGTGGACT	ATGATCCCGG	CTATGCGTGG	840
70	TCTGAACCGA	TAAATATAGA	AGAAGACTGT	GGATGGACTG	ATTTTAATCC	TTTGGGAGCA	900
	CTAAGTATAG	AGATCCAAAT	GATGTTGGAT	GACAATTCGG	ATAATACCGT	GGGTGGAGAA	960
	CGCTCCCAT	ACTTCTGAT	CACTTACCGG	GGCCATTACG	TATATCCGAA	GCAATCTTTC	1020
	AATTTATCTC	CCGGACATAC	ACCGACAAAG	AAAGATCTGG	TCTTTAAACA	CTGTATAGGT	1080
	ATTCCGGCTT	TGGCATACGA	TAACGAAGGC	GATCGTTATC	TGACTACTTT	TCAAGATCAC	1140
75	AATCTAATGA	GATACAGATG	GATCAAAATC	GATGACATTA	ACTCTTTTTA	TGGTGGAGT	1200

WO 99/29870

PCT/AU98/01023

88 / 490

(B) LOCATION 1...1233

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:128

5	ATGAGACAGC	ATTATCTCT	ATTTCTTTT	ATCTTGTTC	TGCTTCTTG	CTTCTTTAT	60
	GTGCGTTGCA	GAACAGTCCG	ACAAACACCT	AAGCAGTCGG	AACGGTACGT	CGTAGTCCCTG	120
	TCTTTGGACG	GCTTCCGACC	GGAATAATCC	GATCGGGCAC	GTACACCGGC	GTTGGATCGG	180
	ATGSCACAGG	AGGGATTGAG	CGGGTCGCTC	CAACCATGCT	TCCCTCGCT	TACATTTCCC	240
	AATCATTACA	GCATGGCTAC	GGGGCTTTAC	CCCGATCATC	ACGGTATCGT	AGCCAATGAG	300
10	TTTGTGGATT	CGCTACTGGG	CATCTTTCT	ATATCCGACC	GAAAGCCGT	GGAGACCCGC	360
	GGATTTTGGG	GCGGCGAGCC	GGTTTGGGAT	ACGGCCGCAC	GCCAAGGCAT	CCGTACCCGT	420
	GTCTACTTTT	GGGTAGGATC	CGAAACGGCT	GTGAACGGAA	ATCGGCCGTG	GCGGTGGAAA	480
	AAATTCTCCT	CCACCGTTCC	GTTTCGTGAC	CGTGCCGACT	CCGTATCGC	GTGGCTCGSA	540
	CTGCCCCGAA	AGGAGCGACC	GCGCTTGCTC	ATGTGGTACA	TGAGGAGCC	GGATATGATC	600
15	GGACACAGCC	AAACGCCCGA	AAGCCCGCTG	ACACTGGCAA	TGGTAGAGCG	GTTGGACAGT	660
	GTGGTCGGCT	ATTTCGCAA	GCGTTGAC	TCTCTGCCA	TAGCCGCACA	GACCGACTTC	720
	ATCATAGTAT	CCGATCACCG	TATGCCACG	TACGAAATG	AGAAATGTGT	CAATCTGTCT	780
	CATTATCTGC	CTGCGGACAG	TTCCTCTAC	ATGGCCACCG	GGGCCCTTAC	CCACTTGTAC	840
	CCGAAGCCCT	CCTATACCGA	GCGAGCCTAT	GAGATCCTGC	GGGCCATTCC	ACATATATCG	900
20	GTTTACCGCA	AGGGGGAGGT	GCCCCAAGCGT	TTGCGCTGTG	GCACCAATCC	TCGTTTGGGC	960
	GAATCGTCTG	TGATTCCGGA	CATAGGCTCC	ACCGTCTTTT	TCGCAATAAA	TGAAGACGTT	1020
	CGTCCGGGAG	CGGCACATGG	CTATGACAAC	CMGACACCGG	AAATGCGGGC	TTTACTCCGG	1080
	GCTGTCCGAC	CCGATTTCGG	TCCGGGCAGT	AGGGTGGAAA	ACCTGCCGAA	TATCACCATC	1140
	TATCCGCTCA	TATGCAGGCT	GTTGGGTATA	GAGCCTGCAC	CCAACGATSC	GGACGAAACG	1200
25	TTGCTGAACG	GCCTGATCCG	AGACAAACGA	CCA			1233

(2) INFORMATION FOR SEQ ID NO:129

30	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 738 base pairs
	(B) TYPE: nucleic acid
	(C) STRAINEDNESS: double
	(D) TOPOLOGY: circular
35	(ii) MOLECULE TYPE: DNA (genomic)
	(iii) HYPOTHETICAL: NO
40	(iv) ANTI-SENSE: NO
	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PORPHYROMONAS GINGIVALIS
45	(ix) FEATURE:
	(A) NAME/KEY: misc feature
	(B) LOCATION: 1...738

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:129

50	ATGAAAGTAG	GTTTGTTCAT	CCCCTGTTAT	GTCAATGCAG	TGTATCCGGA	AGTGGGTATC	60
	GCCACGTACA	AACTGCTGAA	GAGTTTGAC	ATAGATGTCT	ACTACCCGAT	GGATCAGACA	120
	TGTTGGGGCC	AGCCTATGGC	CAATGCCGGA	TTCGAACAGA	AAGCTCAAAA	GCTGGCTTTG	180
	CGATTCCGAG	AGCTGTTCGA	GTCTATGAT	GATGCTGTAG	GGCCATCGGC	CAGTTGCGTT	240
55	GCTTTCTGTA	AAGAAACTA	TGATCATATC	CTCAGACCGA	CAGGACATGT	CTGCAAGTCT	300
	GCAGCCAAAG	TTCCGGATAT	ATGCCAGTTC	TTGCAGGATG	ACCTGAAGAT	CACCAAGCTC	360
	CCCTCCCGAT	TGCCCCATAA	GSTGAGCCTG	CACAACAGTT	GCCACGGTGT	GCGCGAAGTC	420
	CATCTGTCCA	CCCCCAGTGA	AGTGCAACGA	CCGTACCACA	ACAAGGTGCG	CCGGCTATTG	480
	GAGATGGTGC	AGGGCATAGA	GGTATTCGAG	CCGAAGCGAA	TAGACGAATG	CTGCGGTTTC	540
60	GGCGGTATGT	ACTCGGTGGA	GGAGCCGGAG	GTATCCACCT	GTATCGGGCA	TGACAAGGTG	600
	CTGGATCACA	TATCCACAGG	TGCGGAGTAC	ATCAGAGGSC	CGGACAGCTC	GTGCTCATG	660
	CATATGCAGG	GAGTGATAGA	CAGAGAGAAA	TTGCCGATCA	AGACAAATCA	TGCAGTAGAA	720
	ATTTTAGCAG	CAAACTTA					738

(2) INFORMATION FOR SEQ ID NO:130

70	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 738 base pairs
	(B) TYPE: nucleic acid
	(C) STRAINEDNESS: double
	(D) TOPOLOGY: circular
75	(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
10 (B) LOCATION 1...738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130

15 ATGGATATTG TAAGTATGGC CGATAAAGCT CTTGTAGTGG AGATGAGAGA TGTGACGCTC 60
TGTCAGGAGG AAAACGTCAT TTTTCAAAT TTGAATCTGA CCTTTCCGC CGGAGACTTC 120
GTCTATCTGA TAGGCTCAGT GGGATCGGGG AAGAGCACTT TGCTGAAGGC TTTGTATGCT 180
GAGGTGCTTA TCTCTGCCGG TTATGCCCGC GTGATAGATT ATGATCTGGC AAAGTTGAAA 240
CGGAAGCAGT TGCCCTATCT CGGCAGGAAT TTGGGCATTG TGTTCAGGA TTTCAGTTG 300
CTGAACGGAC GTACTGTTGC GGAGAATTG GATTTCSTT TGCGAGCTAC GGAAGTGA 360
20 AACCGAGCG ATCGCGAGCA GCGATCGAG GAGGTTTGA CCCGTGTGGG AATGTCTCGG 420
AAGGCTTATA AGAGACCGCA CGAACTGTCC GGAGGGGAGC AACCAAGTGT GGGTATAGCC 480
ACAGCTTTCG TGGCGAAGCC TCGGTTGATC CTGGCCGAGC AACCCACAGG CAACCTCGAT 540
TCGGTGACCG GATTGCAGAT CGCTTCTCTG CTCTACGAAA TCAGTAAGCA GGGCACTGCA 600
GTACTTATGA GCACGCACAA CAGCAGCCTG CTGTCGCATC TGCCGGCAGG GACATGGCC 660
25 GTTCGTAAGA ATGGCGATGC CTCCTCTTG GTGAGCTGA GTGCAGATCC TGTTCGAAGA 720
AAAAATACGG AAATAGAT 738

(2) INFORMATION FOR SEQ ID NO:131

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 723 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

40 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

45 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...723

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:131

ATGGCCGATA AAGCTCTTGT AGTGGAGATG AGAGATGTGA CGCTCTGTCA GGAGGAAAAC 60
GTCATTTTTC AAAATTTGAA TCTGACCCIT TCCGCCGAG ACTTCGTCTA TCTGATAGGC 120
TCAGTGGGAT CGGGGAAGAG CACTTTGCTG AAGGCTTTGT ATGCTGAGGT GCTATCTCT 180
55 GCCGCTTATG CCCGCGTGAT AGATTATGAT CTGGCAAAAT TGAAACGGAA GCAGTTGCC 240
TATCTGCGCA GGAATTTGGG CATTTGTTT CAGGATTTC AGTTGCTGAA CGGACGTACT 300
GTTGCGGAGA ATTTGGAATT CGTTTGCGA GCTACGGACT GGAATAACCG AGCCGATCGC 360
GAGCAGCGTA TCGAGGAGGT TTTGACCCGT GTGGGAATGT CTCGGAAGGC TTATAAGAGA 420
CGGCACGAAC TGTCCGAGG GGAGCAACAA CGTGTGGGTA TAGCCAGAGC TTTGCTGGCG 480
60 AAGCCTCGCT TGATCCTGGC CGACGAACCC ACAGGCAACC TCGATTGCGT GACCGGATTG 540
CAGATCGCTT CTCTGCTCTA CGAAATCAGT AAGCAGGGCA CTGCAGTACT TATGAGCAGG 600
CACACAGCA GCCTGCTGTC GCATCTGCCG GCACGGACAT TGGCCGTTG TAAGAAATGGC 660
GATGCTCTCT CTTTGGTCTG GCTGAGTGCA GATGCTGTT CAAGAAAAAA TACGGAAATA 720
65 GAT 723

(2) INFORMATION FOR SEQ ID NO:132

70 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 696 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

75 (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- 5 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 10 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...696
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132
- | | | |
|----|---|-----|
| 15 | ATGAGAGATG TGACGCTCTG TCAGGAGGAA AACGTCATT TTCAAAATTT GAATCTGACC | 60 |
| | CTTTCGSCGS GAGACTTCGT CTATCTGATA GGCTCAGTGG GATCGGGGAA GAGCACTTTG | 120 |
| | CTGAAGGCTT TGTATGCTGA GGTGCTTATC TCTGCCGGTT ATGCCCGCGT GATAGATTAT | 180 |
| | GATCTGGCAA AGTTGAAACG GAAGCAGTTG CCCTATCTGC GCAGGAATTT GGGCATTGTG | 240 |
| 20 | TTTCAGGATT TCCAGTTGCT GAACGGACGT ACTGTTGCCG AGAATTTGGA TTTCGTTTTG | 300 |
| | CGAGCTACGG ACTGGAAAAA CCGAGCCGAT CCGAGCAGC GTATCGAGGA GGTITTGACC | 360 |
| | CAAGTGTGG GTATAGCCAG AGCTTTGCTG GCGAAGCCTG CGTTGATCCT GCGCGACGAA | 420 |
| | CCCACAGGCA ACCTCGATTG GGTGACCGGA TTGCAGATCG CTCTCTGCT CTACGAAATC | 480 |
| | AGTAAGCAGG GCACTGCACT ACTTATGAGC ACGCACAAAC GCAGCCTGCT GTCCGATCTG | 540 |
| 25 | CCGGCACGGA CATTGGCCGT TCGTAAGAAT GGCGATGCCT CCTCTTTGGT CGAGCTGAGT | 600 |
| | GCAGATGCTG TTTCAAGAAA AAATACGGAA ATAGAT | 660 |
| | | 696 |
- (2) INFORMATION FOR SEQ ID NO:133
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 657 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 30 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 45 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...657
- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133
- | | | |
|----|--|-----|
| | ATGATTGAAA TCAGCAACCT CACCAAGGTT TTCAGAACAG AAGAAATAGA GACGGTAGCC | 60 |
| | CTCGATGGCG TATCGCTCAA AGTGGACAAA GGCGAATTTA TCGCCATAAT GGGGCCTTCG | 120 |
| 55 | GGATGCGGTA AGTCCACTCT GCTCAATATC CTCGGCCTTC TCGACAATCC CACTTCCGGT | 180 |
| | ATCTACAAAG TCGATGGGGC AGAAGTGGGC AACCTCCGGG AAAAAAGACG GACTGCCGTC | 240 |
| | CGTAAGGGCA ATATCGGCTT CGTATTCCAG AGCTTCAACC TCATCGAAGA GATGACGGTA | 300 |
| | AGCGAGAACG TGGAGTTGCC GCTCGTCTAT CTGGGTGTGA AGGCCTCCGA CCGGAAAGAG | 360 |
| | CGAGTGGAGG AGGCACTGCG CAAGATGAGC ATCAGCCACC GGGCCCGCCA CTTCCTCCAT | 420 |
| 60 | CAGCTCTCCG GAGGACAACA GCAGCGGTG GCTATCGCCC GTGCCGTGGT GCGCAATCCG | 480 |
| | AAGCTCATCC TCGCCGATGA ACCCAGGGGT AACCTCGACT CCAAAAACGG AGCCGATGTC | 540 |
| | ATGGA/ACTGC TCAGAGGTCT CAATCGCGAA GGTGCAACCA TCGTCATGGT GACGCACTCC | 600 |
| | GAGCACGATG CAGTAGTGC CGGCCGATC ATCAATCTGT TCGACGGTAA GATTCCG | 657 |
- 65 (2) INFORMATION FOR SEQ ID NO:134
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1785 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 70 (iii) MOLECULE TYPE: DNA (genomic)
- 75 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1785

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134

ATGAAGAAT	TTTTAAAAT	TTTTTCGCC	TCGATCCTCG	GGGTATAAC	GGCAGGAATC	60
ATCTTGTCT	GTATCTTCT	ATTTATCTTT	TTCCGGCATCG	TAGCCGGTAT	TGCTCCCAAG	120
GCAACGGGAG	GAACCATTC	GAAGATCGAA	GCAAACTCCA	TCCTACATAT	ANACAATTCT	180
TCTTTCCCTG	AGATCGTATC	GGCCAATCCC	TGGAGCATGC	TCACAGGCAA	AGACGAGTCC	240
GTATCGTCT	CACAGGCAST	CGAAGCCATC	GGCCAAGCCA	AAAATAATCC	CAACATAACC	300
GGTAICTTCC	TCGATCTGSA	CAACCTTTCC	GTCCGTATGG	CATCGGCAGA	GGATTGCGT	360
CGCGCGTTC	AGGATTTCAA	GATGTCCGGC	AAGTTCGTGC	TATCCTATGC	CGACAGATAC	420
ACCCAAAAGG	GTTACTACCT	CTCCAGTATT	GCAGACAAAC	TCTACCTCAA	TCCGAAAGGA	480
ATGTTGGGGC	TTATCGGGAT	TGCGACCCAA	ACAATGTTCT	ACAAAGATGC	CCTCGACAAA	540
TTCCGCGTGA	AGATGGAGAT	CTTCAAGSTA	GGCACCTACA	AGGCAGCCGT	AGAGCCATTTC	600
ATGCTCAACA	GGATGAGCGA	TGCCAATCGC	GAACAAATCA	CCACATACAT	AAACGGGCCT	660
TGGGACAAGA	TCACATCCGA	TATTGCGAGG	TCGCGCAAGA	CGGCAATGGA	TTCCGTGAAA	720
ATGTTTGGCG	ACAAAGGCGA	AATGTTCCGT	CTTGCCGAGA	AAGCGGTGGA	GATGAAGCTC	780
TGGGATGAGC	TGGCTTACCG	TACCGATGTG	GAGAAAGAAC	TCAAAAAGAT	GTCCCAACGC	840
GGAGAGAAAG	ATGAACTTCG	GTTCTGATCG	CTTCTCAGG	TTCTGCCCAG	TGCCCCGATG	900
AACAAAACGA	AAGGCAGTCG	GATCGCCGTT	CTCTTTGCCG	AAGGTGAAAT	AACGGAAGAA	960
ATAATAAAGA	AGCCGTTCGA	CACGTACCGT	AGCTCCATCA	CACAAGAACT	CGCCAAAGAA	1020
ATCAAGGCGC	CAGCCGATGA	CGATGATATC	AAAGCCGTAG	TACTTCGTGT	CAATTCTCCG	1080
GGAGGTAGTG	CTTTCACTTC	CGAACAGATA	TGGAAGCAGG	TAGCCGATCT	CAAGGCCAAA	1140
AAGCCTATCG	TGGTCTCCAT	GGGCGACGTA	GCAGCCTCGG	GCGGATACTA	CATAGCCTGC	1200
GCAGCCAAAC	GTATCGTGGC	AGAGCATACG	ACTCTGACCG	GCTCCATCGG	CATATTCGGC	1260
ATGTTCCCGA	ACTTCGCGGG	CGTAGCCAAAG	AAGATAGGAG	TGAATATGGA	CGTCGTACAG	1320
ACATCCAAAT	ATGCAGACTT	GGGCAACACC	TTCCGCTCCGA	TGACGGTCCA	AGATCGTGCC	1380
CTCATCCAAC	GCTACATAGA	GCAGGCGTAC	GACCTCTTCC	TCACTCGCGT	ATCGGAAGGC	1440
CGCAACCGCA	CCAGGCACAC	GATCGACAGC	ATCGCTCAAG	GCCGTGTATG	GCTCGGCGAC	1500
AAAGCTCTTG	CACCTCGGTT	GGTGGATGAG	CTTGGAGGTT	TGGACACAGC	TATCAAACGG	1560
GCCGCGAAGC	TGGCTCAGCT	CGGTGGCAAC	TACAGCATAG	AGTATGGCAA	GACCAAGCGC	1620
AACCTTCTCG	AAGAGTTGCT	CTCCTCATCA	GCAGCGGATA	TGAAGTCTGC	CATCCTGAGT	1680
ACCATTCCTC	CCGATCCGGA	AATAGAAGTT	CTGCGCGAAC	TCCGCTCCAT	GCCGCCCCGT	1740
CCTTCGGGCA	TACAGGCACG	TCTCCCTAT	TACTTCATGC	CGTAC		1785

(2) INFORMATION FOR SEQ ID NO:135

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1767 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1767

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135

ATGTTTTTCG	CCTCGATCCT	CGGGGTTATA	ACGGCAGGAA	TCATCTTGT	CTGTATCTTT	60
CTATTTATCT	TTTTCGGCAT	CGTAGCCGGT	ATTGCCCTCA	AGGCAACGGG	AGGAACCAT	120
CCGAAGATCG	AAGCAAATC	CATCCTACAT	ATAHACAATT	CTTCTTTCC	TGAGATCGTA	180
TCGGCCATTC	CCTGGAGCAT	GCTCACAGGC	AAAGACGAGT	CGGTATCGCT	CTCACAGGCA	240
GTGGAAGCCA	TCGGCCAAGC	CAAAAATAAT	CCCAACATTA	CCGGTATCTT	CCTCGATCTG	300
GACAACCTTT	CGGTCCGTAT	GGCATCGSCA	GAGGAATTGC	GTCCGCGGTT	GCAGGATTTC	360
AAGATGTCCG	GCAAGTTCGT	CGTATCCTAT	GCCGACAGAT	ACACCCAAAA	GGGTACTACT	420
CTCTCCAGTA	TTGCAGACAA	ACTCTACCTC	AATCCGAAAG	GAATGTTGGG	GCTTATCGGG	480

WO 99/29870

PCT/AU98/01023

92 / 490

	ATTGCGACCC	AAACAATGTT	CTACAAAGAT	GCCTCGACA	AATTGCGCGT	GAAGATGGAG	540
	ATCTTCAAGG	TAGGCACCTA	CAAG3CAGCC	GTAGAGCCAT	TCATGCTCAA	CAGGATGAGC	600
	GATGCCAATC	CGGAACAAAT	CACCACATAC	ATAACGGGC	TTTGGGACAA	GATCACATCC	660
5	GATATTGCA3	AGTCGCGCAA	GACGGCAATG	GATTCCGTGA	AAATGTTTGC	CGACAAAGGC	720
	GAAATGTTCC	GTCTTGCCGA	GAAAGCGGTG	GAGATGAAGC	TCGTGGATGA	GCTGGCTTAC	780
	CGTACCGATG	TGGAGAAAGA	ACTCAAAAG	ATGTCCTAAC	GCGGAGAGAA	AGATGAACTT	840
	CGGTTCTGAT	CGCTTTCTCA	GGTTCTGGCC	AATGGCCCGA	TGAACAAAC	GAAAGGCAGT	900
	CGGATCGCCG	TTCTCTTTGC	GGAAGGTGAA	ATAACGGAAG	AAATAATAAA	GAAGCCGTTT	960
10	GACACTGACG	GTAGCTCCAT	CACACAAGAA	CTCGCCAAAG	AAATCAAGGC	AGCAGCCGAT	1020
	GACGATGATA	TCAAAGCCGT	AGTACTTCGT	GTCAATTCTC	CGGGAGGTAG	TGCTTTCACT	1080
	TCCGACAGCA	TATGGAAGCA	GGTAGCCGAT	CTCAAGGCCA	AAAAGCCTAT	CGTGGTCTCC	1140
	ATGGGCGGAG	TAGCAGCCTC	GGGCGGATAC	TACATAGCCT	GCGCAGCCAA	CAGTATCGTG	1200
	GCAGAGCATA	CGACTCTGAC	CGGCTCCATC	GGCATATTCC	GCATGTTCCG	GAACTTCGCG	1260
	GGCGTAGCCA	AGAAGATAGG	AGTGAATATG	GACGTCGTAC	AGACATCCAA	GTATGCAGAC	1320
15	TTGGGCAACA	CCTTCGCTCC	GATGACGGTC	GAAGATCGTG	CCTCATCCA	ACGCTACATA	1380
	GAGCAGGGCT	ACGACCTCTT	CCTCACTCGC	GTATCGGAAG	GCGGCAACCG	CACCAAGGCA	1440
	CAGATGGACA	GCATCGCTCA	AGGCGGTGTA	TGGCTCGGCG	ACAAAGCTCT	TGCATCGGCT	1500
	TTGGTGGATG	AGCTTGGAGG	TTTGACACACA	GCTATCAAAC	GGGCGCGGAA	GCTGGCTCAG	1560
	CTCGGTGGCA	ACTACAGCAT	AGAGTATGGC	AAGACCAAGC	GCAACTTCTT	CGAAGAGTTG	1620
20	CTCTCTCAT	CAGCAGCGGA	TATGAAGTCT	GCCATCCTGA	GTACCATTCT	CTCCGATCCG	1680
	GAAATAGAAAG	TTCTGCGCGA	ACTCCGCTCC	ATGCCGCCCC	GTCCTTCGGG	CATACAGGUA	1740
	CGTCTCCCTT	ATTACTTCAT	GCGGTAC				1767

25 (2) INFORMATION FOR SEQ ID NO:136

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 939 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

35 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

40 (ix) FEATURE:

(A) NAME/KEY: misc_feature

(D) LOCATION 1...939

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136

	ATGAGAGCAA	ACATTTGGCA	GATACTTCC	GTTCGGTTC	TCTTTTCTT	CGGGACAGCG	60
	ATCGGACAGG	CTCAGAGTCG	AAACCGTACA	TACGAGGCTT	ATGTGAAACA	GTACGCCGAC	120
50	GAAGCTATCC	GACAGATGAG	CCGCTACAA	ATACCGGCAA	GCATCACCAT	AGCACAGGCT	180
	TTGGTGGAGA	CAGGAGCCGG	AGCCAGTACA	CTGGCCAGCG	TACACAACAA	TCACTTCGGG	240
	ATCAATGCC	ACAAATCGTG	GACGGGCAAG	CGCACCTATC	GTACCGACGA	TGCGCCGAAC	300
	GAATGCTTCC	GCAGCTATTC	GGCGGCTCGC	GAATCGTATG	AAGATCATTC	CCGATTCTG	360
	CTCCAACCAC	GCTATCGTCC	CCTGTTCAAA	CTCGACAGAG	AAGACTATCG	GGGCTGGGCT	420
55	ACGGGGTTGC	AACGCTGTGG	CTATGCCACC	AATCGGGGCT	ATGCCAATCT	GCTGATCAAG	480
	ATGGTGGAGC	TGTATGAGCT	ATATGCTTTG	GATCGCGAGA	AGTACCCCTC	ATGGTTCCAC	540
	AAGTCTTACC	CCGGGTCCAA	CAAAAAATCC	CATCAACGA	CCAAGCAGAA	GCAGAGCGGA	600
	CTCAAGCAGC	AAGCTTACTT	CAGCTACGGA	CTGCTCTACA	TCATAGCCAA	GCAAGGCGAT	660
60	ACCTTCGATT	CTTTGGCGCA	AGAGTTGAC	ATGAGAGCCT	CCAAACTGGC	CAAAATCAAC	720
	GATGCTCCCG	TGGATTTCCC	GATCGAAAAG	GGCGATGTGA	TCTATCTGGA	GAAAAAGCAC	780
	GCATGCTCCA	TCTCCAAACA	CACACAGCAC	GTAGTGCCTG	TGGGCGATTG	GATGCACAGT	840
	ATCTCCCAAC	GCTATGGCAT	CCGGATGAAG	AACCTCTACA	AGCTCAACGA	CAAGGATGGC	900
	GAATATATAC	CCCAAGAGGG	CGATATACTG	CGCTTGCGC			939

65 (2) INFORMATION FOR SEQ ID NO:137

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1569 base pairs

70 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

75

WO 99/29870

PCT/AU98/01023

93 / 490

(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
5 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
(ix) FEATURE:
(A) NAME/KEY: misc_feature
10 (B) LOCATION 1...1569
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137

15	ATGGACGGAC	GTGATATTC	GGATGGCCTC	CATCAGGCTA	TGGAAGCCAA	AGAGCATGTG	60
	AAAGTAGAGG	CTGCCGACCA	GACATTGCA	ACTATCACTT	TGCAGAACTA	TTTCCGCATG	120
	TATCATAAGC	TGGCAGGGAT	GACCGGTACT	GCTGAAACTG	AAGCGGGAGA	GCTTTGGGAC	180
	ATCTACAAAC	TGGACGTTGT	AGTTATTCCG	ACAAACAAGC	CTATCGCCCG	TAAGGATATG	240
	AATGATCGTA	TCTATAAGAC	GGCACGTGAA	AAATATGCAG	CAGTTATCGA	AGAGATTGTA	300
20	CGTCTTGTG	AAGAGGGCAG	ACCTGTACTT	GTCCGTACTA	CTTCGGTGGG	AATATCCGAA	360
	TTGTTGAGCC	GTATGTTACG	CTTGGGTGGC	ATCCAACACA	ATGTAICTCA	TGCCAAATTG	420
	CATCAGAAAG	AGGCCGAGAT	TGTAGCTCAG	GCCGCTCAGA	AAGGAACITG	TACCATCGCA	480
	ACGAACATGG	CCGGTCGTGG	TACCGACATC	AAGCTCTCTG	CCGAGGTTAA	GAAAGCCGGG	540
	GGTTTGGCTA	TCATTGGTAC	GGAAAGGCAC	GAATCCAGAC	GAGTGGACAG	ACAGCTTCGT	600
25	GGTCGTTCCG	GCCGTCAGGG	TGATCCCGGT	TCGTCCATAT	TCTATGTTTC	CCTTGAAGAT	660
	CATCTGATGC	GCCTCTTTGC	CACAGAAAAG	ATTGCATCAT	TGATGGATCG	TTTAGGTTTC	720
	AAGGAAGGAG	AAGTGCTCGA	AAACAACATG	CTGAGTAAGT	CCGTGGAGCG	TGCTCAAAAG	780
	AAGGTGGGAG	AGAACAACCT	CGGTATCCGT	AAACATCTGC	TTGAGTACGA	TGATGTAATG	840
	AATTCGCAGC	GTGAAGTCAT	TTATACCCGT	CGCCGTCTATG	CTTGTATGGG	AGAGCGTATC	900
30	GGTATGGATG	TACTCAATAC	CATATACGAC	GATGTAAGG	CTCTGATTGA	CAATTATGCA	960
	GAAGCCATAT	ATTTCGSAAG	CTTCAAGGAA	GATCTGATGC	GTGCACTCGC	GATAGAATCT	1020
	CCTATCACGC	AAGAAATATT	CAGAGGTAAG	AAAGCAGAA	AGCTGACCGA	TATGCTTTTC	1080
	GATGAAGCTT	ACAAGTCTTT	CCAACGTAAG	ATGGATCTGA	TCCGAGAAGT	GGCCCAACCT	1140
	GTGGTTCAAT	AGGTATTCTA	GACCAAGGCC	GCCGTGTACG	AGCGCATCTT	AATCCGCATT	1200
35	ACGGATGGTA	AACGTGTCTA	TAACATAGGA	TGCAATTTCG	GTGAAGCGGA	TGAAACTCAA	1260
	GGGAAAGCA	TCATCAAGA	ATTGAGAGAA	GCTATCGTAC	TGCATACTAT	CGATGAGTCT	1320
	TGGAAGAAG	ATCTGCTGTA	GATGGACGAG	CTTCGTAATT	CCGTTTCAAA	TGCCAGCTAC	1380
	GAAACAAAG	ATCCACTACT	TATCTATAAA	CTCGAATCTT	ACGAACCTGT	CCGCAAGATG	1440
	GTAGAAGCCA	TGAACCGTAA	GACCGTAGCG	ATCCTAATGC	GTGCTCGGAT	ACCGGTACCG	1500
40	GAGGCTCCTT	CCCAAGAAGA	GCTGGAACAC	AGGCGGCAAA	TAGAAATCCG	ACATGCAACC	1560
	CAACAACGT						1569

(2) INFORMATION FOR SEQ ID NO:138

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

50 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
55 (iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
60 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1125
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138

65	ATGAATTTCT	TAAAAAAGA	ACCGTTTAAA	ATATTCTCTA	TGATTATCT	GCTGTTAGAT	60
	ACAATAACAA	ACCGTGCCGG	TACAGAACGC	GCCGTGATCA	ACTTGGCTAA	CAACCTGCAT	120
	GCCATGGTTC	ATCGCGTATC	ATTAGTCAGC	GTTTGTACAA	AAGAAGGAGA	GCCTTCCTTC	180
	CAAGTAGAAA	AAGGAATAGA	ACTACACCAT	CTCGGAATTA	GGCTTTATGG	CAATGCATTA	240
70	GCCCCGAAAA	CAGTATATT	CAAGGCTTAT	CGAAGGATAA	AAGCCCTATA	CAAGAAGCGT	300
	GAACCGGTTT	TATTGATAGG	GACTAATATT	TTTATCAATA	CAATTTTGTC	TCAGATCAGT	360
	NACAGAGGCA	GAATATTTAC	GATCGGATGC	GAACATATCT	CTTATGATA	TGCCCGCCCT	420
	ATTACAAAA	GCATAAGGGG	GTTTCTGTAT	TCAGGGCTTG	ATGCCGTGTG	AGCACTGACA	480
	AAAAGAGATC	AGCAATCGTT	CGAGGCAATC	TTACGTGGAC	GCTCTAAGC	ATATGTCATA	540
75	CCCAATCAAG	TTTCATTTAC	TACAGTCCAA	AGAGATGCTA	CTACTCACA	ACAAATGTTG	600

5 GCGATTGGCA GGCTTACCTA CCAGAAGGGT TTTGAATTCA TGATAGAAGA TGCATCACGA 660
GTGCTGGGAG AAAGGCCTGA TTGGAAGCTT ATCATAGTCG GAGATGGCGA AAATGAATCG 720
ATGCTACGTA AAGAAATTGC ATCTCGCAAT ATGGAGTCGC AAATAGAAAT ACATCCATCT 780
ACACCGGAAA TTCGCAATA CTACGAATCA TCTGCTATTT ATCTAATGAC GTCCCGTTTC 840
GAAGGACTAC CAATGGTACT TCTCGAAGCA GAAGCATATG CACTACCTAT AATCTCATAC 900
GATTGTCCGA CCGGCCCGAG GGAAGTGATC GAAAACGGTC GCAATGGTTT CCTTGTGCCA 960
ATGGAAGCAC ATGAAGACTT CCGGGATAAG TTACGCTTAT TGATGGATGA TGAAGCTCTT 1020
CGTAAGAAAA TGGGACAAAG ATCAGAGTTG ATGGTCAAAT CCTACTCTCC GGCAAAATATC 1080
10 TATGAATGTT GGAAGAAACT ATTGCTCGAA ATGGGCTACA TGAAT 1125

(2) INFORMATION FOR SEQ ID NO:139

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1086 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 20 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 25 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 30 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION: 1...1086

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139

35 ATGATTTATC TGCTGTTAGA TACAATAACA AACCCTGCCG GTACAGAACG CGCCGTGATC 60
AACTTGGCTA ACACCTTGCA TGCCAAATGGT CATCGCGTAT CATTAGTCAG CGTTTGTACA 120
AAAGAAGGAG AGCCTTCCTT CCAAGTAGAA AAAGGAATAG AAGTACACCA TCTCGGAATT 180
AGGCTTTATG GCAATGCATT AGCCCGCAAA ACAGTATATT TCAAGGCTTA TCGAAGGATA 240
AAAGCCCTAT ACAAGAAGCG TGAACCGGTT TTATTGATAG GSACTAATAT TTTTATCAAT 300
40 ACAATTTTGT CTCAGATCAG TAACAGAGGC AGAATATTTA CGATCGGATG CGAACATATC 360
TCTTATGATA TTGCCCGCCC TATTACAAAA CGCATAAGGG GGTTCCTGTA TTCAGGGCTT 420
GATGCCGTTG TAGCACTGAC AAAAAGAGAT CAGCAATCGT TCGAGGCAAT CTACGTGGA 480
CGCTCTAAG CATATGTCAT ACCCAATCAA GTTTCATTIA CTACAGTCCA AAGAGATGCT 540
ACTACTCACA AACAAATGTT GCGGATGGGC AGGCTTACCT ACCAGAAGGG TTTTGAATTC 600
45 ATGATAGAAG ATGCATCACG AGTGCTGCCG GAAAGGCCTG ATTGGAAGCT TATCATAGTC 660
GGAGATCGCG AAAATGAATC GATGCTACGT AAAGAAATG CATCTCGCAA TATGGAGTCG 720
CAAAATAGAAA TACATCCATC TACACCGGAA ATTCCGAAAT ACTACGAATC ATCTGCTATT 780
TATCTAATGA CGTCCCGTTT CGAAGGACTA CCAATGGTAC TTCTCGAAGC AGAAGCATAT 840
GCACTACCTA TAATCTCATA CGATTGTCCG ACCGGCCGSA GGGAACTGAT CGAAAACGGT 900
50 CGCAATGGTT TCCTTGTGCC AATGGAAGCA CATGAAGACT TCGCGGATAA GTTACGCTTA 960
TTGATGGATG ATGAAACTCT TCGTAAGAAA ATGGGACAAG AATCAGAGTT GATGGTCAA 1020
TCCTACTCTC CGGCAAAATAT CTATGAATGT TGGAAAGAAC TATTCGTCGA ATTCGGCTAC 1080
ATGAAT 1086

(2) INFORMATION FOR SEQ ID NO:140

- 60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1920 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 65 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 70 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 75 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION: 1...1920

WO 99/29870

PCT/AU98/01023

95 / 490

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:140

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5  ATGGGAAAAA TCATTGGAAT TGAATTAGGC ACAACGAACT CTTGTGTCTC TGTATTGGAA 60
   GGTAACGAAC CTATCGTTAT TACAAACAGT GAGGGCAAGC GCACAACGCC CTCGGTAGTG 120
   GCTTTTGTGG ATGGTGGCGA GCGTAAGGTG GCGATCCGG CCAAGCGTCA GGCCATCACC 180
   AATCCGACCA AGACGATATA CTCTATCAAA CGCTTCATGG GCGAACTTA CGATCAGGTT 240
   TCCAGAGAAG TGGAGAGAGT GCCATTCAAG GTAGTACGTG GGGACAATAA TACTCCGCGC 300
   GTAGATATAG ACGGTCGTCT CTATACGCGG CAGGAAATTT CGGCCATGAT CCTTCAGAAG 360
10  ATGAGAAGA CGGCCGAAGA CTACCTCGGT CAGGAAATTA CGGAGGCCGT GATCACTGTG 420
   CCCGCATACT TCAACGACGC TCAACGTCAG GCAACGAAAG AAGCAGGAGA GATCGCCGGC 480
   CTGAAAGTTC GCGCTATTGT GAACGAGCTT ACGGCAGCTT CTCTGGCCTA CGGTCTGGAC 540
   AAGTCCAATA AGGATATGAA GATCGCTGTC TTCGACTTGG GTGGCGGTAC CTTGATATC 600
   TCTATCTTGG AATTGGGCGA CGGCGTTTTC GAAGTGAAT CGACCAACGG TGATACGCAC 660
15  CTCGGAGGAG ACGACTTCGA CCACGTGATC ATTGACTGSC TGGCAGAAGA GTTCAAGTCT 720
   CAGGAAGGTG TGGATCTTCG CCAGGATCCT ATGGCTATGC AGCGTCTGAA AGAAGCTGCC 780
   GAAAAAGCCA AGATAGAGCT CTCACGACT TCATCTACGG AGATCAACCT CCCCTATATC 840
   ATGCCCGTGA ACGGCATCCC CAAGCACTTG GTGATGACCG TTACAAGGGC TAAGTTCGAG 900
   CAGTTGGCCG ATCGTCTGAT TCAGGCATGT GTGGCACCCT GCGAAACGGC CTTGAAAGAT 960
20  CCGGATATGT CAGGTGGCGA TATCGATGAA GTGATTCTCG TAGGTGGTTC CACACGTATT 1020
   CCTGCTATTC AGGAGATTGT GGAGAAGATC TTCGTAAGG CTCGGTCCAA GGGTGTGAAT 1080
   CCCGACGAAG TGGTAGCTGT GGGTGCCGCT ATTCAGGCG GTGTTCTGAC CGGTGAGGTA 1140
   AAGGATGTCT TGCTGTGGG CGTTACCCCC TTGTCTGTCG GTATCGAGAC TATGGGAGGC 1200
   GTGATGACTC GCTTGATCGA TGCCAAATAC ACTATCCCGA CGAAGAAGAG CGAAATCTTT 1260
25  ACCACAGCAG TGGACAATCA ACCCTCGGTA GAGATTCTAT TACTTCAGGG TGAGCGTTCT 1320
   TTGGCTAAGG ACAATAAGAG CATCGGCCGT TTCNACTTGG ACGGTATTGC TCCGGCGGCC 1380
   CGTCAGACAC CGCAGATCGA AGTAACGTTT GACATCGATG CCAACGGTAT CCTGAATGTA 1440
   ACGGCTCATG ACAAGCTAC CGGCAAGAG CAGAAATATC GCATCGAAGC CTCACGCGGT 1500
   TTGTCCGATG ATGAGATCAA GCGCATGAAG GAAGAGGCGC AGGCCAATGC CGAAGCAGAT 1560
30  AAGAAAGAGA AAGAAGCTAT CGACAAGATC AATCAGGCCG ACAGCATGAT CTTCCAGACG 1620
   GAAAAGCAGT TGAAGGAGTT GGGAGACAAA TTCCCGGCCG ACAAGAAGGC TCCGATCGAT 1680
   ACCGCTCTCG ACAAACTGAA AGAAGCACAC AAAGCACAGG ATGTAGCTGC TATCGATACA 1740
   GCCATGGCCG AACTGCAAAAC CGCTCTTTCC GCAGCGGGCG AAGAGCTTTA CAAGAATGCC 1800
   GGAGCAGCCC AAGGTGGCGC ACAACCCGGT CCGGACTTCG GCGGTGCTCA AGGTCCCTCT 1860
35  GCGGTGATC AGCCCTCTCA CGACAAGAAC GTCACAGACG TAGACTTCGA GGAAGTGAAG 1920

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(2) INFORMATION FOR SEQ ID NO:141

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40  (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 1347 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: double
     (D) TOPOLOGY: circular
45  (ii) MOLECULE TYPE: DNA (genomic)
     (iii) HYPOTHETICAL: NO
50  (iv) ANTI-SENSE: NO
     (vi) ORIGINAL SOURCE:
     (A) ORGANISM: PORPHYROMONAS GINGIVALIS
55  (ix) FEATURE:
     (A) NAME/KEY: misc_feature
     (B) LOCATION 1...1347

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(x1) SEQUENCE DESCRIPTION: SEQ ID NO:141

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60  ATGCGCTACG ACTTAGCTAT CATCGGTGGA GGGCCGGCCG GTTATACGGC TGCCGAACGT 60
   GCTGCCAAGG GTGGCCTGAA AACCTCCTTA ATTGAGAAGA ATGCTCTCGG TGGTGTATGC 120
   CTCACGAAGG GATGTATACC GACCAAGACG CTACTCTACT CGGCCAAAGT GCTACATCAA 180
   ATTGCTACGG CATCTAAATA TGCAGTAAGT GGAACGGCCG ATGGACTTGA CCTCGCCAAG 240
65  GTGATTGCCA GAAAAGGTAA AATCATTTCG AAGCTGACTG CAGGCATCCG TTCACGCCCTG 300
   ACAGAGGCCG GAGTAGAGAT GGTGACGGCA GAAGCTACCG TAACGGGATG CGATGCAGAC 360
   GGCATCATCG GCATTACTGC GGGCGAAGCA CAGTACAAAG CTGCCAACCT GCTACTATGT 420
   ACCGGTTCCG AGACGTTTAT TCCACCCATC CCGGAGTGG AGCAGACAGA GTATTGGACA 480
   AACCGTGAAG CTCTACAGAA CAAAGAGATT CCGACCTCTC TCGTCATCAT CGGTGGTGGG 540
70  GTGATCGGAA TGGAGTTCCG TTCTTCTTC AACGGTATCG GTACGCAAGT GCACGTGGTG 600
   GAGATGCTGC CGGAAATACT CAACGATATC GATCCCGAAC ATGCAGCTAT GCTACGCGCT 660
   CACTATGAAG AAGAAGGAAT CAAATCTTAC CTCGGGCACA AAGTAACATC GGTTCGCAAC 720
   GGAGCTGTTA CGGTAGAATA CGAAGGAGAA AGCAAAGAGA TCGAAGGAGA ACGTATCCTG 780
   ATGAGTGTGG GACGTCGCCC CGTGCTGCAA GGATTGAGT CGCTCGGATT GGTGCTTGGC 840
75  GGCAAAGGTG TAAAGACTAA TGAGAGGATG CAAACTTCCC TGCCCAATGT CTATGCTGCA 900

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WO 99/29870

PCT/AU98/01023

96 / 490

5
GGTGATATTA CAGGCTTCTC GCTTTTGGCA CATACGGCTG TACGGGAAGC AGAGGTAGCA 960
GTAGATCAGA TTTTGGGCAA AACAGACGAA ACGATGAGCT ACCGTGCCGT ACCAGGTGTG 1020
GTGTACACCA ATCCUGAGGT CGCCGGTGTG GGAGAGACGG AAGAATCGCT TCGCAAAGCA 1080
GGACGTGCGT ACACGTGTTG TCGCCTTCCT ATGGCCTTCT CGGTCGATT TGTAGCAGAA 1140
AACGAACAA GCAATGGAGA GTGCAAACTA CTACTTGATG AAGAGAACCG CTTGATCGGA 1200
GCACACCTCA TTGGCAATCC GGCCGGCGAA CTCATCGTAA CCGCTGCCAT GGCCATCGAG 1260
ACCGGCATGA CGGATCGACA AATCGAACGA ATCATATTCC CTCATCCGAC TGTAGGCGAA 1320
ATCTAAAG AAACCTCTCC CGGAGGT 1347

10

(2) INFORMATION FOR SEQ ID NO:142

15

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2823 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

20

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(1iv) ANTI-SENSE: NO

25

(v1) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

30

(1x) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...2823

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:142

35
ATGGAATTGA AAAGATTTT ATCACTTGGT CTTCTGCTTG TGGGATTCAT TCCGATGAAG 60
CTTCTGCCCC AACAGGCTCA GCCACTCCCT ACAGATCCGG CTGTTCCGTG CGGTAAGTTG 120
GACAACGGAT TGACTTATTT CATCCGTCAC AACGAGAACC CGAAAGATCG TCGCGATTTC 180
TTTATCCGAC AAAAGGTAGG TTCTATTCTT GAAGAAGATA GCCAGTCCGG TTTGGCTCAC 240
TTCTTGGAAC ACATGGCTTT CAACGGTACG AAGAAGCTCC CCGTAAGAA CTTGATCAAC 300
TATCTCGAAA CGATCGGTGT ACGTTTCCGT CAGAACCTGA ACGCTTCTAC CGGATTCGAC 360
AAGACGGAAT ATACGATAAT GGAATGTCCG ACTACACGTC AGGGAATCAT GACTCCCTGC 420
TTGCTTATCC TGCATGATTG GAGTAACAAT ATTACCCCTG ACGGGCATGA GATCGACGAG 480
GAGGCGGGTG TGATCCAGGA AGACTGGCGT GCTCGTCGCG ATGCCAACCT TCGTATGTTT 540
GAGGCTATAC TTGCCAAGGC TATGCCGGGT AATAAATATG CAGAACGCAT GCCCATCGGT 600
CTGATGGAGC TCGTGTCAA CTTCAAGCAT GATGAGCTGC GCAACTATTA TAAGAAATGG 660
TATCGTCCCG ACCTGCAAGG TCTGGTGATC GTGGGAGATA TCGATGTGGA CTATGTGGAG 720
AACAAGATCA AAGAACTCTT CAAGGACGTT CCGCTCCCG TGAATCCAGC AGAGCGTATC 780
TATACGCCGG TAGAGGACAA CGATGAGCCT ATCCTAGCCA TTGCTACCGA TGCTGAGGCT 840
ACTACCACGC AGCTCTCCAT CAGCTTCAAG AGCGACCCCA CTCCTCAAGA AGTGGGAGGA 900
TCGATATTCC GACTTGTGGA AGACTATATG AAACAGGTGA TCACTACAGC CGTGAATGAG 960
CGTCTGTCGG AGATTACTCA CAAGCCTAAC GCTCCTTTCC TCAGTGCAGG AGCTTTCTTC 1020
TCTAACTTCA TGTACATCAC CCAGACTAAG GACGCATTCA ATTTTGTTCG CACGGTTCGT 1080
GAGGGTGAA GCGAGAAAGC GATGAACGCA TTGGTGGCAG AGATAGAAAG CCTCCGTCAG 1140
TTCCGTTATCA CCAAGGCGGA ATACGATCGT GCACGCACGA ATGTGCTCAA GCGATACGAG 1200
AATCAATACA ACGAAAGAGA CAAGCGTAAG AACAAATGCT ATGCCAATGA ATACTCCACC 1260
TACTTCACCG ATGGCGGCTA TATCCCGGGT ATTGAGGTGG AATATCAGAC GGTGAATGCT 1320
TTTGTCTCTC AGGTTCCTCT GGAAGCATTC AATCAGGCTA TTGCCCAAT GATCGATCCG 1380
GTGAAGAATG CTGTCGTTAC CCTCACCGGT CCTTCAAAGG CTGAAGCCAA GATTCCGAGC 1440
GAAGCAGACT TCCTCGCTGC TTTCAAAGCT GCTCGTCAGC AGAAAGTAGA AGCCAAGAAA 1500
GACGAAGTCT CCGACCAAAA ATTGATGGAG AAAGCTCCTA AGGCCGAAA GATCGTTTCC 1560
60
GAGAAGAAAG ATCAGAAGTT CGGTACCACG GAACCTACCC TTAGCAATGG CATCAAAGTA 1620
TACCTCAAGA AGACCGATT CAAATCAAAC GAAATCTGA TGAGTGCTCT CAGCCCGGCT 1680
GGTATCTCT CCGGAAAGCA TGCTCCCAAC CAATCTGTGA TGAATTCGTT CATGAACGTG 1740
GGTGGCTTGG GCAACTTCGA TGCTATCCAG CTGGATAAGG TGCTGACAGG TCGTCTGTCT 1800
TCCGTATCTC CTTCTTTGTC TCTGCTCAGT GAAGGTCTTT CGGGCAAAAC GACTGTAGAA 1860
65
GATATGAAAA CTTTCTTCCA GTTGATCTAT CTCCTAATGA CTGCTAACCG CAAGGATCCC 1920
GATGCGTTCA AGGCGCACCA GGAAGAGTTG TACAATAACT TGAATAATCA GGAAGCCAAC 1980
CCGATGGCTG CGCTTATGGA CTCTATCCGT CATACCATGT ACGGCGATAA TCCGATGATG 2040
AAACCCATGA AAGCTGCTGA CGTGGAGAAA GTAAATACG ATCAGGTAAT GGCCTTCTAC 2100
AATGAGCGAT TCGCTGATGC CGGCGACTTT ATGTTCTTCT TTATCGGTAA TCTGGATGAA 2160
70
GCCAAGATGA AGCCATTGAT CGAAACTTAT CTTGCTTCAT TGCCCAACCT CAAGCGTGCC 2220
GATAAGATGA ATAAGGCTCA GCTACCGGCT GCCCGTTCGG GAAAGATCGA TTGCAAGTTC 2280
GAGAAGGAAA TGGATACTCC TTGCACTACT ATATTGATG TCGTGTCCGG AAATGTGGAA 2340
TATACGCTCA AGAACAGTCT CTTGCTGGAA GTCTTCTCAG CCGTAATGGA TCAGGTGTAC 2400
ACGGCTACCG TTCCGAGGAA GGAAGGCGGT GCATACAGT TGGCTGCATT CGGCGTCTC 2460
75
GAGCAATATC CTCAGCCCAA GGCTCTGATG CAGATCTATT TCCCCACGGA TCCTGCTCGT 2520

5	GCCGAGGAAA TGAATGCTAT CGTTTTGCT GAGTTGGAGA AGCTTGCCAA GGAGGGCCCC 2580 AATGTGGAAT ACTTTAAGAA GACTATCGAA AACCTGAATA AGCAGCAGAA AGAAAAGTCTG 2640 CGTGAGAATC GTTTCCTGGCT CGAAGCCATG AAGGCGTCTT TCTTCGAAGG AATGACTTC 2700 ATCAGAGACT ACGAATCCGT ACTGAACGGT CTTACTCCTG CTGAATTGCA AAAGTTTGG 2760 GCAGACCTCT TGAAGCAGCA GAATCGGGT GTTGTATGA TGGCTCCTGT TGCAGAGGCT 2820 CAA 2823
10	(2) INFORMATION FOR SEQ ID NO:143
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 2052 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular
20	(ii) MOLECULE TYPE: DNA (genomic)
25	(iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
30	(ix) FEATURE: (A) NAME/KEY: misc feature (B) LOCATION 1...2052
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143
40	ATGAGTAAGA AAGGAACAAT CGGGGTAACG AGCGACAATA TATTCCCGGT CATCAAAAAA 60 TTCCGTGTACA GCGACCATGA GATATTCCCTG CGTGAGATCG TCTCCATGC CGTGGATGCT 120 ACGCAGAAAGC TGAAAACGCT TACATCCGTC GCGGAATTCA AAGGCGAGAC GGGTGACCTC 180 CGCGTAACCG TCAGCGTGGG TGAAGTGGCA CGCACGATCA CGGTCAAGCA CCGCGCGTA 240 GGGATGACCG AAGAGGAGGT GGAGAAGTAC ATCAATCAGA TTGCTTTCTC CAGTGCAGAA 300 GAGTTTCTTG AAAAGTACAA AGACGACAAG GCCGCCATTA TCGGCCACTT CGGACTCGGA 360 TTTTACTCGG CTTTCATGGT GTCCGAGCGA GTGGACCTGA TCAGCGGCTC TTTCCGAGAA 420 GATGCTACGG CGGTGAAATG GAGCTGCGAC GGATCGCCCG AATACAGCT CGAACCTGCG 480 GACAAAGGCTG ACCGTGGCAC CGACATCGTG ATGCACATCG ATGAGGAGAA TAGCCAGTTC 540 CTCAAAAAAG AAAAGATAGA GGGGCTCCTC GGCAATACT GTAAGTTCTT TACCGTGCCG 600 ATCATTTCG GCAAGAAGCA GGAATGGAAA GACGGCAAGA TGCAAGATAC GGACGAGGAC 660 AATCAGATCA ACGACACACA TCCTGCCTGG ACCAAAAAGC CTGCCGACCT CAAGGACGAA 720 GACTATAAGG AATTTTACCG TTCGCTCTAT CCCATGTCCG AAGAGCCTCT CTTCTGGATC 780 CACCTCAATG TGGACTATCC GTTCAATCTG ACAGGTATCC TCTATTTCCT GAAGTCAAA 840 AACAACTGG ATCTGCAGCG CAACAAGATT CAGCTCTACT GCATCAGGT TTACGTCACC 900 GATGAAGTAC AGGCTATCGT GCCGGACTTC CTCACCTCC TGCACGGGGT CATCGATTCC 960 CCGGATATTC CCTCAACGT ATCGCGCTCC TATCTGCAGA GCGATGCCAA TGTGAAGAAG 1020 ATCTCGTCTC ATATCACCAA GAAGGTGGCA GACGCTCTGG AAGAAAATTT CAAAAACGAC 1080 CGCCCCACAT TCGAGGAGAA ATGGGATAGT CTGAAGCTCT TCGTCGAATA CGGTATGCTG 1140 ACGGATGAGA AGTTCTATGA GCGTGCAGCC AAATTCTTCC TTTTCACCGA TATGGACGGA 1200 CACAAGTACA CGTTCGACGA ATACCGAAGC CTGTCGAAG GTGTACAGAC GGATAAGGAC 1260 GGACAGGTAG TGTATCTCTA TGCTACGGAC AAGCATGGAC AGTACAGCCA CGTGAAACGT 1320 GCATCCGACA AAGGCTACAG CGTGATGCTG TTGGATGCTC AGTTGGATCC GCATATCGTG 1380 AGCCTGCTGG AGCAAAAGTT GGAGAAGACA CACTTTGTCC GTGTGATAG CGATACGATC 1440 AACAACTGTA TCCGCAAGGA GGAAGAGACC GAAGTGAAAC TGTCCGATAC GGAGCGCGCC 1500 ACTCTCGTGA AGCTGTTGGA AGCACGCGCTG CCACGGGACG AGAAGAAGCA CTTCAATGTA 1560 GCTTTCGAAT CGCTCGGAGC CGAAGGTGAA GCCATCCTTA TCACACAAGC CGAATTCATG 1620 CGCCGTATGC GCGATATGGC ACAGCTGCAG CCGCGAATGA GCTTCTACGG CGAACTCCCC 1680 GATTCGTACA ATCTGGTACT TAATACCGAT CATCCGCTCA TCGACAGGGT ACTCTCCGGT 1740 GAGAAAGAAAT CCGTAGAGCC TTCGCTCACA GAGCTTAGAG CGAAAATCGC CGAGCTGAAA 1800 GCGGAAGAGG CCAAGCTGCT CGATGAGGAA AAAGGGGAAG AACCGGAGGA AATCCCTGTT 1860 GCCACGAAGG AAGCCAAAGG GAACAAAGCC GTCGAACAGG CCAAAACCGA AGGCAGTATC 1920 AACGATCAAC TGACCAATA TGCTCAGGAC AACGAGCTGA TAGGTGAGCT CATCGACTTG 1980 GCTCTGCTCG GAAGCGGATT GCTGACGGGA GAGGCTTTGG CGGAATTCAT TCGTCCGAGC 2040 CAGCGTCTTC TC 2052
70	(2) INFORMATION FOR SEQ ID NO:144
75	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1392 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1392

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144

ATGGAAGAAC	TGATCGATAT	TTTGGTCGTA	GACGATGATG	TGGCAGTCTG	TGCCGCACTG	60
CGTCTGGTGC	TCAAGCGAGC	GGGCTATAAT	CCCGTTATAG	CCAACAGTCC	CGACGAAGCT	120
TTGTCCATAA	TGCGGAATCC	TGATGGCGGC	TGTAAGCCGG	CTGTGATTCT	GATGGATATG	180
AAATTTCTCC	TTTCGACCTC	CGGCAGGGAA	GGATTGGAAC	TACTGGAGAA	GATGCAGATA	240
TTCACTTCCT	GCCCTGTCT	ACTGATGACG	GCTTGGGCTT	CGATTCCACT	GGCAGTGGAG	300
GGAAATGAGG	TTGGAGCTTT	CGACTTCATA	GGCAAGCCAT	GGGACAACGA	TCCGGCTCCTT	360
CGTACCATAG	ATACGGCCTT	GCATCTGGCT	GCTCCCTCAG	CTGTGGCGAA	TCCATCGGAA	420
CAGTCTGACA	GAGATACAGC	CGTCAGCCCG	AAAGCTACAG	TCCAAGAGAA	TGACCCCTGT	480
GCCCATATCA	TAGGCCGGAG	CGATGCCATC	TGTAAGATCA	AGGAACGGAT	ACGCCGCATA	540
GCTCCCAACC	ATGCCTCTGT	GCTGATCAGC	GGCGAGAGCG	GTACGGGCAA	AGAGTTGATA	600
GCCGAAGCTC	TGCACCGTGG	GAGCAAAACGA	GCCTCAGCCC	CATTCTGTCA	GGTCAATTTG	660
GGTGGGATTC	CCGAAAGTTT	GTTGAAAGT	GAGCTGTTCC	GACATAAGAA	AGGAGCTTTT	720
ACCAATGCTT	TTTCCGACAG	GAAAGGACGG	TTCCGAGCTGG	CTGATGGGGG	CACGATCTTT	780
CTGGACGAAA	TACGCGAACT	ACCGGTCGGC	AACCAAGTAA	AACTGCTGCG	AGTGCTACAG	840
GAACAGACAT	TCCAGCCGTT	GGGCGAGAGC	GTCTCCCAAC	GAGTGGACAT	CCGTGTGGTA	900
TCCGCTACGA	ATGCTTCCTT	GGAGCGAATG	GTAGCCGAAG	GACGTTTCAG	AGAGGACCTC	960
TACTATCGAA	TCAACCTGAT	ACATCTGCAT	CTGCCTCCGC	TGCGTGAGCG	TCAGGAGGAT	1020
ATACAGCTGC	TGGTGGAAAG	CTTCAGTGAA	GCCTTTGCCC	AATCGAACGG	ATTGCCCCAT	1080
GCCGTTTGA	GTGCGGAAGC	TATGCGAGCT	ATCTGTGCCA	TGCCCTTACC	GGGCAATGTA	1140
CGCGAACTGA	AAAACGTAGT	GGAGCGTAGC	CTATTGCTCT	CGGGATCGAG	AGAAATCAGT	1200
GCCCGGATG	TGGCTGACTT	CGGTTCGCAG	GTGACGGCAG	CAGACCACTC	CGACGAACGG	1260
GCTTTGACCG	ACATGGAGGA	AGCTGCTATC	CGAGAGACGC	TGACTAAATA	CAACGGCAAC	1320
GTTAGTCGTG	CTGCACGAGC	CTTGGGATTG	AGCCGGGCAG	CTCTTTACCG	GCGAATGGAG	1380
AAATACGGAC	TG					1392

(2) INFORMATION FOR SEQ ID NO:145

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 750 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145

ATGCTTAAGA	TAAAGAACCT	CCACGCCACA	GTACAGGGCA	AAGAGATATT	GAAAGGAATC	60
AACTCTGGAG	TCAATGCCCG	AGAGATTGAT	GCTATCATGG	GGCCGAACGG	ATCGGGGAAA	120
AGTACGCTCT	CTTCGTTTTT	GGTGGGACAT	CCCTCCTTTG	AAGTCACGGA	AGGAGAGGTG	180
ACATTCAATG	GAATCGACCT	GCTCGAACTC	GAACCGGAAG	AACGTGCACA	CCTCGGACTC	240
TTTCTCAGTT	TCCAATATCC	GGTCGAGATC	CGGGGCGTCA	GCATGGTGAA	TTTCATGAGG	300
GCAGCTGTCA	ATGAACATAG	GAAAGCGATC	GGAGCAGAAC	CGTATCGGC	AAGCGACTTC	360
CTCAAGATGA	TGCGAGAGAA	CGGTGCCATT	GTGGAGCTGG	ACAACAAATT	GGCCAGCCGT	420
TCTGTGAACG	AAGGCTTCTC	CGGTGGAGAA	AAAAAGAGCA	ACGAATCTTT	CCAAATGGCT	480
ATGCTCGAAC	CCAAGCTGGC	TATTTTGGAC	GAAACCGATA	GCGGGCTCGA	TATCGACGCT	540
CTCCGCATCG	TAGCAGCGCG	GGTAAACCGA	CTCCGCTCTC	CGGAGAATGC	TGCTATTGTG	600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146							
30	ATGGCTAAGG	AGAAAACGAT	CTACGCTGCG	CGTTCGTGCG	GAACCAATA	CGCCAAATGG	60
	CAAGGCAACT	GCAATGCGCTG	TGGAGAGATGG	AATTGCATTG	ATGAGAGAGAA	GGTGCCGGCA	120
	CGGGCATCGG	GCAAGCATCT	AGCCAAAGAT	TTTATGCTGT	GGGAGCAGGA	CAACCGGCCA	180
	AGACTCTTAC	AGGATGTGGA	GTCCGGCGAT	GAAGAGCGTA	TTGCGCTCGG	CGATGAAGAG	240
	TTCCAGCTTG	TACTGGGTGG	AGGAATTGTC	AAAGAGCAT	TTGCTCTGCT	TGGCGGCGAG	300
	CCGGGAATCG	GTAAGTCCAC	GCTTATCCTC	CAGACGGTGC	TGCGCTTGGC	CGAGTTGGCG	360
35	AGCGCTCATG	TGTCGGGCGA	AGAAAGTGCC	CGACAACTGA	AGATGCGGCG	CGAACGACTG	420
	GGCCAGCGCA	TGAATGGGTG	CTACGTATAC	TGCGAAACGA	ATATAGAGAG	GTAACCTCTG	480
	CCGTGCAGAA	AACCTCACAC	CGATCTCCTC	GTGATAGACT	CTATACAGAC	GGCTCTATACC	540
	GAGGAATAAT	AAAGCTCGGC	CGGCAGCGTG	GGGACAGTCC	GGGAATGTCG	CGCCTTACTG	600
	CTCAAAATAG	GCAAGACTAC	GGGTATCCCC	GTCATCGTCA	TCGACACAT	CACCAAGAGAA	660
40	GGTAGCATAT	CCGGACCGAA	GGTGCTGGAG	CATATAGTGG	ATACGGTGCT	TCTCTTCGAC	720
	GGGGATAGGC	ATCATCTCTA	CCGGATACTC	CGAGGACAGA	AGAACCGCTA	TGGCAGTACT	780
	TCCGAGCTTG	GGATATCTGA	GATGGCGCAG	CACGGTCTCG	TGGGCGTGGG	GAATCCGAGC	840
	GAACA'TCTCA	TCACACGCA	TAGGGAAGAC	GTCAGTGCCA	TAGCCATAGC	CGTAGCGATG	900
45	GAGGGCATTG	CGCCGATACT	CACTGGAAGC	CAGGCTTTGG	TCAGCTCGGC	CATTATTGCC	960
	AATCCCGAGC	GTTCCGGCAC	GGGCTTCGAT	ATTCCGGCGA	TGAACATGGT	CTTAGCCGTA	1020
	CTGGAGAAGC	GTCCCGGCTT	CAAGCTCATG	CAGAAGGATG	TGTTTCTGAA	CATTGCCCGA	1080
	GGTATCAAAA	TACCGCATCC	GGCTACGAGT	CTGGCCGTTA	TCTCGGCAGT	GCTGSGCGTCG	1140
	AGTCTGGACA	TCGTATCCCG	GCCCGCCGTA	TGCATGACGG	GCGAGGTGCG	ACTCTCGGGA	1200
	GAGATACGTC	CGGTGAGCCG	CATCGAGCAG	CGCATAAACG	AAGCGCGCTG	CATAGGGGAT	1260
50	CAAGAGATAT	TGGTACCGGC	CGATAAATTC	CGGCAGGAGG	ATGCCGCGCG	CTTCGGTATT	1320
	CGGCTCGTGC	CGGTGAGAAA	GGTGAGGAAA	GCCTTCCCCC	ATCTGTCTCT	GAAAGGAAGA	1380
	GAA						1381

SUBSTITUTE SHEET (Rule 26) (RO/AU)

100/ 490

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:147

5 ATGAATAGCA GACATCTGAC AATCACAATC ATTGCCGGCC TCTCCCTCTT TGTACTGACA 60
TTGGGCGGCT GCTCCGTAGC CCAACAAGAT ACGCAGTGGG CTCTCGGCGG AAAGCTCTTT 120
ACTTGGCGGT SGATACACGG TTCGGCCGAA TATCAAGCGC TTTCATTCA GGCATACAC 180
ATCGCTACGG AAGAGTGGG CGCTCTACCG GCAGAACGTA AACCAAGGAGA TAGGCCTTAT 240
GCCATCGTAA CGGACATAGA CGAAACCATT TTGGACAATA CGCCTAACTC CGTGTATCAG 300
GCTCTCAGCG GCAAGGATTA TGATGAAGAG ACTTGGGGGA AATGGTGTGC ACAGGCCGAT 360
GCCGACACAC TGGCAGGAGC TTGTCTTTC TTCTCCATG CAGCGAACAA GGGGATCGAG 420
10 GTCTTTTACG TCACCAACCG CAGAGACAAT CTGCGCGAAG CAATCTTCA GAACCTTCAG 480
CGTTACGGAT TCCCTTTGCG CGATGAAGAA CATTTGCTTA CGACCCATGG GCCATCCGAC 540
AAAGAACCCC GTCGGCTCAA AATACAAGAA CAGTATGAAA TAGTATTGCT CATAGGAGAC 600
AACTTGGGCG ACTTCCACCA CTCTTCAAT ACGAAGAAG AGTCCGGACG CAACAGGGCT 660
CTGGGCGTGA CAGCGCGGGA GTTTGGCGGG CACTTCATCA TGCTGCCCAA TCCCACTAC 720
15 GCATCTTGGG AACCGGCATG GTACGGCGGG AAGTATCCGC CACTGCCCGA AAGAGACAAA 780
GCATTTAAAC AACTGCACCTC ACAGAACAGC AGA 813

(2) INFORMATION FOR SEQ ID NO:148

- 20 (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1251 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO
30 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
35 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1251

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:149

45 ATGAGCACCA ATATAGATGT ACAACAGATC AACAGCGTT TCGGCATCAT CGGTAGCAGT 60
CCGCTGATGG AACATGCCAT ACGAGTGGCA GCACAGGTGG CTCTACCGA CATGTCCGTC 120
CTCGTGACGG GGGAGAGCGG TTCGGGGAAA GAGTTCTTCC CACAGATAAT CCACTACTAC 180
AGCGCCCGGA AACATCATAG CTACATTGCA GTCAATTGCG GAGCCATCCC CGAAGGAACC 240
ATCGATTCCG AGCTGTTCGG ACACCGCAAA GGTTCCTTTA CCGGAGCCGT ATCGGATCGC 300
AAGGGGTACT TCGAAGAAGC ATCCGGCGGC ACGATCTTTC TGGACGAAGT GGGCGAACTG 360
CCTTTGCCCA CGCAGGCGAG GCTGCTGAGG GTGCTGGAGA CGGGCGAGTT CATCCCGTA 420
GGAGCCAGCC AGTCGCAGAA GACGGATGTC CGTATCGTAG CCGGCGAAGT TGTGAACCTC 480
50 AAGGAGCGGG TAGCGAACGG GAAGTTCGGG GAAGACCTCT TCTTCCGGCT CAATACGGTA 540
CUGATCGAGG TGCTCGCGCT GCGTATGCGA CCGGACGACG TGCCCTTGCT TTTTCGCCGA 600
TTCCGCCCGG ACAGCGCCGA GAAGTATCGG ATGCCTCCGC TGCGCCTATC GGACGAAGCC 660
CGTACCATAT TAATGCGTTA CCGCTGGCCC GGCATGTGCG GAGAGCTGCG CAATATAACC 720
GACAGGCTGA GCATCTGGA GAGGAGCGG ACGGTATCGG CAGAGACCAT CACTCGCTAC 780
55 CTGGACGCTG AGGGGATGCA AGACCTCCAC CCGTCTGTA TCCGACGGAA CGAAACGACC 840
GAAGCGGACA AACAAATCCC CCATTACGAG CGCAATCA TCTACCGGT GCTATACGAT 900
ATGAAGAAAG AGATAGCCGA TTTGAAGGGG ATGATGAACC GCCTGGCGCA CCACGAACAG 960
CCCTCATGGC CTGTAGGGTC GGCCTCTGG GGCACGACG ACAAGCGCAC CGCAGATCCG 1020
AAGTGGGGCG TCAGACGCA CAAGGCCCCC ATCGCGAAGC CGGAGAACCG CGTGGAGCCG 1080
60 ATACAGGAAG CCAGCGAATA CACCGAGGAT CCGGTTTCGC TGGAGGAGGT AGAGAGAGAA 1140
ATGATTTCCC TTGATTGGA ACGCCACGGC GGAAGGCGCA AGCAGACAGC CAGGGAACCTG 1200
AASATTTCCG AGCGGACACT ATACCGTAAA ATCAAGGAGT ATGGACTGGA A 1251

(2) INFORMATION FOR SEQ ID NO:149

- 65 (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1806 base pairs
70 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)
75 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1806

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149

ATGATCTAC	TCTTCGGCGG	TACTACGGAA	GGCGGTGCGG	CAGCTCGCGT	GCTGGATGAA	60
GCGGGAAGTC	CGTTTTCTA	CTCCACCAA	GGCAATCTGC	AAGAGATCCA	GAGTAGCCAC	120
GGCCATCGTC	TGACAGGAGC	CATGACGGTT	GCGACATGG	TTTCGTTTG	TCGGAAGAA	180
GAGATCCGAC	TGATCGTGG	CGCGGTCAT	CCTTTCGCG	AAGAATTGCA	CGCTTCAGTG	240
GCAGAAGCCT	CTGAACAAAC	AGGTATCCCC	GTAGTAAGAT	ACGAGAGACA	ATACCTCCA	300
CGCGAAGAAG	GTATCGTCTG	GTGTGCAAAC	TACGATACGG	CTGCCGAGCG	GATGCTTGGC	360
GATGGCGTGC	AGCGTCTGCT	GATGCTCACA	GGAGTGANTA	CGATCCCCAA	GCTGGCTGCT	420
TTCTGGAAAG	AGCGCACAC	CTTTGCGCG	ATATTGAAGC	GAGACGAATC	GTTGCTTTG	480
GCAGAGAAGA	ACGGCTTTCC	TGCCGAGCGC	ATCGTTTCT	TCGAACCGCA	TGCCGACGAG	540
GAGCTGATGC	AAGCCGTTCC	CCCCGATGCC	ATTATCACAA	AAGAAAGCGG	AGAGAGCGGT	600
TACTTCCGAG	AAAAGATAGA	AGCTGCCCGA	CGGATGGGCA	TCCGTATATA	TGCCGTCGTA	660
CGTCCCCCTT	TGCTCCTTC	ATTCATTCCT	GTAGGCGGGC	CTGTGCGTTT	GAGACGGGCG	720
GTAGAACGCC	TCGTGCGGG	ATTCTTTTCA	CTCCGAAGCG	GATTCACTAC	CGGCACCAAC	780
GCTACCGCTG	CAGTAGTAGC	AGCCATGTAC	CGATTGATGG	GGCTTGSGTC	TCTCGCCGAA	840
GCTCCCGTAG	AATTGCCTTC	GGGCGAATA	GTCACTCTGC	CCATAGCGGA	AATTCGAGAG	900
GAAGAAGATC	CTGTCGTATC	CGCAGTCTCG	AAAGATGCG	GTGATGATCC	GGATGTGACC	960
AATGGCATGG	CGGTATGCGC	TACGATCAGG	CTCAATCCCC	AACATGAGGA	AGTCCGCTTC	1020
CTGCAGGGTG	AAGGGGTGGG	GGTAGTGACG	CTCCCCGCG	TCGGTCTGGA	GGTCGGAGST	1080
CCGGCTATCA	ACCTCGTACC	TGCAGCAATG	ATGACAGCAG	AGGTAGCGCG	ACTCTATGCG	1140
CAGGAGGGTG	TGGATATTAC	GATTAGCGTA	CCGGAAGGCC	GAGAGGCTGC	TACCCAGACA	1200
TTCAATCCCC	GACTCGGCAT	ACGGGACGGC	ATCTCTATTA	TCGGAACATC	GGGAGTCGTG	1260
AAACCTTTT	CGGCCGAAGC	GTTCTGTTGT	GCCATCCGTA	AGCAAGTGGG	TATTGCCACC	1320
GCCTTGGGAG	CCAATCATAT	CGTCTCAAT	TCGGGAGCCA	AGAGTGAGCG	TTATGTAAAA	1380
GGAGCCTATC	CGGCACTCAT	TCCACAGGCC	TTTGTGCACT	ATGGCAATTT	CGTCGGCGAA	1440
TCACTCAGTT	GTGTAGCTTC	CTTCCCTTCT	GTCCGTTCCG	TAACGGTAGG	AATCATGCTC	1500
GGCAAAGCAG	TGAAACTCGC	CGAAGGCTAT	CTGGATACGC	ACAGTAAAAA	GGTAGTGATG	1560
AATCGGGATT	TCCTGCACGA	ACTGGCTCGT	CAGGCAGGTT	GTTCCGGAAGA	CATCCATGCC	1620
ATATATAGACA	GCCTGAATTT	GGCTCGTSG	CTATGGACTA	TGCCGAGTGC	GGAGGACAGC	1680
GATCGACTGC	TACGAAGAT	TGCCGAACGA	TCTTGGGAAA	CTTCCGCCCC	ATCGGTACCA	1740
TCGGCCGAAT	TAGAACTCCT	GCTGATCGAT	GAGTCCGAG	CGATTGCTTT	TCGTATCGGT	1800
GGAGAA						1806

(2) INFORMATION FOR SEQ ID NO:150

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1329 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150

ATGTTGAGGA	CTTCCGAAT	CGGTGGTATT	CACCCCCCG	AAAACAAGTT	GTCCGCGAGC	60
AAGCCCGTAG	AGGTGTTGCC	TATCCCTCA	CAGGTAGTCA	TCCCTCTGG	TCAGCACATC	120
GGTGACCCGG	CAACTGCCAC	GGTCAAGAAA	GGGGATGAAG	TTAAGGTCCG	GAATATCATT	180
GCTCAGGCCG	GAGGATTCGT	ATCAGCTAAT	ATCCACTCAT	CTGTGTGCGG	TAAGGTGCTG	240
AAGATCGATA	ACGTATACGA	CTCAAGCGGC	TATCCCAAGC	CGCGAGTCTT	CATTAGCGTA	300
GAAGGTGACG	AATGGGAAGA	GGGCATCGAT	CGCTCACCAG	CCATCGTCAA	AGAATGCAAT	360
CTGGATGCAA	AAGAAATCGT	AGCCAAAATT	TCTGCAGCCG	GTATTGTGSG	TCTTGGCGGT	420

102/490

5 GCTACCTTCC CTACCCATGT GAAGCTGTCC CCTCCTCCGG GCAACAAAGC TGAGATCCTG 480
ATCATCAACG CCGTAGAGTG CGAGCCTTAT CTGACGAGCG ACCATGTCCT TATGCTGGAG 540
CACGGCGAAG AGATCATGAT CGGCGTGAGT ATCCTGATGA AAGCCATTCA GGTAAACAAG 600
GCCGTCAATCG GAGTTGAGAA TAATAAGAAA GATGCTATTG CTCACCTCAC CAAACTGGCC 660
ACTGCATATC CGGCGATAGA GGTAAATGCC TTGAAGGTGC AATATCCTCA AGGCGGTGAG 720
AAGCAGCTGA TCGATGCAGT GATCCGCAAG CAGGTAAAAA GCGGTGCCTT GCCTATCAGC 780
ACAGGTCCCG TAGTACAAAA CGTGGGTACG GTATTGCGCG TGTACGAAGC AGTACAGAAG 840
AACCAAGCCTC TGGTCCGAGCG CATCGTGACG GTTACAGGAA AAAAACTGTC TCGTCCGTCT 900
AACCTCCTCG TTGCTATAGG TACTCCTATT GCGGCTTTGA TCGAAGCAGC AGGTGGCTTG 960
10 CCGGAGAATA CCGGCAAGAT CATCGGCGGA GGTCCGATGA TGGGACGCGC TCTGCTGTCA 1020
CCGGA'GTGC CTGTGACCAA AGGCAGCTCC GGAGTATTGA TTCTCGATAG AGAAGAGGCA 1080
GTTCCGAAGC CTATGCGCGA CTGTATCCGA TCGCCCAAGT GCGTCGAGT GTGTCCGATG 1140
GGACTCAATC CCGCTTTCTT TATGCGCGAC ACCTTATATA AGAGCTGGGA AACAGCGGAA 1200
15 AAAGGCAACG TGGTTGACTG TATCGAATGC GGTTCGTGCA GCTTCACCTG TCCGSCCAAC 1260
CGTCTCTGCG TGGATTATAT CCGCCAAGCC AAGAAGACTG TGATGGGTAT CCAAAGAGCA 1320
CGTAAGCAA 1329

(2) INFORMATION FOR SEQ ID NO:151

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1437 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151

ATGAAAAGAA TACAACAAAC TCTTATCGCT CTCTTCGCGG CTGTTGCCGG TTTGGTCGCT 60
CAAAATGCTT ACGAGGGAGT AATTTTCATAT AAAATTTGCT TGGACAAAAC CGGAACAAG 120
GTTGTACTGA ATGGTGCGGC AGATATGAGT AATTAAAGC TCAAGAGCAC TCAGATGATC 180
45 ATTGTTACGC CTATTCTTGG TTCAGAAGAT GGTACCAAGC GGGTGGAAAT TCCTTCGGTA 240
GTCATTACAG GCGCAATAG AACAAAAGCT CTCAGGCTG AAATCGCATT TAGTTCGGCT 300
TTGCCCAAG CAAAACATGC AGCTCAATAC ATTCGCCGTC ATAATGGGAA GAGCGAGCAG 360
TTTGCTTTTA CAGGAGAACA TGCTTATGCA TCAATGGATGA TGGATGCCAA GTTTGTGGTT 420
CGTGAGGAGG TACGAGGTTG TGCTAAATGC CCTGTAGGTC TCTCGAGTAA TATTGTTCTT 480
50 TTTGATCCAC TCTTCAATCC GGCAGAGGCT CCTTATTGTT TGGCACACAT TACTCCGGCA 540
GAAGAAGTGG AAAAAACAGC AGAGTCCAGC TTCGATGCTT ATATCAACTT CAAAGTCAAT 600
AAGCAGATG TCCTTCCTGA GTATCGCAAC AATAAGGCGG AGTTAGAGAA AATCAAGAA 660
TTTGTAAGCA CCGTTAAGGC TAATCCAAAC TATTCCGTCA ATAAATGAT CATCGAAGGG 720
TTTGCTTCTC CCGAGGCTTC AATAGCCAC AATAAGGCTT TGTCGGAGCG CCGTGTCTAA 780
55 AGACTCGCGG AAGAATTGGT GCGTAAGTAT GGCAAAACAT TGCCGAATAT AACCACTGAA 840
TTCGGCGGTG AAGATTGGAA GGGGCTGAAA CTGGCTATCG AAAAGAGTGA TATAGCCGAT 900
CGTGACCGCG TATTGGAGAT AATCAACTCC GATAAATATG CCGATGATGA TGCAGGTGAA 960
CAGGCTCTGA AGCAACTTTC GTCTTATCGT TATATCTTGG ATCAGATCTA TCCGAATTGG 1020
CGTCGCAATA CGATAACCAT GGGGTATATC GTTCGTGATT ATACCCTCGA AGAAGCTCGT 1080
60 GAAATCATTG AGACTGCTCC GAAAGAACTT AGTGAGGCGG AATGTACCG TGTGGCAATG 1140
TCTTATCCTG AGGGGACCA AGAGCGTTTG TTTGCTCTGA ATACGACCCT TAAGTATTTC 1200
CCTGAAAGTG TAACGGGCGG AATCAATTG GCTGTAGCCG CTTTAAATGG TGGAGACGTT 1260
CAACAGGCAA TTGCTCTGTT GAGTCCGATT CAGACAGAAA AGGGTGTAA CAATATCCTT 1320
GGAGCTGCTT ATGCTCGTAC GGGAGATTIT GCTCGTGCCG AACCTTCTT CCGTAAGGCC 1380
65 GTTCAGAAAG GAGATGCAAA TCGCAGCGC AACCTCGATA TGCTGCTTGG CAAAVAG 1437

(2) INFORMATION FOR SEQ ID NO:152

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1149 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
5 (iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
10 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1149
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152
15
ATGGCAGAAA AAAGAGACTA TTACGAAGTC CTCGGTGTAT CGAAGAATGC CACCGACGAT 60
GAACTGAAAA AAGCATATCG CAAGAAGGCT ATCCAATACC ATCCTGATAA GAACCCCGGT 120
GACAAGGAGG CCGAAGAGCA CTTCAAAGAG GTAGCTGAAG CCTACGACGT ATTGAGCGAT 180
CCGCAGRAGC GCAGTCAATA TGACCAAGTC GGCATGCGG GATTGGGCGG AGCTGCCGGT 240
20 GGAGGTTTCA GCGGAGGCGG TATGTCCATG GAGGATATTT TCAGTCCGCTT CGGTGATCTA 300
TTCGGTGGGT TCGGCGGTTT CCGCGGATTC TCCGATATGG GCGGTGGCAG TCGCAGACGT 360
GTTCCGAGAG GGTCTGACCT GCGAGTACGA GTGAAGCTTT CTTGGCCGA TATAGTAAA 420
GGTGTGAGA AGAAAGTGAA GGTAAAAAAG CAGGTAGTGT GCAGCAAATG TCGTGGCGAT 480
GGCAGCGAAG AAGCCAATGG CAAGACTACC TGCCAGACCT GCCATCCAAC CGGCGTGGTT 540
25 ACACGTGTGA GCAACACTTT CTTGGGGGCC ATGCAGACCC AGAGCACTTG TCCCACTTGC 600
CACGGAGAGJ GTGAGATCAT CACGAAGCCA TGCTCCAAGT GTAAGGGCGA AGGTGTGGAG 660
ATCGCGAAG AGGTGATCTC ATTCCACATC CCTGCCGCTG TAGCCGAAGG AATGCAAAATG 720
TCCGTGAACG SCAAGGGAAA TGCCGCGCCC CGAGGAGGCG TGAAATGGCGA CTTGATAGTC 780
30 GTGATCGCG AGGAACCGGA TCCGAATCTG ATCCGCAATG GCAACGATCT GATATACAAT 840
CTGCTTATAT CCGTTCGGTT GGCTATAAAA GGAGGTAGTG TGGAAATGCC GACGATAGAC 900
GGACGAGCCA AGATCCGCAT CGAGGCGGGG ACACAACCCG GCAAGATGCT GCGTTTGGCG 960
AATAAGGGGT TGCCAGCGT AAACGGCTAT GGCATGGGAG ACCAACTGGT GAATGTCAAT 1020
GTCTATATCC CCGAATCGAT CGATGCCAAA GATGAGCAGG CTATCGCAGC GATGGAAAAC 1080
35 TCGGACAGCT TCAAACCTAC CGATGCTGCT CGTAAGGATA TAGACAAGAA ATACAGAGAG 1140
ATGCTGGAT 1149
(2) INFORMATION FOR SEQ ID NO:153
40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 879 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
45 (D) TOPOLOGY: circular
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
50 (iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
55 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...879
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153
60
ATGAAAAAAC TGATTTTAGC GACTTTGGGA CTTATGGCCA TTGCCATGCT CTCATGTTCA 60
AGCAACAACA AGGATTGGA GAACAAAGGG GAGGCTACTC TTTTGGTAAC GTTTGGTAGC 120
TCCTATAAAG CTCCACGCGA AACCTATGCG AAGATTGAGA AGACTTTTGC CGCACCTTAT 180
CCCGATCAAA GGATAAGCTG GACATACACG TCTTCTAATTA TCCGAAAGAA ACTGGCTCAG 240
65 CAGGGTATTT ATATCGATGC TCCGGATGAG GCTTTGGAGA AATTGGCTCG TCTGGGTTAT 300
AAGAAGATCA ATGTACAGAG TCTTCATGTG ATTCGCCGCC GAGAATATGA TGAGATGATC 360
GACTTTGTCA ATAAGTTTAA GGCAGCACAT AGTGATATTA CTGTGAAGGT AGGGGCTCCG 420
CTTTTCGATA CCGATGAAGA TATGCGCGAG GTGGCAGAGA TCTTGCACAA GCGTTTTCAG 480
CAAAAGATAG AGAAAGGTGA AGCTATTGTA TTCATGGGAC ACGGCACCGA GCATGCTGCC 540
70 AATGACAGGT ATGCCCGTAT CAATAAGATC ATGAAGAACT ATAGCAAGTT CATGATCGTC 600
GGAACCGTGG AGTCCGATCC CTCTATCAAT GATGTTATTG CCGAACTGAA AGAAACCGGT 660
GCCACGGCCG TAACAATGAT GCCCGTGATG AGTGTGGCAG GCGACCATGC TACGAATGAT 720
ATGGCCGGAG ATGAGGACGA TAGCTGGAAG ACGTTGCTGA CCAATGCCGG CTACACAGTT 780
TCTATAGACA AGCTGGACAA TGGCAATTTC TCAGCTCTTG GAGATATAGA AGAGATCCGG 840
75 AATATCTGGC TCAAGCATAT GAAGGCCACC TCTGCTCGC 879

(2) INFORMATION FOR SEQ ID NO:154

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1068 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 10 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 15 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 20 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1068
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:154

ATGACATCCG	TCAGCCACTT	ACGTACAATT	TCGTGCGCAG	GTATCCTGGC	TGCGCTGGGA	60
GGGGCTGTAC	TCATTCTCTT	CGGGGTTAAI	CTCTTCCTCG	GCTCGGTGGC	TATTCCGATG	120
AGCGAGATCT	TCGGACATCT	TTTTTCAGAT	CGTCCCGAAG	GAGGAGAAGC	ACTCGTGAC	180
TACAATATCC	TATGGAAATC	CCGCCTGCCC	GAAGCCCTCA	CGGCTGCTTT	TGCCGGCGCA	240
GGTTTATCCG	TTASTGGCTT	GCAGATGCAG	ACCGTCTTTC	GCAATCCITT	GGCCGCTCCG	300
TCCGTCTCTG	GCATCAGCTC	CGGTGCCAGT	TTGGGTGTG	CTTTGGTCGT	TCTGCTGAGC	360
GGCTCGCTGG	GAGGAGTGGC	ATTGAGTAGC	CTGGGTATA	TGGGCGAGGT	GGCCATGAAT	420
ATAGCCGCTG	CCGTAGGCTC	GCTGGCAGTA	ATGGGGCTGA	TCGTTTTTGT	CAGCACCAAG	480
GTGCGCAGCC	ACGTTACGCT	GCTCATTATC	GCGGTTATGA	TCGGATATGT	AGCCACTGCC	540
GTGATCGGGG	TATTCAAGTT	TTTCAGTATC	GAAGAAGATA	TTCCGGGCATA	CGTAATTGG	600
GGGTTGGGCA	GCTTTTCCCG	TGCCACGGAT	TCGCAACTGA	GTTTCTTTGC	CATTCTGATG	660
TTGATCTTTA	TTCCGGCCCG	TATGCTCCTT	GTCAGCAGT	TGAATCTCTT	ATTGCTGGGA	720
GAAAGCTACG	CACGTAATCT	GGGACTGAAT	ACTCGTCGGG	CACGGCTGCT	CGTGATCTCT	780
TCCGCGGGTT	TGCTCATCGC	TACCGTCACG	GCCTATTGCG	GTCCCATCGG	CTTTTGGGG	840
ATGGGTGTGC	CACACTTGGC	ACGGGTTATC	TTTCACACAT	CGGATCATCG	GATCCTGATG	900
CCTGCTACCT	GTTTGATTGG	AAGTGCTCTG	GCTCTTTTCT	GCAATATCAT	TGCTCGTATG	960
CCGGGGTTTG	AGGGGGCTTT	GCCGTCAT	TCCGTAACGG	CTTTGGTGGG	AGCACCTATT	1020
ATCGTCACCG	TTTTGTTCCG	GCGCAGACGC	TTCAAGGAAG	AAACCGAC		1068

(2) INFORMATION FOR SEQ ID NO:155

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2271 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 55 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 60 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...2271
- 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:155

ATGCGGACAA	AAACTATCTT	TTTTGCGATT	ATCTCTTTTA	TTGCTCTATT	GTGCTCTTCT	60
CTGTGCGCTC	AGAGCAAAAG	CGTTTAAACC	GGTAGTGTGT	CGGATGCCGA	AACCGGAGAG	120
CCTCTTGCCG	GTGCTCGAAT	CGAAGTCAAA	CACACCAACA	TAGTAGCCGG	TGCCGATGCC	180
GGCGGACATT	TCGAGATCAA	GAACCTGCCG	GCAGGGCAGC	ATACTATTAT	ATGTTCTGTT	240
GGGGGGTATG	GACAGAAAGA	GGAGGTGGTT	GCCATCGAAG	CCGGACAGAC	CAAAACGATC	300
TCTTTTGAT	TGCGACTGCG	AACGAACAAC	TTGGAGGAAG	TCGTCGTAC	CGGTACCGGT	360
ACACGTTACC	GCTTGGTCGA	TGCTCCTGTG	GCAACGGAAG	TCCTTACCGC	TAAGGACATA	420

5	GCCTCTTCT	CGGCTCCTAC	TTCCGAGGCC	TTATTGCAGG	GGCTGAGTCC	GTCTTTTGAC	480
	TTCCGCCCCA	ATCTGATGGG	CTCTTTTCATG	CAGCTGAACG	GCCTTAGCAG	TAAGTATATC	540
	CTCATCCTTA	TCGATGGTAA	GGGTGTGTAC	GGCGATGTAG	GCGGTCAGGC	CGATTTGAGT	600
	CGTATTCTTC	CTGATCAGAT	CGAACGGATC	GAATGGTGA	AAGGTGCTTC	GAGTTCGCTC	660
	TACGGATCCG	ATGCCATCGC	CGGGGTAATC	AATGTGATCA	CAAAAAAGAA	TACGAATCGA	720
	CTGAGTGCAT	ATACGTCACA	TCGCATATCG	AAGTACAACG	ATCGGCAAC	CAATACTTCG	780
	CTCGATATAA	ACATCGGTAA	GTTCAGTAGC	AATACCAACT	ATTTCTTCTA	CCATACGGAT	840
	GGCTGGCAGA	ATAGTCCGTT	CGAAATAAAA	AAGAAAAAAG	GATCCGGCGA	ACCGGTCTTG	900
10	GAGGAAACGT	ATAAGAAAAC	TTTTCTGTCA	CAGGAAAAATC	AGGGTGTAA	CCATCGCTT	960
	TCCTATTATG	CAACTAACAA	TCTTAGCTTC	AGCGGAAATG	TGCAGTACAA	TAAACGTCAG	1020
	ATCTTCACTC	CGACTTTTTC	CGAAAGAAG	GCCTATGACA	TGGATTATCG	TGCTTTGACG	1080
	GCTTCACTCG	GTACGAACTA	TCTTTTCCCC	AATGGTCTGC	ATACGCTTTC	TTTCGATGCC	1140
	GTCTACGATC	GCTTCCGTTT	CGGATATTTC	TATCATGACA	AGGACAGCAG	TGAGAGCCTG	1200
15	ATCAACAACC	AAGGTCAGAC	CGAGCAACCC	ACATTCTTTC	CGGGTCAGCT	ACGCAATAAA	1260
	AACGATCAGA	TCCGATACAC	GGCAGAGGCT	CGCGGTGTAT	TTACACTGCC	TTATGCGCAG	1320
	AACTGACCG	CGCGTTTGGG	GTATTTCCGT	GAGGAATTGA	TCTCTCCCTA	TAATTTGATT	1380
	ACCGACAAGG	CAGATGCTTC	CACGCTCTCT	GCTTATGTAC	AAGATGAATG	GAAACCGCTC	1440
	GATTGGTTCA	ATATGACAGC	CGGTTTCCGT	CTGGTACACC	ATCAGGAGTT	CGGTACACGA	1500
20	ATGAGCCTTA	AGGTATCCAT	ACTCGCCAA	TATGGGCGCG	TGAACCTCCG	CGCTACGTAT	1560
	GCTAACGGCT	ATAAGACTCC	CACGCTGAAA	GAGCTTTTTC	CACGGAACGA	ACTCACCCT	1620
	ATGGGTTCCG	ACAATCTCTA	TCTCGGCAAT	GCGGATCTTA	AGCCACAGAT	GTGGGATTAT	1680
	TATGCTTTGG	GCTTGGAGTA	CAATCAAGGC	CCTATCTCGT	TCAGTGCAAC	GTTTATGAC	1740
	AATGAATTC	GCAATCTGAT	CTCCTTTATG	GATATACCGA	CTCACCCTGA	GCACGAAGCT	1800
25	CAGGGAATCA	AGAAAACCAA	GCAGTATGCC	AACATAGGAA	AAGCTCGCAG	CCGCGGCCTT	1860
	GATGTCCTAT	GTGATGCCTC	TATCGGTTGG	GGTATCAAGT	TAGGAGCCTG	ATACAGCCTC	1920
	GTGGAAGCTA	AGAATCTCCA	GACGGATGAG	TGGCTGGAAG	GAGCTGCACG	TCATCGTGCC	1980
	ATGTGCACG	CCGATTGGGT	TCACTACTGG	GGTCAGTATA	GACTTGGCGT	GAGCCTTTTC	2040
	GGCCGTTATC	AGAGCGAGCG	TTACTACAAA	GACGGCAATG	CTCGGACTA	TACCTTGTGG	2100
30	USACTCGCCA	CATCGCATCG	TTTCGCTCAT	TTCCGCCACA	TCATCCTGGA	TGGAACGCTC	2160
	GGTATAGACA	ACCTGTTTGA	CTACGTGGAT	GATCGTCTTA	TGGGTGTCAA	TTATGCTACC	2220
	GTAAACCCGG	GACGTACTTT	CTTTGCTCAA	ATAGCGGATTC	GATTCAACAA	C	2271

(2) INFORMATION FOR SEQ ID NO:156

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 993 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- 40 (ii) MOLECULE TYPE: DNA (genomic)
- 45 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS
- 50 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...993
- 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:156

60	ATGACGGACA	ACAAACAACG	TAATATCGTA	TTCCCGGCGT	TTCTCTCTTT	GCTGGGAGTC	60
	ATCGCAGTGG	TGACGATCGT	TGGTTTTTTC	ATGCTCAGAC	CGGCCGAGGA	GATTATCCAA	120
	GGACAGATAG	AAGTGACCGA	ATACCGAGTG	TCCAGCAAAG	TGCCCGGGCG	CATCAAGGAA	180
	CTTAGGGTAT	CCGAGGGGAC	GCAGGTGCAG	GCCGGCGATA	CCCTCGCTGT	CATCGAAGCC	240
	CCCGACGTAG	CGGCTAAGAT	GGAGCAGGCA	AAGGCTGCCG	AAGCAGCTGC	ACAGGCTCAG	300
	AACGCCAAGG	CTCTCAAAGG	AGCACGCGAG	GAACAGATAC	AGGCAGCCTA	TGAGATGTGG	360
	CAGAAAGCTC	AGGCGGCGGT	AGCCATAGCG	ACCAAGACAC	ACCAGCGCGT	GCAGAACCTC	420
65	TATGACCAGG	GAGTGGTACC	GGCTCAGAA	TTGGACGAAG	CCACTGCCCA	GCGCGATGCG	480
	GCCATCGCTA	CGCAAAAGC	GGCCGAAGCC	CAGTACAATA	TGGCTCGCAA	CGGTGCCGAA	540
	CGCAAGACA	AGCTGGCAGC	TTCTGCCCCC	GTCCGATAGAG	CGAGAGGAGC	CGTCCCGGAG	600
	GTGGAGTCGT	ACATCAACGA	AACTTACCTC	ATCGCCCCAC	GGGCAGGCGA	AGTGTCCGAG	660
	ATATTTCCCA	AAGCCGGCGA	ACTCGTAGGT	ACCGGGGCAC	CTATCATGAA	TATCGCCGAG	720
70	ATGGGCGATA	TGTGGGCCAG	CTTTGCCGTT	CGTGAGGATT	TCCTCAGCAG	CATGACCATG	780
	GGAGCCGTTT	TGGAGACTGT	GGTGCCGGCT	CTGAATGAAG	AAAAAGTACG	CTTCAAGATC	840
	ACATTTCATC	AGACATGGG	TACCTATGCT	GCCTGGAAAG	CGACCAAGAC	AACAGGGCAG	900
	TACGACCTGA	AGACCTTCGA	GGTAAAGGCC	ACCTTGCGG	ATAAAGACAA	GGCAGAAAG	960
75	CTACGCCCGG	GTATGTCCGT	GATCATAACG	AAG			993

(2) INFORMATION FOR SEQ ID NO:157

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 801 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 10 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 15 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
20 (B) LOCATION 1...801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157

25 ATGCGTATTG TCAGTAATTT TTGTTGCTG TCTTTTTCGG TTTTGCTTTT TGCATCATGC 60
CGTTCCACGC GAGAAAAGGT CGTTTACCTG CAAGATATCC AAACCTTTTAA TCGGGAGATT 120
ATCGCTAAAC CATATGACGT AAAAATTGAG AAGGACGATG TGCTGAACAT CCTTGTCAGC 180
AGTAGAGACC CGGAGCTTTC AACGCCCTAC AACCAAGTGT TGACCACTCG TGCACTGGCC 240
CGCAACGGCT ATGGAACGAA CTCGAACGAA GGCTTCCTGG TCGATTGAA AGGGTACATC 300
AATTATCCTA TTTTAGGCCA GATCTATGTA GAGGGCCTTA CTCGTACCGA ACTGGAGAAG 360
GAGATACAGA AGAGGATTAT TTCCAGTGGG TTTATCAAGG ATCCTACGGT AACGGTGCAG 420
CTTCAAAATT TCAAGGTGTC GGTTTTGGGA GAGGTGAATC ATCCGGGTTC GATGTCGGTA 480
AAAGGAGAGC GAATAACTCT TTTGGAAGCG ATCGGAATGG CCGGAGACCT GACAATCTAT 540
GGTCCCGCGC ATCCGGTTT TGTGATTAGA GAAACCGATG GGCATCGCGA GGTTTTCCAG 600
ACGGATCTCA GAAAGGCCGA CTGCTCGCA AGCCCGGTGT ACTATCTGCA TCAGAACGAC 660
35 GTCATCTATG TGGAGCCGAA CGACAAGAAA ACACAGATGA GCGAGATCAA CCAGAATAAT 720
AACGTAAACG TATGGCTGAG TGTTACCTCC ACTTTGGTAT CCATTTCCAC GCTGACGATT 780
ACGATAATAG ATAAGACCAA A 801

40 (2) INFORMATION FOR SEQ ID NO:158

- 45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1707 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 50 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 55 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
60 (B) LOCATION 1...1707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158

65 ATGAAAAAGA CCAATCTGTT TTTATCTCTG CTGGTGATCT TTATCACCGG TAGTTTTATG 60
ACTGCCCTGTG CACAGAAGTC CAAGACGAAC AAATCACCAG AAGAAGATCG GAGCCGCAAT 120
GAGTATGTAC AGTCGATGGA TGTGCTTAGC AATATTATCG GTAACGTCAG GCTGATTTTC 180
GTGATACCA TAAGTATCAA ACATATGACT CGGCGTGGA TAGATGCGAT GTTGGGCGGG 240
CTTGACCCCT ATACCGAATA CATTCTTAC GAGGAAATGG ATGAACTGAA ATTGATGACT 300
ACGGGAGAGT ATGCCGAGT CGGAGCTATC ATATCGCAGC GCCCGGATAG TGCTGTGATT 360
ATCCAGAGAC CTATGGAAGG TATGCCCGCA GACGAAGCAG GATTGATAGC AGGCGACCGC 420
ATCCTGACTA TCGATGGGAA AGACTTCCGC AAATCCACCA CACCGAAAGT AAGCCAAAGCA 480
CTGAAAGGGA TAGCCGGTAC TGTTCGAAAG GTGACAGTAA TGCGCTATGG CGAAACCAAA 540
CCTCGTACTT TTTCCGTGAA ACGTCAAAAA GTGATTATGA ATTCGCTCAC TTACAGCGGA 600
ATGCTCGATG GCTCGATAGG ATATATCCGC TTGAACAACT TTACGGACAA AAGTGCAGAA 660
GAGGTGCGCA CGGCCCTTGT GATCTTCGT GACAACCAAG GAGCGAAAGG TCTCATTTTG 720
75 GATTTAAGAG GCAATGGTGG CGGACTGATG CAGGCTGCTA TCGAGATAGT CAATCTGTTT 780

WO 99/29870

PCT/AU98/01023

107 / 490

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GTCCCTAAGG	GCAAAGAGGT	GGTAACGACC	AAAGTCCGCA	TTGCAGAGTC	GGCGTCCGTA	840
TTTCGCACAT	TGACTGAACC	GATCGACACG	AAACTCCCGA	TAGTAGTCCT	GATCGATGGA	900
CAATCGGCAT	CTTCCTCGGA	GATTGTAGCC	GGAGCACTGC	AGGATATGGA	CAGGGCTGTA	960
CTGATGGGAC	AAAAGAGCTA	TGGCAAAGGG	CTTGTACAAA	CGACTCGTCA	GCTACCATAC	1020
AACCGCGTGA	TCAAATTGAC	TACGGCCAAG	TACTACATCC	CAAGCGGACG	TTGTATTTCAG	1080
CGTTTGGACT	ACAGCCGCAC	CAATCGGACA	GGTATGGCAA	CGGCCATTCC	TGACAGTCTG	1140
CACAAAATCT	TTTACACTGC	TGCCGGAAGA	CGTGTAGAAG	ATGCAGGAGG	AATCCTGCCT	1200
GACATCGAGG	TCAAACAAGA	TACAGCTGCG	ACATTACTTT	ATTATATGGC	CATCAATAT	1260
GACGTTTTCG	ATTTCGTAC	AGGTTATGTG	CTCAAGCATA	AAACGATTCC	CAAGCCGGAG	1320
GATTTTTCCT	TAACGAACGA	GGACTATGCA	GCTTCTGCA	AGATGATGGA	AGAAAAGAAA	1380
TTTGACTATG	ATCGCCAGAG	TGGCAAGATG	CTTGACAAAC	TGGAGGAACT	GGCTAAGATA	1440
GAAGGCTACC	TGCGGGAAGC	CAACTCGGAG	CTTAAAGCNC	TACGCGAAAA	GCTAAAACCC	1500
AACCTGTCGC	GTGATCTGCT	ACGATTCAAA	AAGGAGATAA	CAAACTATCT	CAACAATGAG	1560
ATTGTCACTC	GCTATTATTA	TGAGCGAGGC	AGTATCCGCC	AGAGTTTGCC	GGAGATAAG	1620
GTAGTCAAAG	AAGCTATTAA	GCTGCTGAAG	GACCATCCGG	AACAAATTCG	ACAGATCCCT	1680
GCAGCTCCGA	AAGCAGAGAA	TAAAGGG				1707

(2) INFORMATION FOR SEQ ID NO:159

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2943 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2943

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159

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ATGCAAAACA	AAGGATTGTT	GATTGTTATC	ACATCGGGTC	TGGCCATCAT	CTGTGGGTTT	60
TACCTGTGAT	TCTCTTTTCT	TACGAACCGT	TACGAAAAGA	AGGCTAAGGC	GATGGGCGAT	120
GTGGCCGGAA	TGCCCTATCT	TGATTCCATG	TCGAATGAGA	AGGCTGGTTT	CGGCTACACG	180
CTGAAGAAGG	CTCAAGCCCA	GCAAAATGGT	CTTGGCCTTG	ACTTAAAGGG	GGGTATGAAC	240
GTATCTTTGA	AACCTAACGC	AAGCGATCTG	CTTCGTAAAC	TCTCTAAACA	AAGTTTGGAT	300
CCCAACTTCA	ACAAAGCTCT	GGAGATGCT	GCCAAAGACA	CGGAGCAATC	CGACTTCATC	360
GATATTTTCG	TGAAGGAATA	TCGCAAGCTC	GATCCCAACG	GTCCGTTGGC	CGTTATCTTC	420
GGTTCGGGTG	ACCTTCGCGA	CCAGATTACC	GCAAAAGCTA	CGGATGCAGA	CGTAGTGCCT	480
CTGCTCAAAAG	AAAAATATAA	TAGTGCTGTA	GAAGCTTCGT	TCAATGTGCT	CCGTGCTCGT	540
ATCGATGCTT	TCGGTGTGGT	TGCACCTAAT	TTGCAGCGAT	TGGAAGGGCA	AGGGCGTATC	600
CTTGTGCAAC	TCGCCGAGT	GAAAGACCGT	GAGCTGTGTC	GTACCCCTTT	GCAACGCGAT	660
GCCAACCTAC	AGTTCTGGCG	TACATACAAA	TTGGAAGAGG	TCAGCGGAGA	CTTGATCGCT	720
GCCAATGATC	GTCTGAGCGA	ATTGGCTATG	AACAACACGG	ATGCTACCCC	GGAACAGAG	780
CCTGCAACTA	CTGACTCTGT	AGCTGCAACA	GCCGATTCTG	CTGCTGTACA	AGCTGTAGCT	840
GATTCTGCTA	CTGTAGCACA	AAAAGAGGCG	AAGGATGCTA	CTGTAAGA	CGCACTCTTC	900
TCTCTGCTTA	CTCCCGTGAA	TCGTGGCGGT	GCAGTAGTGG	GTGTGGCTCG	TCGTGCTAAT	960
ATGGCTCAGA	TATCTGAAAT	GCTCCAGCAA	GCTCACGATC	TGAAGGTTAC	ACGTGAAGAT	1020
GTGCTTTTCC	TCTGGGGTGC	TAAAGCAATC	GAAGACCCCG	AAACCAAAAA	GGAGACCGAC	1080
CTCTACGAAC	TCTATGCTAT	TCGTACCAAT	CGTACGGGAG	ATCCTGATTT	GGGAGGTGAT	1140
GTAGTGACTT	CCGCCAAGAG	TGATATCCAA	AATGACTTCG	GTGTTCCGA	ACCGATCGTT	1200
TCGATGACGA	TGAATGAAGA	AGGTGCTCGT	AAATGGGCGC	GTATCACAAA	GGATAACGTG	1260
GGACGGGCAA	TCGCTATCGT	TTTGGATGGT	GTGGTTTATT	CTGCTCCGAA	CGTGAATGAT	1320
GAGATCACGG	GCGGTGCTC	TCAGATCTCC	GGGCACCTCA	CCGTGGAGGA	GGCCGGTGAC	1380
CTTGCCAACG	TACTCAACTC	CGGTAAAATG	GATGCTACGG	TAAGCATCGA	ACAGGAAAC	1440
GTGATTTGTC	CTACGCTGGG	TGCCGAGTCC	ATTAAAGCCG	GATTCTTGTC	GTTCCTGCTC	1500
GCTTTGGTTA	TCCTGATGTG	TTACATGTGT	CTGGCTTAAG	GTTCCTTGCC	GGGTCTTATC	1560
GCAACGGGCG	CATTGATTGT	AAACAGCTTC	TTACATTGGG	CGGTATTGGC	TTCTTTCCAT	1620
CCCGTGCTCA	CCCTCTCGGG	TATCGCAGGT	TTGGTGTGTA	CGCTGGGTAT	GGCTGTGGAT	1680
GCCAACGTAC	TTATCTTCGA	GGGTATCAAA	GAAGAGCTTC	GTGCGGTAA	GACTCCGATT	1740
CGTGCGGTAA	CGGATGGTTA	TGGCAACGCT	TTCTTGCCA	TCTTCGACTC	GAACGTTAGC	1800
ACTATTATTA	CCGATATCAT	CCTATTCTTC	TACGGGACGG	GGCCGATTCC	CGGTTTGCC	1860
ACTACGTTGA	TTATCGGTCT	TATCGCTTCT	TTCAATACGG	CTGCTTCTT	GACTCGTATC	1920
GTCTTCGAGA	AACCTGGCAA	AAAAGTCTGT	TTGGATAAGA	TTACATTCAC	TACGAGCATT	1980
ACTCGCAATC	TCCTTTGTCAA	TCCCTCATAC	AACATCTTGG	GTAAGCGCAA	GACCGGCTTT	2040

108 / 490

5 ATCATTCGGG TGATTATCAT CGTTTTGGGA CTTATAGCTT CATTTACAAT CGGTCTCAAT 2100
AGGGGTATTG AATTCTCCGG AGGACGTAAC TACGTAGTAA AATTCGACCA GCCTGTATCT 2160
TCCGAAGCCG TTCGTTCCGG CTTGTCTTCT CCCCTGCAGG AAAAGGTATT GGTTACCTCC 2220
ATCGSTACTG AAGGGACAGA GGTGCGTATA TCTACGAACT ATAAGATCCA GGAGGAAAGC 2280
GAAGAACTG AAGCAGAGAT TACTGACAAA TTGTATCAGA GCCTGAAAGG TTTCTACACC 2340
CAGCAGCCTA CTGCTGATCA GTTCTTGGAC AATATCATTG GCTCTCAGAA AGTAAGTCCC 2400
AGTATGTGCA GTGACATCAC GAGAGGTGCT ATTTGGGCTG TGCTGTTATC GATGATCTTC 2460
ATGGCCATTT ATATTCTGAT TCGCTTCCGT GACATTTCTT TCTCTGCCGG GGTATTCGTA 2520
TCTGTGGCCG CTAATACATT CTGCATTATT GCTCTGTATG CGTTGCTGTG GAAGATTCTG 2580
10 CCCTTCACCA TGGAGATCGA TCAGAACTTC ATCGCTGCTA TTCTGGCTAT CATCGTTTAC 2640
TCGCTCAATG ACACCGTGGT TGTATTTGAC CGTATCCGAG AGACGATGAA ATTTGATCCC 2700
AACAGAGATC GCTATCAGGT GATCAACGAT GCCCTTAATT CAACATTGGG TCGAACATTA 2760
AATACGCTCT TGAATACGTT TATCGTTATG TTGGTAATCT TCATCTTTGG AGGTGCTACG 2820
ATGCGTAGTT TCACGTTCTC GATCCTGCTC GGTATCGTTA TCGGTACATA CTCTACGCTC 2880
15 TTTGTTGCTA CACCCCTTGC CTACGAGATC CAAAAGCGCA AGCTCAACAA AGCAGCTAAG 2940
AAA 2943

(2) INFORMATION FOR SEQ ID NO:160

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3051 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: circular
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
30 (iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
35 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...3051
40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:160

ATGAAAAGAA TGACGCTATT CTTCTTTGCG TTGCTGACGA GCATTGGGTG GGCTATGGCC 60
CAGAATAGAA CCGTGAAGGG TACAGTTATC TCCTCCGAGG ATAATGAGCC CCTGATCGGC 120
45 GCGAATGTGG TGGTTGTCCG AACACCACTC ATCGGTGCTG CAACCGACTT GGATGGCAAC 180
TTACGCGCTTA GCGTGCTTGC CAATGCCAAA ATGTTGAGAG TGTCTTATTC CGGTATGACT 240
ACCAAGAGAG TCGCCATCGC TAATGTGATG AAGATCGTAC TGGATCCGGA CTCTAAGGTT 300
CTGAGGAGAG TAGTTGTATT GGGTTACGGT ACGGGACAGA AACTCAGCAC TGTTCGGGT 360
TCTGTGGCCA AAGTGTCCAG CGAAAAGCTC GCGGAAAGC CGTTGCCAA TATCATGGAT 420
GCCCTCCAAG GTACAGTAGC CGGTATGCGA GTTATGACTA CATCCGGTGA CCCTACTGCC 480
50 GTCGCTCTG TGGAGATCCA TGGTACAGGG TCGTTGGGSC CAAGCTCTGC ACCATTGTAT 540
ATCGTGGATG GTATGCAAAAC TTCTTTGGAT GTTGTGGCTA CGATGAATCC GAATGATTTT 600
GAATCTATGT CCGTTTGTAA AGATGCTTCT GCAACATCTA TTTATGGAGC TCGTGCTGCA 660
AACGGAGTCG TTTTCATTCA AACGAAGAAA GGTAAAATGA GCGAGAGAGG TCGTATTACC 720
TTTAATGCCA GTTACGGGAT TTCTCAAATC CTGAATACTA AGCCCTTGA TAATATGATG 780
55 ACTGGAGATG AATTGCTGGA TTTTCAGGTG AAGGCAGGTT TTTGGGGGAA CAATCAAACC 840
GTTCAGAAGG TTAAGATATG GATCCTTGCC GGAGCTGAAG ATTTGTATGG CAATTATGAT 900
TCTTTGAAGG ATGAGTATGG TAAGACATGG TTCCAGTGG ATTTTAATCA TGATGCAGAC 960
TGGCTCAAGG CTTTGTTTAA AACAGCACCC ACCAGTCAAG GTGATATTTT TTTCTCCGGA 1020
GGGTCTCAGG GAACCTCATA TTATGCCTCT ATAGGCTACT TCGATCAGGA AGGTATGGCT 1080
60 CGTGAACCCG CAAATTTTAA GCGCTATAGT GCGCGGCTCA ACTTCGAAAG TCGTATCAAT 1140
GAATGGCTGA AAGTTGGTGC AAATTTGTCT GGTGCGATAG CGAATAGACG ATCTGCCGAC 1200
TATTTTGGAA AGTATTATAT GGGGTGAGT ACTTTCGCTG TGTTAAGCAT GCCTCGTTAT 1260
TATAACCCCT TTGATGTGAA TGGGGATTTA GCAGATGTCT ATTACATGTA TGGAGCTACC 1320
AGACCTTCTA TGACAGAACC GTACTTCGCA AAAATGAGAC CGTTCAGTTC CGAATCACAT 1380
65 CAGGCCAATG TAAATGGTTT CGCCAGATT ACTCCGATCA AAGGCCCTTAC TTAAAGGCA 1440
CAGGCTGGTG TTGATATTAC TAATCTGCGC ACTTCTTCTA AGAAGATGCC CAATATCCG 1500
TATGATTCTA CTCCTCTTGG GGAAAGAAGA GAAAGAGCTT ATCGAGATGT TAGCAAGTCT 1560
TTTACAAATA CCGCTGAATA TAAGTTTCA ATTGATGAAA AACATGATCT TACAGCATTC 1620
ATGGGGCATG AATATATTGA ATATGAAGGG GATGTTATTG GGGCATCTTC TAAAGGATTT 1680
70 GAAGGTGATA AGTTGATGTT ACTGAGCCAG GGAAAACCG GAAATAGTTT GTCTTTGCTT 1740
GAACACAGAG TCGCTGAATA TGCCTATTG TCTTTCTTTA GTCGTTTAA TTACGGTTTT 1800
GACAAATGGA TGTATATAGA TTCTCTGTT CGTAATGACC AATCCTCTCG ATTCGGATCC 1860
AATAATAGAA GCGCGTGGTT CTATTCTGTC GGTGGAATGT TTGACATATA TAATAAATTC 1920
ATTCAAGAAA GTAATTGGCT CAGTGATCTT CGACTGAAA TGAGTTATGG TACAACGGGT 1980
75 AACTCGGAGA TTGGTAATTA CAACCACCAA GCATCTGTTA CTGTGAACAA TTATCTGAA 2040

WO 99/29870

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109/490

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GATGCTATGG GGCTTAGCAT TTCTACAGCA GGCAATCCCG ACCTCTCGTG GGAAAAGCAG 2100
TCTCAGTTCA ACTTCGGTTT GGCTGCAGGG GCTTTCAATA ATCGCTTATC TGCAGAGGTA 2160
GATTTCTATG TCCGCACTAC GAATGATATG TTGATTGATG TCCGATGCC TTATATCAGT 2220
GGTTTCTTCT CACAGTATCA GAATGTAGGC TCTATGAAA ATACGGGTGT AGACCTTTCT 2280
CTTAAGGGGA CGATCTACCA AAATAAGGAC TCGAATGTAT ATGCTTCTGC GAATTTCAAC 2340
TACAATAGAC AGGAAATAAC AAAGCTTTTC TTGGTCTCA ATAAGTACAT GTTGCTTAAT 2400
ACCGGACTA TATGGGAAAT TGGGTACCCG AATTCGTTCT ATATGGCTGA ATATGCTGGA 2460
ATCGACAAAA AAACCGGTAA GCAGTTGTGG TATGTTCTG GTCAAGTCGA TCGGATGGT 2520
AATAAAGTTA CAACAAGCCA GACTCAGCT GACTTGGAGA CACGAATTGA TAAGTCTGTT 2580
ACTCCTCCTA TTACAGGTGG TTCTCCTTA GGTGCTTCTT GGAAAGGACT TTCTTTAGAT 2640
GCTGATTTTG CCTACATCGT TGGTAAATGG ATGATCAATA ATGACCGTTA CTTTACAGAG 2700
AATGCAGGTG GATTGATGCA ATTAAATAAA GATAAAATGC TATTGAATGC CTGGACAGAG 2760
GATAATTAAG AAACAGATGT TCCAAAATTG GCACAGTCTC CTCAGTTTGA TACGCATTG 2820
TTGGAGAATG CTTCTTTCTG GCGTTTGAAG AATCTCAAAC TCACCTATG ACTCCCAAT 2880
AGTCTTTTGG CTGGGCAGAA TGTGATTGGT GGAGCTCGTG TCTATTGAT GGCAGCAAT 2940
CTGTAACTG TTACGAAGTA TAAAGGCTTT GACCTGAAG CAGGGGGGAA TGTGGGAAA 3000
AATCAATATC CTAATCTAA GCAGTACGTT GCGGGATTTC AGTTGTCTTT C 3051

20 (2) INFORMATION FOR SEQ ID NO:161
25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3042 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
30 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
35 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...3042
40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:161

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ATGACGCTAT TCTTCCTTTG CTTGCTGACG AGCATTCCGGT GGGCTATGGC CCAGAATAGA 60
ACCGTGAAGG GTACAGTTAT CTCTCCGAG GATAATGAGC CCTGTATCGG CGCGAATGTC 120
GTGGTTGTGG GAAACACCAC TATCGGTGCT GCAACCGACT TGGATGGCAA CTTACGCTT 180
AGCGTGCCTG CCAATGCCAA AATGTTGAGA GTGCTCTATT CCGGTATGAC TACCAAGAG 240
GTGCGCCATG CTAATGTGAT GAAGATCGTA CTGGATCCGG ACTCTAAGGT TCTGGAGCAG 300
GTAGTTGTAT TGGGTTACGG TACGGGACAG AAACCTCAGCA CTGTTTCCGG TTCTGTGGCC 360
AAAGTGTCCA GCGAAAAGCT CGCGGAAAAG CCGGTGGCCA ATATCATGGA TGCCCTCCAA 420
GGTCAGGTAG CCGGTATGCA GGTATGACT ACATCCGGTG ACCCTACTGC CGTCGCTTCT 480
GTGGAGATCC ATGGTACAGG GTCGTTGGGG GCAAGCTCTG CACCATTTGA TATCGTGGAT 540
GGTATGCAAA CTTCCTTTGA TGTGTGGCT ACGATGAATC CGAATGATT TGAATCTATG 600
TCCGTTTGA AAGATGCTTC TGCAACATCT ATTTATGGAG CTCGTGCTGC AAACGGAGTC 660
GTTTTCAATC AAACGAAGAA AGGTAAAATG AGCGAGAGAG GTCGTATTAC CTTTAAATGCC 720
AGTTACGGGA TTTCTCAAAT CCTGAATACT AAGCCCTTG ATAATATGAT GACTGGAGAT 780
GAATTGCTGG ATTTTCAGGT GAAGGCAGGT TTTGGGGGA ACAATCAAC CGTTCAGAG 840
GTTAAAGATA TGATCCTTGC CGGAGCTGAA GATTTGTATG GCAATTATGA TTCTTTGAAA 900
GATGAGTATG GTTAGACATT GTTCCAGTG GATTTTAATC ATGATGCAGA CTGGCTCAAG 960
GCTTTGTTTA AAACAGCACC CACCATGCAA GGTGATATT CTTTCTCCGG AGGGTCTCAG 1020
GGAACTTCAT ATTATGCCTC TATAGGCTAC TTCGATCAGG AAGGTATGGC TCGTGAACCG 1080
GCAAAATTTA AGCGCTATAG TGGCCGGCTC AACTTCGAAA GTCGTATCAA TGAATGGCTG 1140
AAAGTTGGTG CAAATTTGTC TGGTGGGATA GCGAATAGAC GATCTGCGCA CTATTTTGA 1200
AAGTATTATA TGGGGTCAGG TACTTTCGCT GTGTTAACGA TGCCCTCGTTA TTATAACCTT 1260
TTTGATGTGA ATGGGGATTT AGCAGATGTC TATTACATGT ATGGAGCTAC CAGACCTTCT 1320
ATGACAGAAC CGTACTTCGC AAAAATGAGA CCGTTCACTT CCGAATCACA TCAGGCCAAT 1380
GTAAATGGTT TCGCCAGAT TACTCCGATC AAAGGCCTTA CTTTAAAGGC ACAGGCTGGT 1440
GTGATATTA CTAATACTCG CACTTCTTCT AAGAGAATGC CCAATAATCC GTATGATTCT 1500
ACTCCTCTTG GGGAAAGAAG AGAAAGAGCT TATCGAGATG TTAGCAAGTC TTTTACAAAT 1560
ACGGCTGAAT ATAAGTTTTC AATTGATGAA AAACATGATC TTACAGCATT GATGGGGCAT 1620
GAATATATTG AATATGAAGG GGATGTTATT GGGGCATCTT CTAAGGATT TGAAGTGAT 1680
AAGTTGATGT TACTGAGCCA GGGAAAAACC GCAATAGTT TGTCTTTGCC TGAACACAGA 1740
TTCGCTGAAT ATGCCATTTT GTCTTCTTCT AGTCGTTTAA ATTACGGTTT TGACAAATGG 1800
ATGATATAG ATTTCTCTGT TCGTAATGAC CAATCCTCTC GATTCGGATC CAATAATAGA 1860
AGCGCGTGGT TCTATTCTGT CGGTGGAATG TTTGACATAT ATAATAAAT CATTCAAGAA 1920
AGTAATTGGC TCAGTGATCT TCGACTGAAA ATGAGTTATG GTACAACGGG TAACTCGGAG 1980

110/490

5	ATTGGTAATT ACAACCACCA AGCACTCGTT ACTGTGAACA ATTATACTGA AGATGCTATG 2040
	GGGCTTAGCA TTCTACAGC AGGCAATCCC GACCTCTCGT GGGAAAAGCA GTCTCAGTTC 2100
	AACCTCGGTT TGGCTGCAGG GGCTTTCAAT AATCGCTTAT CTGCAGAGGT AGATTTCTAT 2160
	GTCCGCACTA CGAATGATAT GTTGATIGAT GTCCGATGC CITATATCAG TGGTTTCTTC 2220
	TCACAGTATC AGAATGTAGG CTCTATGAAA AATACGGGTG TAGACCTTTC TCTTAAGGGG 2280
	ACGATCTACC AAAATAAGGA CTGGAATGTA TATGCTTCTG CGAATTTCAA CTACAATAGA 2340
	CAGGAATATA CAAAGCTTTT CTTCGGTCTC AATAAGTACA TGTTCCTTAA TACCGGTACT 2400
	ATATGGGAAA TTGGGTACCC CAATTCGTTT TATATGGCTG AATATGCTGG AATCGACAAA 2460
10	AAAACCGGTA AGCAGTTGTG GTATGTTCCCT GGTCAAGTCG ATGCGGATGG TAATAAAGTT 2520
	ACAACAAGCC AGTACPCAGC TGACTTGGAG ACACGAATIG ATAAGTCTGT TACTCCTCCT 2580
	ATTACAGGTG GTTCTCCTT AGGTGCTTCT TGGAAAGGAC TTTCTTTAGA TGCTGATTTT 2640
	GCCTACATCG TTGGTAAATG GATGATCAAT AATGACCGTT ACTTTACAGA GAATGCAGGT 2700
	CGATTGATGC AATTAAATAA AGATAAAATG CTATTGAATG CCTGGACAGA GGATAATAAA 2760
15	GAAACAGATG TTCCAAATTT GGGACAGTCT CCTCAGTTTG ATACGCATTT GTTGGAGAA 2820
	GCTTCTTTCC TGCGTTTGA GAATCTCAA CTCACCTATG TACTCCCAA TAGTCITTTT 2880
	GCTGGGCAGA ATGTGATTGG TGGAGCTCGT GTCTATTGA TGSOGCGCA TCTGTTAACT 2940
	GTTCAGAGT ATAAAGGCTT TGACCCTGAA GCAGGGGGGA ATGTGGGAAA AAATCAATAT 3000
	CCTAATTCTA AGCAGTACGT TGGGGGTATT CAGTTGTTCT TC 3042
20	
	(2) INFORMATION FOR SEQ ID NO:162
	(i) SEQUENCE CHARACTERISTICS:
25	(A) LENGTH: 2463 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: circular
30	(ii) MOLECULE TYPE: DNA (genomic)
	(iii) HYPOTHETICAL: NO
	(iv) ANTI-SENSE: NO
35	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
	(ix) FEATURE:
40	(A) NAME/KEY: misc feature
	(B) LOCATION 1...2463
	(x) SEQUENCE DESCRIPTION: SEQ ID NO:162
45	ATGAAGAAAA AGAATTTTTT GCTTCTTGCC ATTTTCGTTG CTTTGCTGAC TTTTCATCGGC 60
	AGCATGCAGS CACAACAGGC CAAAGATTAT TTCAACTTTG ACGAACGGGG CGAGGCGCTAC 120
	TTCTCACTTA AAGTGCCTGA TAGGGCCGTT CTACAAGAGC TGGCTCTGAT CATGTCCATC 180
	GACGAGTTTG ACCCCGTAA CAAATGAAGC ATTGCCTATG CCAGCGAAGA GGAGTTCCAG 240
	GCATTCTTGC GCTATGGGCT CAAGCCTACA TTCTTGACTC CTCCATCCAT CGAGCGCGCT 300
50	GTGAGATGT TCGACTACCG CTCAGGAGAA AAATACGAAT GGAATGCTTA CCCCACCTAT 360
	GAAGCCTATA TCAGCATGAT GGAAGAGTTC CAAACAAAGT ATCCATCACT TTGTACTACT 420
	TCCGTCATTG GCAAGTCCGT AAAGGATCGT AAATCTGATG TTTGCAAGCT GACGTCCTCT 480
	GCCAATACAG GGAAGAAAGCC TCGCGTGCCT TATACTTCTA CGATGCACGG AGACGAAAGC 540
	ACCGGATATG TGGTACTGCT CCGACTCATA GACCATCTGC TGTGCAACTA CGAATCCGAT 600
55	CCGAGGATTA AGAATCTTCT GGATAAAGC GAAGTATGGA TCTGCCCTTT GACCAATCCG 660
	GACGGAGCAT ACAGAGCCGG AAACCAACACC GTACAAGGAG CTACTCGCTA CAATGCCAAC 720
	AATGTGATTT TGAACCGTAA CTTCAGGAT GATGTAGCCG GTGATCACCC CGATGGAAAA 780
	CCTTGGCAGC CGGAGGCCAC TGCAATCATG GATTGGGAG GAACACCTC TTTCTGTCTC 840
	GGTGCATAA TACATGGAGS AACAGAGGTG GTGAACATC CATGGGATAA TAAAAAGAA 900
60	AGACATGCAG ACGATGAGTG GTACAACTG ATCAGTCGCA ACTACGCAG CGCTTGTGAC 960
	AGTATTTCCG CCGCTACAT GACCTCCGAA ACCAATTCGG GAATCATCAA CGGTTGAGAC 1020
	TGGTATGTAA TTCGCGGAAG TCGTCAGGAC AATGCAAAAT GTGCCGGCCT CTCAACTTCC AAAGTATTGG 1080
	ATTACCTTGG AAATCAGCAA CACGAAGTTG ATCGAAGAAT CCTTATACGG CATCCATGGT 1140
	AATCTGAACA AAGAATCTCT GCTTGCTCTG ATCGAAGAAT CCTTATACGG CATCCATGGT 1200
65	ACAGTGACTT CCGCTGCGAA CGGACAGCCT CTCAATGCC AGATCTTGAT AGAAACCAT 1260
	GACAAGCGCA ACTCCGATGT TTACTCGAT GCTACACAG GCTACTAGT ACGTCCATATC 1320
	AAAGCCGGCA CTTATACGGT GAAATACAAA GCGAGGGT ATCCTGAGGC AACTCGTACC 1380
	ATTACGATCA AGGACAAAGA AACCGTCATC ATGGACATG CATTTGGGCA CTCGGTTCTT 1440
	CTCCGTGTAC CCGATTTCAC AGCTTCTCCT ATGACCAATC CAGTAGGCGA AAGCGTCCAA 1500
70	TTCCAAGATC AAACGACAAA TAACCCACAG AATTGGGAGT GAGCGTTTGA AGGCGGACAG 1560
	CCTGCCATGA GTACAGAGCA GAATCGGCTC GTATCCTATA GTCATCCCGG TCAGTACGAC 1620
	GTTACGCTCA AAGTGTGGA TGAAGTGGT TCCAACACGA TTACGAAAGA AAAATTCATC 1680
	ACTGTCAATG CCGTTATGCC TGTAGCTGAA TCGTGGGTA CCCGACGGA AATAGAGAG 1740
	GGCCGACCGG TATCTTTCCA AAACCAATCC ACCAATGCCA CCAACTAGCT ATGGATATTC 1800
75	GATGCGGSCA CTCCGCTAC CAGTGAAGAC GAARACCGGA CTGTGCTTTA CAGCAAAGCC 1860
	GGCCAATACG ATGTACAGCT CAAGGCGATC AGTGCTTCCG GTGAAACGGT GAAGACGAAA 1920

111/ 490

5 GAAAAATACA TCACTGTCAA GAAAGCTCCG GTCCCTGCTC CGGTAGCCGA CTTGGAAGGA 1980
 ACACCTCGAA AAGTAAAGAA AGGCGAGACA GTTACTTTCA AAGACTTGTC TACGAACAAT 2040
 CCGACTTCAT GGCTTTGGGT GTTCGAAGGC GGCTCTCCTG CCACCAGCAC GGAGCAAAAC 2100
 CCGGTGGTCA CCTACAATGA AACAGGCCAAG TACGATGTCC AGCTGACTGC CACCAACGAG 2160
 GGGGGAAGCA ATGTGAAGAA AGCAGAAGAC TACATTGAGG TTATCCTCGA TGACAGTGTC 2220
 GAGGACATAG TGGCACAGAC GGGTATCGTC ATTGCTCCGC AAAACGGGAA GAAGCAGATC 2280
 CTCATAGAAG CCAACGCTGC TATCAAAGCG ATCGTTCTCT ATGACATCAA TGGACGGGTC 2340
 GTACTCAAAA CTACTCGAA TCAGCTCCGC TCGACCGTAG ATCTTTCCAT CTGCCCCGAA 2400
 10 GGAATCTACA CCATCAATAT CAAAACGGAA AAATCCGCTC GCACGGAAAA GATCCATATC 2460
 GGG 2463

(2) INFORMATION FOR SEQ ID NO:163

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 228 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
 20 (ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
 25 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 30 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...228
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:163

35 ATGGGACTGA TCAAGGCTTT TCTCGTGCAA CTCTTACTGC TCCCCATTTT CTTCTACAAG 60
 CGGTTTATAT CGCCGCTTAC ACGGCTTCA TGCCGGTTTA CCCCCTCATG TTCGTCTTAT 120
 GCCATCGAAG CTTTACGTAA ATATGGCCCG GGCAAAGGAC TATTGCTGAG CATCAAGCGT 180
 40 ATTCTCCGCT GTCAACCCGTG GGGTGGAAAT GGCTATGACC CCGTTCCG 228

(2) INFORMATION FOR SEQ ID NO:164

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2577 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
 50 (ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
 55 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 60 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...2577
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164

65 ATGGCATACG ACTTTACACA AACATTCCGC AACAGCCTGG AGTACAGCTA TCAGGAAGCA 60
 ACCCGTCTCG GCGTCGTAGC CGTGACGCAA GATATGCTCG TACTCGGTAT CATTCGCGAC 120
 GGAGACAATG GCGGATCGA CATCATGGGG CACTATGGGA TCAACTTGTA CGAACTCAAA 180
 CGGTTGATCG AGTTGGAAGC CATCGCCGAG AGTTTGCTCG CTTGCGCTGA GGGATCGCCC 240
 70 ATCTTCACCC CTTGCGCTCG GGAGGCTATC GATGATGCLA CAGACATCTG TGCCGACATG 300
 GAGGACGAGG CCGTCAGCCC GGTCCATCTG TTGCTGAGTA TCCTCAACTC GACACAGGAG 360
 AGCTTAGTAC AAAAGATATT TATGAAACAA GGTATAAAAT ACGACACCAT CTTGTCCGGAT 420
 TACTTCGGAC AGCGCAACCC CTCGGAAGGG AAGTCTCCT CCGAAATGGA GATCCTCGAC 480
 GGGTACCAAG ACAACGACTT CGACGACGAA GAGGACGAAT CCTCTCGGCC TTCCGGGAAT 540
 75 AGCGGACAG GCGGAGGCTC CGGCGACGCC CCCGAACAGA ATACCGGCGG AGGCGATACT 600
 ACCACCACGA CACGGAGTGG AGGCGACACG CTTGCACTGG ACACCTTCGG CACCGACATC 660

ACTGCCATGG CGGCAGCAGG CAAGCTCGAC CCGGTAGTGG GTCCGGAGCA GGAGATCGAA 720
AGGGTGATAC AGATACTCAG CCGGCCGAAA AAGAACATC CGGTGCTCAT CGGCGAAGCC 780
GGGTGATAGCA AGAGTGCCAT CGTGGAAGGA CTGGCCGAAC GCATCGTGAA CAGGAAGGTG 840
AGCCGTATTC TTTTCGACAA GCGGATCATC AGCCTCGATT TGGCTCAGAT GGTAGCCGGC 900
ACCAATATC GCGACAGTT CGAAGAGCGG TTGAAAGCCG TGCTCGATGA GCTGAAGAAG 960
AATCCGCAGA TCATCTCTT CATCGACGAG ATACATACCA TCGTGGGAGC AGGCTCTGCA 1020
GCCGGATCGA TGGATACGGC CAATATGCTC AAACCCGCTC TTGCCCGTGG ACAGGTACAG 1080
TGATCCGGAG CCACTACGCT GGATGAGTAT CGTAAGAACA TAGAAAAGGA CCGAGCACTC 1140
GAAGCCCGCT TCCAGAAAGT GCGGATAGCC CCTCGACTG CAGAAGAAAC GCTGACCATC 1200
CTGCAAAACA TCAAGAGAA ATACGAGGAC TATCACGGTG TACGCTATAC GGACGAAGCG 1260
ATCAAAAGCG CAGTGGAACT GACCGATCGC TATGTATCCG ATCGTTTCTT CCCAGATAAG 1320
GCGATAGATG CCAATGGACGA GGCCTGGCGG AGCGTCCATA TCACCAATGT GGTGGCTCCG 1380
AAAGAAATCG AGATACTGGA GGCCTGAATT GCATCGGTGC GAGAGAACAA GCTCTCGGCC 1440
GTAAGAGCTC AGAACTACGA ACTGGCTGCC TCCTTCGGCG ATCAGGAGCG GCGCACTCAG 1500
CAGCAGATAG CGGAAGAGAA GAAAAAATGG GAAGAGCAGA TGTCCAAGCA CCGCGAGAGC 1560
GTGACAGAGA ATGTAGTGGC GCATGTAGTG GCGTTGATGA CAGGCGTTCG GGTGAGCGG 1620
CTGAGCACGG GCGAAGGCGA ACGTCTGGCG ACGATGGCAG ATGATCTCAA GACCAAAGTA 1680
GTAGGTGAGG ACACAGCCAT CGAAAAGATG GTGATGCCA TCCAGCGCAA TCGTCTGGGA 1740
CTTCGCAATG AAAAGAAACC GATCGGTTCT TTCTTTTCC TCGGCCCCAC GGGGGTAGGC 1800
AAGACCTATT TGGCCAGAA GCTCGCGGAA TACCTGTTCG AGGATGAGAA TGCATGATC 1860
AGGGTGATGA TGAGCGAGTA TATGGAGAA TTCTCGTTT CCGCTCTCGT GGTGCGCCCT 1920
CCGGGATATG TGGGCTATGA AGAAGCGCGC CAAGTACGCG AGCGCGTAAG ACGCAAAGCC 1980
TATTCCTGTT TTCTCTTGA TGAGATCGAA AAGGCGCATG CCGATGTCTT CAATCTGCTC 2040
TTACAGGTGA TGGACGAAGG TCAGCTGACC GACAGTCTGG GACGGCGCGT GAATTTCAAG 2100
AACACCGTGA TCATCATCAC CTCCAACGTC GGTACACGCC AGCTCAAAGA CTTCGGGCAG 2160
GGTATCGGCT TCCGTTCGGA AAAAGACGAG GAAGCGAACA AGGAGCATAG CCGTTCCGTG 2220
ATCCAAAGAG CTCTGAACAA GACGTTACGC CCCGAATTC TCACCGTTT GGACGATATC 2280
ATCTCTCTCG ACCAACTGGG CAAGACGGAG ATTCCGCGGA TGGTGGACAT AGAGCTTAAA 2340
GCGCTCTTGG CCGCATCCCA TCGTGCCGGA TACGACCTCG TCCTTACCGA TGAAGCCAAG 2400
GATGTGATAG CGACGAAGGG ATACGACCTC CATTACGGAG CAGGACCGCT CAAGCGCACA 2460
CTCAGTAAGC AAGTGGAGGA TCGCTCACG GATCTTATCC TCTCGGACA GATCGAGAA 2520
GGGCAGTCCG TTACGCTCTC TGCTCGCGAT GCGGAGATCA TCGTACAGA ACAAGCA 2577

35 (2) INFORMATION FOR SEQ ID NO:165

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1251 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

45 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- 55 (A) NAME/KEY: misc_feature
(B) LOCATION 1...1251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165

ATGAATTACC TGTACATACT GATTACACTT TTACTCTCCG GCTTTTTTTC CGGTGCTGAG 60
ATTGCTTTTC TTCTTCGGA CAAGCTGCGT CTTGAGTTGG ACAGGAATAG AGGCGATCTC 120
ACAGGCAGAG CGTTAAACTT GCTGTATCGA CATCCGGACC AACTGGTGAC TACTCTCCTT 180
GTGGGTAATA ATATCGTTTT GGTAGTCTAT GGTCTGCTGA TGGCGGGATT GCTGGCCGCA 240
CCTTTGGCGC AATGGATTGA TAACGATGCT ATGATCGTCG TTCTCCAATC TGTCTTATCC 300
ACTATCATCA TACTGTTTAC CGGGGAATT CTACCCAAAG CCATTTTCAA GACCAATGCC 360
AATATGATGA TGAGGGTATT CCGCTCCCT ATCGTAGCGA TCTATTATCT GCTTTATCTT 420
CTGTCTAAAC TCTTCACCGG TTTATCTGCG TCTTTTATTC GTCTGGTGGG CAAGAATTAT 480
GTGCTTACAA CAGTAGGGTT GGGGCGCGTA GATCTCGATC ATTATTTGGC AGAAAATATG 540
TCCGAGAAAA ACAGAACAGAA CCACTTGACT ACCGAAGTGA AATCATCCA GAATGCGCTG 600
GATTTTTCGG GTATTACGCT GCGAGACTGC ATGATCCAC GCAATGAGAT GATAGCATGT 660
GAGTTGCAAA CCGATATTGA AGTACTCAA ACGACTTTTA TCGATACCGG TTTGTCCAAG 720
ATCATTTATC ACAGACAGAA CATAGATGAC GTAGTAGGAT ATATCCATTC GAGCGAAATG 780
TTTGTGGGGC AAGACTGGCA AAAACGTATC AATACTACTG TATTCGTACC CGAAAGCATG 840
TATGCCAATA AACTGATGCG ACTACTCATG CAGCGCAAGA AAAGCATTGC GATCGTCATC 900
GATGAACITG GAGGTACGGC CGGAATGGTC ACATTAGAGG ATTTGGTAGA AGAGATTTTC 960
GGTGACATTG AGGACGAACA CGACACTCGC AAGATCATAG CCAACAGACT CCGCCCTCAT 1020
ACCTATCTGG TCAGTGGTGC TATGGAAATA GATGATGTA ACGAAGCTTT TGGGTTGTCC 1080

TTGCCTGAST CTGACGACTA CTTACCGTG GCCGGATTTA TCCTGAATAG CCATCAAAAT 1140
 ATCCACACAGG CCAATGAGGT CGTGAGATT GCTCCTTATA CTTTACCAT TCTCAGATCT 1200
 TCTTCCACCA AGATCGAAGT GGTGAAAATG TCCATCGACG ACCAATCGAA C 1251

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(2) INFORMATION FOR SEQ ID NO:166

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 879 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1...879

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166

30 ATGAAACAGA ACTACTTCAA AAGAGTCTGC TCACTGCTTT GGCTGGTTTT ACCCATGCTT 60
 ATTATGCCAT TCGAAGTAGC AGCTCAGAG ATTATTCCGA ACGAAGAGGT GTTGAATCA 120
 TTGACTTTTCG TTGCACCGGT TGAGGAGACA GACGCAATAG AGGCAGAGGT AGAAGCTCTG 180
 CAGGAGATAG TCGCTACTGA GGAGATTGCG GAGCAGGCTG TTCGTTCTTA TACCTACAG 240
 GTCTATCGTG ATGGCGTGAA GATTGCTTCA GGATTGACTG AGCCCACTTT TCTCGATGAA 300
 GATGTTCCCTG CCGGCCGAACA TACCTACTGC GTAGAAGTAC AGTATCAGGG AGGCGTATCC 360
 35 GACAAAGTAT GCGTGGACGT AGAGGTGAAG GACTTCAAAC CGGTTACCAA TCTCACCAGG 420
 ACTGCTTCCA ATGACGAAGT TTCTTTGGAC TGGGACGGTG TGGGAAGAGAA AGCTGAAGAG 480
 CCGGCAAGTG ATAAAGCAGT CAGCTACAAC GTCTACAAGA ATGGAACCTT GATCGGTAAT 540
 ACAGCTGAAA CTCATTATGT GGAGACCGGT GTAGCCAATG GTACATACAT CTACGAAGTG 600
 GAAGTAAAGT ATCCTGACGG TGTATCTCCG AAGGTGGCTG TAACCGTGAC CGTGACCAAC 660
 40 AGCTCATTTGA GCAATGTAGA TGGACAGGCT CCTTACACAT TCGGAGTAGA AGGCAAGAG 720
 ATTATTGCGG AAGCCCATGG TATGATCAGG CTCTACGACA TCAACGGAGC TACCGTGGCC 780
 GTAGCCCGGA ATCGATTGGA ATACATGGCG CAACCGGTT TCTATGCAGT GCGCTTCGAT 840
 GTGGGGAATA AACACCATGT ATCGAAAATA CRAAGTAAGA 879

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(2) INFORMATION FOR SEQ ID NO:167

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 936 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1...936

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167

70 ATGATTCTCT TAAGCGAGAG TTTGAATCA GGTATTCAG CTATATGGAA GACCATTGAC 60
 GCAGATGCGG ATGGCTATAA TTGGATGCAT TTGACCAATT TCACGGGACA GAGTGGTCTC 120
 TGTGTCTCTT CCGCTTCATA CATAGGCGGC GTCCGAGCTT TGACTCCGGA CAATTATCTG 180
 ATACACCCCG AATTAAAACT ACCACAGAC GCGTTGGTGG AAATAATCTA TTGGGTATGT 240
 ACTCAAGATC TCACTGCTCC ATCGGAGCAC TATGCGGTTT ATTCTCTTTC TACAGGCAAT 300
 AATGCTGCTG ACTTGTATA TCTCTTATAT GAAGAGACTT TGACTGCCAA ACGGATACAA 360
 75 TCCCCCGAGT TGATCCGCGG AATCGGACA CAAGGTGTTT GGTATCAAAG AAAGGTGGTA 420

114/ 490

5 CTCCCTAAGC ATACTAAATA TGTTGCTTTC CGCCATTTTA ATTCCACGGA TAATTTCTGG 480
CTCAATTTGG ATGAAGTATC TATCCTGTAT ACCCCTCTTC CCCGAAGAGC TCCGTGTCCG 540
CATCCGGGTG GTTACACTTA TTCTGTATTC CGTGATGGAC AAAAGATAGC GAGTGGATTG 600
TCGGCATTGG CATATATCGA TACGGATGTA CCGTATGGGA CTCAGACTA TTGTGTCCAA 660
GTCAATTATC TGCAAGGAGA CTCGTATAAA GTCTGCAAAA ATATAGTGGT GGCAAAATCT 720
GCAAACTATC ATGGGGCGGA TAAGCCTTTT GCGTTGACCG TGGTTGGCAA GACCAATTGT 780
GCGAGTGTCT TCAAAGGAGA GATCACTCTT TATGACATTC GTGGCCGGCT GATAGCTTCC 840
GGCTGCGATA CGCTTAGGTA CAAAGCGGAA AATGGTITTT ACCTCATTAA AATACAGGTA 900
10 AACGGAACCTG TCTATACTGA GAAATCCAA ATCCAA 936

(2) INFORMATION FOR SEQ ID NO:168

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2529 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 20 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 25 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORPHYROMONAS GINGIVALIS
- 30 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...2529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168

35 ATGAAAAA GTTTTCTTT AGCCATAGTA ATGCTCTTTG GCATTGCCAT GCAGGGACAT 60
TCTGCTCCGG TTACGAAAGA GCGAGCTTTG AGTCTGGCTC GGCTGGCTTT GCGACAGGTA 120
TCCTTGGCAA TGGGACAAAC AGCAGTATCT GACAAGATT CCATCGATTA CCGTTATCCG 180
CAAGGAGATG CTGAGAGGGG TATCAGATCA CAAGAGGAAG GCTCTCTGTC ATATTTTAT 240
GTAGCTAATC GTGGAATATA TGAGGGCTAT GCTCTGTAG CAGCAGATGA CAGAATACCG 300
40 ACAATTTTAG CCTATTCCAC CATTTGGCCGT TTCGACATGG ACAGTATGCC GGACAATCTT 360
CGCATGTGGC TACAAATTTA CGATCAGGAA ATAGGCCCTGA TACTTTCCGG AAAAGCTCAG 420
CTCAATGAAG AGATATTACG TACCGAGGGC GTACCGGCTG AAGTACATGC TCTGATGGAT 480
AAGCGTCATT TTGCAACGTA TCCCATGCGA TCGAATCAAG GTTACCCATG GAACAATAAG 540
GAACCACTGC TTCTAATGG CAATCATGCC TATACCGGCT GTGTTGCTAC TGCTGCAGCA 600
45 CAAATCATGC GCTACCATAG CTGGCCGCTT CAAGGTGAAG GCTCTTTGGA TTATCATGCA 660
GGTTCAATTAG TTGGCAACTG GTCCGGCCACA TTTGGTGAAA TGTACGACTG GATCAATATG 720
CCCGGAAATC CCGACCTTGA TAATCTGACT CAATCTCAAG TGGATGCTA CGCCACACTG 780
ATCGGTGATG TGAGTGCATC TGTTCGATG AGTTTTATG AAAATGGAAG TGTGACGTAC 840
50 AGCGTTTATG TAGTAGGAGC CTTGCGAAAC AACTTTGCTC ACAAGCGTTC ACTGCAGCTA 900
CATGTACGCG CCTTATATAC CTCACAGGAG TGGCAGGATA TGATCCGCGG GGAACCTGCC 960
TCCGGAAGGC CGGTCTATTA TGCAGGGGAT AACCAGAGCA TAGGACATGC TTTCGTTTGC 1020
GATGTTATG CTTCGGATGG TACTTTCCAT TTCAACTGGG GTTGGGGAGG TGTTTCCAAC 1080
GGTTTACCA TTTATCAAGA GATCATCACC GGTATCGAAC CGGCTAAGAC TCCCGCTGAA 1140
55 GCCGGTACAG ATGCGTTGCC GATCTTGGCA CTGAAAGACA TAGAAGCCGA GTATAAAGT 1200
GAATCCGGAT TGAACGTAGG GTATTGATA TATAATACAG GTGAAGAGCA ATCAAACTCT 1260
GACCTCGGAT ACAGATTGAA CAAGGCTGAC GGAGAAGTCA TAGAGGTGAA AACTTCATCT 1320
ATCAATATCT CTTGGTAGGG ATACGGAGAG CATCCCGAGA GTTCTCATC GGCACCTAAT 1380
CAGTTGTGAC AAGGAATCAA CACCATCACC CTACTTTATC GTGCGACAGG CACCGAACAG 1440
60 TGGGAGCCGG TACGGCATGC ACAGGGGAGG TATGTCAATA GCATTAAAGT AAATACGACA 1500
GACCCGAACA ATGTGCTAGT CACGGTAGAT AATAACGAAG GCAAGCTCAG TATCGTCCCG 1560
AACAGCTTTG TCGCAGATCT GAATTCCTAT GAACATAGTA CGATTACAGT ACAGTTCAAT 1620
AGCGACAGCC CTGATGAGAT CCGTACACCC GTAGCCTTTG CTCTATCTAC ACGAGCTACT 1680
CGCGACGATG TAATATCTTT GGGCTGGGTA ATGGCTGAAG TTCCGGGGCGG TAGCAGCAAC 1740
65 TATCCGGTGG TTTGGTCTAA AGACGTTCTC ACTCTCTCGG AAGGCGACTA TACATTGTGG 1800
TATAGATTTT CCATCAACAA CCAAAAGGAT GAATGGAAAA AGATCGGAAG CGTGTCACTA 1860
TATACGCTGG ATGGTGAATT GGTGTGTGTT TTCCGCGGAA CACAATCTCT ATCTGCGGCT 1920
TTGCGCTTCA ATGGTGAATT GGTGTGTGTT TTCCGCGGAA CACAATCTCT ATCTGCGGCT 1980
70 TTATGGGCGC CTCAAGAAAC AGTACATATC AAGCAAGGAG AAATTTCTGT ATATAAAGCT 2040
GTTGTGCAAG GCCCTATACC TGATGGATCC TATCGTGCGA CCGTCCATGC ATTCGTAAC 2100
GGACAACAAC AGTTGTACCT CAAGGGGAAA AGGAACTACA CCGTGAAGAT CGTCAATGGT 2160
ACAGCGGTAG AAGCAATAGA ATGCTCAGAA GAGATCAGAG TATTCCTTAA TCCGGCACGC 2220
GATTATGTGG AAATATCGGC ACCTTGCAAT CCCCAGAAA CATCTATCAT TCTTTCTGAT 2280
75 CTGTGAGGCA AGATTGTCTAT GAAGAATAGT TTATCAGCGG GGCATGGCAG AATGGATGTC 2340
2400
2460

AGCCGACTTC CTAATGGGGC CTACATCCTT AAGGTGGATG GATATACGAC GAAAATAAAT 2520
ATAGTGACAC 2529

5 (2) INFORMATION FOR SEQ ID NO:169

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 870 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

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(ii) MOLECULE TYPE: DNA (genomic)

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(v) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...870

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(x1) SEQUENCE DESCRIPTION: SEQ ID NO:169

ATGAAAAAGC TATTTCTCTC GCTCAGGAGT CTTGTAATGG TCTTCGCTGT TCCAAAGTTGC 60
GATATAATCG ACAAGGATCA AACCTCTCTG CCGGCTCCGA CCAATGTGAC ACCCGATAAT 120
30 CCGGATGACA ATCCTTCGGA GATCGACATT ACGCAGACGC ACACAGAAAA ATATGTTTTG 180
GCTGAAGAAT TTACCGGCCA AAAATGTCTC AACTGTCCGA AAGGTCATCG CAAACTGGCG 240
GCTCTCAAGG AGCAATACGG TAAGAGATTG ACTGTTGTGC GTATACATGC CGGCCCTGGA 300
TCTCTCGTGC CACCTCTTTT CCGTACAGAA GCCGGAGACG CATATTATAG CAAGTTCCGC 360
AATAATACCC CTCTCCCTGC GCTGATGGTT TCGCGCAAAA AGTTGGGCTC TTCTACGTT 420
35 TATGATAAGA GCTACAAAAC GTGGGACGTG CCTATTGCCG AGCAGATGGA CCAAAAGGCG 480
AAGATCAATA TCTTTGCCGT GGCCGAATAC ACCGATACCC AAAAGATCAA GGTGACTGTA 540
AAGGGTAAAA TACTGGAGGG GAATACACTC CCGAAGTCCA TGGTTCAGGT GTATCTGTTG 600
GAGGATAAGC TGATCGCTCC GCAGGTGGAT GGCAATACGA CAGTCGAGAA TTACGAGCAC 660
AATCACTGTG TCGGTGGAGC CGTTAATGGT ATTTGGGGCG AAGAATTGT GAATCTCAA 720
40 GATTATTGT ATACTTACGC CGTTGAACCG CTCTCGGSTA TGTCTTCGT AGCCGAGAAT 780
TATTCGATTG TGGCTTTGT ATACGATGTG CAGACGTCG AAGTGATGA CGTTGTGCAT 840
GTAAAGATCA ATCCGCAATC CGATGGCAAA 870

45 (2) INFORMATION FOR SEQ ID NO:170

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 669 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

50

(ii) MOLECULE TYPE: DNA (genomic)

55

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGINAL SOURCE:

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(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...669

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(x1) SEQUENCE DESCRIPTION: SEQ ID NO:170

ATGAAGAAAT CAAGTGTAGT AGCCTCAGTT TTGGCCGTGG CTCTCGTGT CGCCGGTTGC 60
GGACTGAACA ATATGGCAAA AGSCGGCCTT ATCGGCGCCG GAGTAGGAGG TGCCATTGGT 120
70 GCCGGACTAG GTAAACGTAG CGGAATACG GCTGTCCGTT CCATCGTCGG TACTGCAGTC 180
GGTGGAGCAG CCGGTGCTCT CATCGGAAG AAGATGGACA AGCAGAAAAA AGAAGTGGAG 240
GCCGCACTAC CCGATGCTAC GATTGAGACA GTAAATGACG GAGAGGCTAT TCTGGTTACT 300
TTCCGATAGG GTATCTCTTT TGCGACGAAC TCCAGCACTC TGAGTCCCAA CTCACGCACT 360
75 GCGCTGACGA AGTTTGCTGC AAACATGAAC AAAAACCCCG ACACGGATAT TCGTATCGTA 420
GGCCATACGG ACAATACCGG CTCCGACAAG ATCAACGATC CTCTCTCTGA GAGACGTGCA 480

116/ 490

GCCAGCGTAT ATTCTTTCCT GAATTCTCAG GGTGTGASTA TGTCGCGCAT GGCAGCCGAA 540
GGGCGTGGA GCCATGAACC GGTTCGAGAC AATAGCACAG TTGCGGAGCG TTCGGCCAAC 600
CGCCGTGTGG AGGTTTATAT CTTGCGGAAT GCCAAGATGA TCGAACAAGC ACAGCAAGGT 660
ACGCTGAAG 669

5

(2) INFORMATION FOR SEQ ID NO:171

10

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1011 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

15

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

20

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

25

- (ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1...1011

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:171

30

ATGTCGAAAA AATCGATCCT TCTGCTTTCG TGTCGCTGT GCTTCATTTC TGCTACGAAG 60
GCTGTGACCC CCGTCAGAAA TGTGCGCAAT AGCCAAGTGA ACAGCAAAGC AAAGACCGAA 120
CGTACAAAGC CCGCGACTC TGTACGGTAC ATTAGCAACA TGATTGCAGA TCCGCTGGAG 180
TTCCGCAACA AGATTCTTTC CGAAAAAGAG CTAAAGAAAG CCGAATATGA AATCGGCTG 240
GCGATGGAAG CACTCAATTA CCCTGCCATA GATTATATG GTGAAGATTC TTGGAGCGAG 300
TATGTAAACC CTTTCGTGGG TGCAGGAACC GATGTCGAAA TTCCGAATC CTATGACATT 360
GATTGCTCTT CGTTCGTGAT GCCCGTCGAA GATAAGCAGG TCACCTCTCA ATTGGCTAC 420
CGTCGCGCTT TCGGACGGAT GCACTATGCT ATTGATCTTT CAGTGAATCG TGGCGATACG 480
ATACGAGCAG CCTTTGACGG GAAAGTTCGT GTACGCAGCT ATGAAGCGCG TGGCTATGGC 540
TACTACATAG TCTTGGCCCA TCCGAACGGA CTGGAGACTG TGTACGGACA CATGAGTCGG 600
CAATTGGTAG ACGAGATCA GATCGTTCGA GCAGGACAAC CGATCGGATT AGGAGGCGAG 660
ACGGGTGAAA GCACCGGTCC TCATCTTCAC TTCGAGACCC GCTTCATGGG TATCCCATC 720
AATCCGAGTA CCATTATAGA CTTGATAAC GGAGTGCCGC TCCGAGACAT TTACACATT 780
AAAGGAGGA GCAATTCTCG CTATGCAAAA GCCTCTAAGA CTCTCTCG CTATGCAAAA 840
AAAGGGAAGA AAGGCAGACA AGCTTCTTCT CCTATGACCT ATAGAATCAA AAAAGGCGAT 900
ACTTTGGAAG CAATAGCCAA AAGGCACGGC ACTTCTGTTT AGAAACTCTG TGCTACCAAT 960
GGCATTTGGA AGAGTAAAT TTTGACTCCG GGCAAGCCT TGAGGATCAA A 1011

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(2) INFORMATION FOR SEQ ID NO:172

55

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 453 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

60

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

65

- (ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1...453

70

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:172

ATGSCAAAAA TCAATTCTTA TGCTGAAGGC CTCAGCCTTC CTCGGATCAG AAGACGGATC 60
GTCGTAAGT GGATAGCCGA AGTATGCAGC CGATATGGGA AAGCGGTGGG AGAAATCTCC 120
TATCTTTTCT GTGATGACGA ATATATCTTG AAAGCCAATC AGGAATTTCT CGATCATGAC 180
TACTACACCG ACATCATCAC CTTGATTCC TGCGAAGCGG ATACGGTGAA TGCGACCTG 240

117/ 490

5 CTTATCAGTC TCGATACCGT ACGCTCGAAT GCCCGTGCTC TTGATCTTCG ATACGAAGAC 300
 GAACTGCATC GTGTCAATTAT CCACGGCATA CTGCATCTTT GCGGATTGAA AGACAAGAGC 360
 AAAAAGGATG AAGCCCAAT GCGTGCAGCC GAAGAGAAAG CCCTTGTCAT GCTGCGAGAA 420
 ACCATCGGAT CGGAGCTTTC CCTATTGCAT ACA 453

(2) INFORMATION FOR SEQ ID NO:173

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1173 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- 15 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 20 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 25 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1173
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:173

30 ATGAAGGTAA AGTACTTAAT GCTCACATTG GTTGGAGCAA TTGCACTGAA CGCAAGTGCA 60
 CAGGAGAATA CTGTACCGGC AACGGGTCAG TTACCCGCTA AGAATGTTGC TTTTGCTCGC 120
 AATAAAGCAG GCAGCAATTG GTTTGTAACA CTGCAASGCG GTGTTGCAGC GCAGTTCCTC 180
 AATGACAACA ACAACAAGA CCTCATGGAC CGCTTAGGAG CCATAGGTTT TCTTTCTGTC 240
 GGAAAGTATC ACAGCCCTTT CTTTGCAACT CGTTTGCAAA TTAACGGAGG TCAAGCCAC 300
 35 ACTTTCCTCG GAAAAAATGG CGAACAAGAA ATCAACACCA ATTTTGGTGC AGCTCACTTC 360
 GACTTTATGT TTGATGTGGT TAACTACTTT GCACCATATC GCGAAAATCG TTTCTTCCAT 420
 TTAATTCCAT GGGTAGGTGT TGGCTACCAA CACAAATTCA TCGGTAGCGA ATGGAGCAAA 480
 GACAATGTGG AATCACTGAC GCGCAATGTA GGAGTTATGA TGGCTTTCAG ATTAGGAAG 540
 CGAGTAGACT TTGTGATCGA AGCACAAGCA GCTCACTCCA ATCTCAATCT AAGTCGCGCA 600
 40 TACAATGCCA AGAAAACTCC CGTATTCGAA GATCCGCGAG GACGTTATTA CAATGGATTTC 660
 CAGGGGATGG CTACAGCAGG TCTTAATTTC CGCCTGGGAG CCGTAGGCTT CAATGCCATT 720
 GATCCGAGG AACTCTCAA ACGTCTCTGA TCATGCCCGG AATGTCCTGA AGTAACTCCT 780
 GTTACTAAGA CAGAAAATAT ACTGACGGAA AAAGCTGTAC TGTTCGTTT CGACAGCCAC 840
 45 GTTGTGGACA AAGATCAATT GATCAACCTG TATGACGTAG CTCAGTTTGT AAAAGAAACT 900
 AACGAGCCGA TTACCGTTGT TGGTTATGCT GATCCTACGG GTAATACTCA ATACAACGAG 1020
 AAATTGCTG AGCGTCGGGC TAAAGCGGTT GTTGATGTTT TGACAGGTAA ATATGGTGTG 1080
 CCTCCGAAT TAATCTCTGT AGAATGGGAG GCGGACTCTA CGCAACCGTT CAGCAAGAAA 1140
 50 GCTTGAATC GTGTTGTAAT CGTTCGCTCC AAG 1173

(2) INFORMATION FOR SEQ ID NO:174

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1155 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- 60 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 65 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 70 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1155
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:174
- 75 ATGACATACA GAATTATGAA AGCTAAATCT TTATTATTAG CACTTGCGGG TCTCGCATGC 60

118/ 490

5 ACATTTCAGTG CAACAGCCCA AGAAGCTACT ACACAGAACA AAGCAGGGAT GCACACCGCA 120
TTCCAACGTG ATAAGGCCTC CGATCATTGG TTCATTGACA TTGCAGGTGG AGCAGGTATG 180
GCTCTCTCGG GATGGAATAA TGATGTAGAC TTTGTAGATC GTCTAAGTAT CGTTCCTACT 240
TTGCGTATCG GTAAATGGCA TGAGCCTTAT TTCGGTACTC GTCTCCAATT CACAGGATTC 300
GACATCTATG GATTCCCGCA AGGGAGCAAG GAGCGTAACC ACAATTACTT TGGAAACGCC 360
CACCTTGACT TCATGTTGCA TCTGACGAAC TATTTCGGTG TATACCGTCC CAATCGTGTC 420
TTCCATATCA TCCCATGGGC AGGTATAGGA TTTGGTTATA AATTCCATAG CGAAACGCC 480
AATGGTGAAA AAGTAGGAAG TAAAGATGAT ATGACCGGAA CAGTIAATGT CGGTTTGATG 540
CTGAAATTCG GCCTATCAAG AGTCGTAGAC TTCAATATTG AAGGACAAGC TTTTGCCGGA 600
10 AAGATGAAC TATCGGGAC AAAGAGAGGA AAAGCAGACT TCCCTGTAAT GGCTACAGCA 660
GGTCTAACGT TCAACCTTGG CAAGACAGAG TGGACAGAAA TTGTTCCCTAT GGACTATGCT 720
TTGGTCAATG ACCTGAACAA CCAATCAAC TCACCTCGCG GTCAAGTGGG AGAGTTGAGC 780
CGTCGTCTGT TTTATGCCC TGAATGCCCT GAGCCTACAC AGCCTACAGT TACTCGTGTA 840
15 GTCSTTGACA ATGTGGTTTA CTTCCGTATC AATAGTGCAA AGATTGATCG TAATCAAGAA 900
ATCAATGTTT ACAATACAGC TGAATATGCG AAGACCAACA ACGCACCGAT CAAGGTAGTA 960
GGTTACGCTG ACGAAAACCG CGGTACTGCG GCCTATAACA TGAAGCTTTC AGAGCGTCGT 1020
GCAAAAGCGG TAGCCAAGAT GCTTGAAAAG TATGGTGTTT CTGCGGATCG CATTACAATT 1080
GAATGCAAGG GCTCATCAGA GCAATCTAT GAAGAGAAGC CTGGAATCG TATTGTAGTA 1140
20 ATGACTGCAG CGGAA 1155

(2) INFORMATION FOR SEQ ID NO:175

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 570 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 30 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 35 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 40 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...570
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:175

45 ATGGAATTTT TCATGTTATT CATAGCGCGG GTTTTCGTTA ATAACGTCGT GCTGTGCGAG 60
TTCTCGGTA TATGCCCAT CTAGGCGTA TCGAAGAAGG TAGACAGCTC AATCGGTATG 120
GGTGCAGCCG TGACATTGCT ATTGGCACTG GCTACCTTGG TTACCTTCCT GATTCAAGAG 180
TTGTTTTGG ATCGTTTCGG ATTGGGCTTT ATGCAGACCA TTGCATTTAT TTTGGTCATT 240
GCCGCTTGG TGACATGGT GGAGATCATA CTCAAGAAAG TATCTCCTCC CCTGTATCAG 300
50 GCACTGGGTG TATTCTTCC CTTGATTACG ACGAAGCTGT GTGTGCTCGG TGTGGCTATT 360
TTGGTTATCC AGAAGGATTA TACCCTGCTC CAGAGCTTCG TCTATGCAAT ATCCACGGCT 420
ATCGGTTTCA CTTGGCAAT GGTACTTTTC GCAGGTATTG GAGAGCAAT CGATATGACC 480
AATCTCCCA AAGCTATGAA GGAATACCT TCGGCACTCT TGGTGCCGG TATATTGGCT 540
55 ATGGCTTCA TGGGCTTCAG CGGTATCGCC 570

(2) INFORMATION FOR SEQ ID NO:176

- 60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 558 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 65 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 70 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 75 (ix) FEATURE:
(A) NAME/KEY: misc_feature

(B) LOCATION 1...558

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:176

5	ATGTTATTCA TAGCGGCGGT TTTCGTTAAT AACGTCGTGC TGTGCGAGTT CCTCGGTATA	60
	TGCCCATTCI TAGGGTATC GAAGAAGGTA GACACCTCAA TCGGTATGGG TGCAGCCGTG	120
	ACATTCGTAT TGGCACIGGC TACCTTGGTT ACCTTCCTGA TTCAGAAGTT CGTTTGGAT	180
	CGTTTCGGAT TGGGCTTTAT GCAGACCAAT GCATTATTT TGGTCATTGC CGCCTTGGTG	240
10	CAGATGGTGG AGATCATACT CAAGAAAGTA TCTCCTCCCC TCTATCAGGC ACTGGGTGTA	300
	TTCTTGCCCT TGATTACGAC GAACTGCTGT GTGCTCGGTG TGGCTATTTT GGTATCCAG	360
	AAGGATTATA CCTGCTCCA GAGCTTCGTC TATGCAATAT CCACGGCTAT CGGTTTCACC	420
	TTGGCAATGG TTACTTTCCG AGGTATTGGA GAGCAACTCG ATATGACCAA TCTCCCAAAA	480
	GCTATGAAGG GAATACCTTC GGCACCTCTG GCTGCCGGTA TATTGGCTAT GGCTTTCATG	540
15	GGCTTCAGCG GTATCGCC	558

(2) INFORMATION FOR SEQ ID NO:177

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2499 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(1v) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...2499

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:177

40	ATGAACAAC TAAACATTAT CAGCTTCATC ATTGCTTTCC TATTCTTAGG AACGAGCGCA	60
	TCGGCTCAGC AATCGGGCGG ATCCGTTACA GGTACCGTAG TGGACAAAAG CTCAAAAGAA	120
	CCTATCGCAT ACGTACAAGT ATTTCGTCAA GGAACCACTC TCGGAACCTC CACGGATGCA	180
	AACGGAACCT ACTCGATCAA GGGAAATCCCT TCGGGTAATC AAATATCGT AGCCCGACTC	240
45	ATGGGTTACT CCACTTGCGA AGAAAAAGTA CATATAGAAA AGGGTGGTTC CCGCCACGTA	300
	GACCTCTATC TGACCGAAGA GATTCTCTCT CTCGATGGGG TAGTGGTATC TGCCAATAGA	360
	AACGAGACTT TCCGCGCTCA AGCACCCTCG TTGGTAAAGG TACTGTCCGC GGAACCTTTC	420
	CTCAAAACCA ACTCTACCAA CCTGAGTCAG GGAATTAACT TCCAGCCCGG TCTGCGCGTG	480
	GAGGACAACT GTGAGAACTG CGGTTTCAAC CAAGTTCGTA TCAATGGACT CGAAGGAGCC	540
50	TATTGCAAAA TTCTTATCGA CAGCCATCCC ATCTTCAGIT CGCTTGCCGG TGTCTATGGC	600
	TTGGAGCAGA TGCTGCCAA TATGATCGAA CGTGTAGAAG TAATTCGCGG TGGAGGTTTG	660
	GCTCTGTTCG GCTCTAATGC TGTGGGAGGC GTTATCAACG TAATTACGAA AGAACCCGCT	720
	CGCAATTCGG CCGAGATCAG CCATTCTACG ATGACCTTCG ACCACGCGAA AGGGTGGGGG	780
	AGCTTCCAAA ATACGACCCA GTTCAACGGT TCTATGCTGA CGGAAGACCG CAAAGCCGGT	840
55	GTATGGTAT TCGGCCAACA CAACTACCGT CCGGACAGG ATATAGACGG CGCAACTTT	900
	ACCGAATAC CCAATCTCGC CAACCGCTCG CTCGGTTTCC GCTCATACTA TAAGACCGGT	960
	CTCTACAGCA AAGCAACCTT CGAATATCAC AGCATGCAAG AGTACCGTCG TGGTGGCGAC	1020
	AGCTGGGACA ATCCTCCTTT CGAAGCCAG ATAGCGGAAT ATCTCCAGCA CTATATCAAT	1080
60	GGCGGAAGTT TCAAAATCGA TCAGGGCTTC AGCGGTGGCA AGGATTTCCT CAGTCTGTAT	1140
	GCTTCAGCAC AAGACGTTCA GGTGCTAGC TACTACGGGG GTGGCGACTA TACCAGAAAT	1200
	CTGCTGAACG GAGCAGTTCA GAGTGGAAAG ACCGAATCGG ACGAATACAA CGATGCTTTC	1260
	ACGGCTCTTA CTTCCTACGG GACTACCAAG GGAATCGATT TGCAAGGAGG AGGTATGTAC	1320
	CGTCATACCT TCGGAGAAAA CTGGGACTTT ACCGGCGGAC TCGAATATAT CTACGGCCAA	1380
	CTCGATGACA GAAGCGGCTA CAGACCGAGC AATATAGATC AGAATACCTC TACTTTTAGT	1440
65	CAGTACGACC AGCTCGAATA TAAGACGGAG AAGTTAAGTG CCTTATCGG AGCACGTATC	1500
	GACTATGTTT TCCTCAATCA GGATGCCAAA CGCTATATCG ATCCGCTCTT CATTTTCAGT	1560
	CCTAGAGCCA ACGTACGATA CAATCCCAAT AAGAACTCA GCTTCGGACT CTCATACAGC	1620
	GAAGGATTCC GCGCTCCTCA GTATTTCGAT GAAGATCTGC ACGTAGAGTT GGCCGGTGGT	1680
	ACTCCTATCA CCGGTGTCCT TTCCCCCAAT CTGAAGAAAG AACGTTACAG AAGCATCAGT	1740
70	GCTTCTTTTG ATTATTACCA CAGAGCCGAC GAATGGCAAT TCAATATCAT GGGAGAAGCC	1800
	TTCTCCACCT TTATCAGCAA TCAGTTTCAA CCATCCGATA AGGTGCAAGC CACGAGCGAT	1860
	GGCAAGAAT GGATCATTCT TACCATCTAC AACGACAAGG ATGGAGTATC GAAGGTATAT	1920
	GGTGTGAATC TGGAGGGAAG AATCGCCTAC AACAAATCGT TCGACCTCCA GCTCGGCGGT	1980
	ACATGGCAGA GAAGCCGCTA CGGAAGCATC TATACCGCTG TGAAGCGGGA CAAACAACG	2040
75	GGACAAGCCG AGATCTCTGT GAAAGACTAT GTACGCACTC CGAATCTGTA CGGCTATTTT	2100
	GTGCTACGG TACGTCTTAC CGAGCACTTC GCCATCAATC TCTCCGTTAC ATTCACGGGC	2160

120/ 490

5	AAAATGGATG TAGTACACGA AGCCTATGAA GGCGATATTC CCGCAGAAACA CATAGCTCCG GACGGATCGT TCGACTTTGA AATGAATGGT CAGCAATTC AAGGTTTGGC CGAAGGTCAT GCCAAGCTCG TCAAGACTCC GGCCTTCGCC GATATAGACC TCAAGCTGAG CCACGACTTC CACCTTGCTT CCACTATGAC CTTGGAATTG AATGCCGGAA TACAGAACAT ATTCAACAGC TATCAGAAAG ACACGGACAA GGGACCGGGT AGAGCTTCTA CTTACGTATA CGGTCTCTATG CAGCCCAGAA GGATTTTCGT CGGTACAAAG ATCAATTTT	2220 2280 2340 2400 2460 2499
10	(2) INFORMATION FOR SEQ ID NO:178	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 2673 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular	
20	(ii) MOLECULE TYPE: DNA (genomic)	
25	(iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (vi) ORIGINAL SOURCE: (A) ORGANISM: PORPHYROMONAS GINGIVALIS	
30	(ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION: 1...2673	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178	
40	ATGTACAAA AGATTATTGC CGTAGCAGCT CTCTTCTGCG CCAGCATAGG GATCCTGAAA GGACAGTCC CGGATCTGAC CCCTCAGGAT ACTATATATA GCCTTGAAAT ATCCTATGCC AAGCCTATTC ATAAGACCAT AGCATCTATT GAGATCGAGG GAATGACGTC TTTCGATGAC TTTGTCTTGC GCAATCTTTC AGGCTTGGCT GTAGGTGATG AAGTCTGAT TCCTGGAGAT GCCATGCTCG CTCCTGTGAA TAGAATTATG CGTCAGGGCT ACTTCTCAA TGTGCCAATC ATCGCGGATA AATATGTCGG CAATAAAGTC TATCTGAAAA TCATTGTGAC TGAACGTCCT CGCATCAGTA AGGTTACTTT TAGCGGGGTA AAGAAGTCTG AGAGAGAAGA TCTTGAATG AAAATCGGTC TCGCGAGGG GATTACAGAT ACCAGAAATA ATGAAGACAA GGTCAAGCAA ATCGTACAGA AGTATTTTAC TGAGAAAGGT TATCGCGATG CCAGCATACG GATAACGACG GAACCGGATC TTTCCAAAGA TGGCTTTGTC AATGTGCTTA TCTCGATTGA GAAGAAAAGC AAAACCAAGG TGAATGAAAT TTATTTTTC GGCAACAAGG CCCTTAGCAA TCATAAGCTA AGAATGGCGA TGAAGAACAC CAATGCCAAA TTCAGTCTTA GAAAGCATAT TCGCTCATCT TTCTTGAAAC TTTTATGAT TCATAAGTTT GTGGAAGAGA GCTACCGTGA AGATTTGGTC CGATTGATAG AGAAGTATCA GGAATATGGA TATCGTGATG CTGAAATACT GACCGACAGT GTCGTGAAGG CTCCTGACGG CAAAAGAGTG GATATTTATC TCAACATCGA AGAGGGGACG AAGTATTATA TTAAGGATGT CAATCTTGTG GCAATTCAC AATATCCATC GGAGTATTTG GAACGAGTGC TCGGAATAAA ATCCGGAGAT GTGTACATC AGAGACGATT GGCTAAGCGT CTCAATGAAG ATGAAGATGC TGTGGGGAAC CTGTACTATA ACAATGGCTA TATTTTGGC TGGGTCGATC CCGTGGAAAC AATGTAGTG GGGGATTCTG TTTCCGTTGA TATTCGTATA GCGGAGGGGA AGCAGGCCAA TATCAATAAG CTGATCATCA AAGCCCGGCC AGCTCTTTAG TCGCGAGGAT GAAGACGTAG TACGCGGAGA GCTTACACA AAGCCCGGCC AGCTCTTTAG TCGCGAGGAT ATCATTAAT CTATTCGTCT CATCAATCAG CTGCGGCATT TCGATGCCGA AAAATCTATT CCCCGTCGGA TTCCCAATCC CGAAACAGGA ACAGTGGATA TAGAGTATGA TTTGGTGCCG CGTAGCAGTG ACCAATTGGA GCTTCTGTGC GGTGGAGTC AGTCCGGACT TCTGTCCGA GGAGCCATTA AGTTACAGAA CTCTCTGTGC GGCAACTTGC TCCATCCCTC GATGTATAAG AAAGGGATCA TTCCGCAAGG GGATGGGCAA AACTATCAC TGAGTGCTCA GACCAATGGA AAGTACTATC AGCAGTATAG TGTCACATTT ATGGATCCAT GGTTTGGGG CAAGCGGCCG GATATGTTCA GCTTCAGTGC ATTCTATTCC AAGACTACGG CGATTGACTC CAAGTTCTAC 60 AATAGCAATG CCGGCAACTA CTATAATGCC TACTATAATA GCTACTACAA CAATATAAT AGTTATTACA ACGGTATGTC GAACTATACC GCGGACCTCT ATACTCAGGC CAGCGATCCG GATCGTTCGG TTCAGATGTT AGGTACTTCC ATCGGTTACG GTAAGCGTAT GACTTGGCCG GACAATTGGT TCCAGATTTA TACTTCTCTG AACTACACCT ACTATAGACT GCGAAATTGG AGCTACAATA CCTTCCAAAA TTCCATCAT GGCTCGGCTA ATGATCTCAA CTGGAGCTG 65 CGTCTCTCTC GTACTTCCAT CGATAATCCT ATTTATACCA GAAGCGGATC GGATTTCTATG GTTTCTGTG GCTACTCTCT TCCTTATTCT TTGTGGGACA ATCAATGACTA TGCCAGCCAG AAGCTCAGCG TAAGCGATCG TTACAGATT ATCGAGTATC ACAAGTGGA GTTTAGAGGA ACGCTTTTGA CTCCATTGCT CAATCCTGCT ACGCATAAAT ATACACCGGT GCTCATGAGT CGAGTGGAAG GAGCAGTTCT TGGTTCGTAT AATTCCAAAT AGAAATCTCC TTTCCGGTACT 70 TTCTATATGG GAGGTGATGG TATGTCCAGC TATTATGGTG GCTACATGAA TGAGACTATA GGTTTGGCTG GTTATAAGAA CGGATCTATT GCCGGTAATA ACTACGACTA TGCAATGCT TATATGCGCG TTACGATGGA ACTACGTTTC CCGATTCTGT TTGAAAACCT ATTCAATGCG TGGCTCTTAG CTTTTCGCGA AGCAGGCAAT GCGTGGCGCA GTATCGACAA TTATAATCCC 75 TTAACTCTGA AGCGATCGCG CGGTGTAGGA TTGCGTGTAA CGTTACCGAT GGTCCGAATG CTCGGTATCG ATTGGGGATA TGGCTTTGAC CGTCCGGACA ATTCTCTACA GCGAGGAGGA	60 120 180 240 300 360 420 480 540 600 660 720 780 840 900 960 1020 1080 1140 1200 1260 1320 1380 1440 1500 1560 1620 1680 1740 1800 1860 1920 1980 2040 2100 2160 2220 2280 2340 2400 2460 2520 2580 2640

AGCAATGTCC ACTTTGTGCT CGGACAGGAG TTC

2673

(2) INFORMATION FOR SEQ ID NO:179

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 522 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179

ATGAATGGCG	ATATGAAACG	GTITTTGATT	TTGATCGGCT	TTGCACTGGC	GGTAGCTTTC	60
TCCGGTTTTT	CCCAAAAGTT	CGCTTTGGTA	GATATGGAAT	ATATCCTCAG	GAATATTCCT	120
GACTATGAGA	TGATGAACGA	ACAGCTGGAA	CAGGTGTCCA	AGAAATGGCA	AAATGAAATC	180
GAAGCTCTCG	AAAATGAAGC	CCAATCTATG	TATAAGAAAGT	ATCAGAGCGA	TCTCGTATTC	240
TTGTCTGCTG	CACAGAAGAA	AACCCAAGAA	GAGGCTATCG	TAAAGAAAGA	GCAGCAAGCA	300
TCCGAGCTCA	AGCGGAAGTA	TTTCGGCCCG	GAGGGGGAGC	TGTATAAGAA	ACGCTCCGAT	360
CTGATGAAGC	CTATTCACGA	TGAGATTGG	AATGCTATCA	AAGAGATTGC	CAAGCGTAAC	420
AACTATCAGA	TGGTGCTTGA	TAGAGGTACG	TCCGGAATTA	TCTTTGCCAG	TCCGTCTATT	480
GACATTAGCG	ACCTTGTA	CTACT	GAGCAAGATG	GCCTTTAGCA	AG	522

(2) INFORMATION FOR SEQ ID NO:180

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 510 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180

ATGAACGGGT	TTTTGATTTT	GATCGGCTTT	GCACTGGCGG	TAGCTTTCTC	CGGTTTTTCC	60
CAAAAGTTGG	CTTTGGTAGA	TATGGAATAT	ATCCTCAGGA	ATATTCCTGA	CTATGAGATG	120
ATGAACGAAC	AGCTGGAACA	GGTGCCCAAG	AAATGGCAAA	ATGAAATCGA	AGCTCTCGAA	180
AATGAAGCCC	AATCTATGTA	TAAGAAGTAT	CAGAGCGATC	TCTATTCTTT	GTCTGCTGCA	240
CAGAAGAAAA	CCCAAGAAGA	GGCTATCGTA	AAGAAGAGC	AGCAAGCATC	CGAGCTCAAG	300
CGGAAGTATT	TCCGGCCCGA	GGGGGAGCTG	TATAAGAAAC	GCTCCGATCT	GATGAAGCCT	360
ATTCAGGATG	AGATTGGGAA	TGCTATCAAA	GAGATTGCCA	AGCGTAACAA	CTATCAGATG	420
GTGCTTGATA	GAGGTACGTC	CGGAATTATC	TTTGCCAGTC	CGTCTATTGA	CATTAGCGAC	480
CTTGTA	CTACTG	CAAGATGGG	CTTTAGCAAG			510

(2) INFORMATION FOR SEQ ID NO:181

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 489 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

5 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
10 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORPHYROMONAS GINGIVALIS
(ix) FEATURE:
15 (A) NAME/KEY: misc feature
(B) LOCATION: 1...489
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181

20 ATGAAGAAAT TTTTCTCAT GCTTCTGATG GCTCTTCTT TGAGCTCTT GGCACAAAAG 60
GTGGCAGTGG TAAACACTGA GGAGATCATT TCCAAAATG CGGAACAAGT AGCTGCTACC 120
AAACAGCTCA ACGAATTGGC CGAAAAGTAT CGCCTTGATC TCAAGAGTAT GGACGATGAG 180
TTTGCCAAAA AGACAGAAGA ATTTGTAAAG GAAAAAGACT CTCTACTGGA GAACATCCGC 240
AATCGTCTGC AGCAGGAACT TCAGGATATT CAAACTCGTT ATCAGCAGTC ATACCAAACG 300
25 ATGCAGGAGG ATTTGCAAAA GCGCCAACAA CAGCTTTTGG CTCCTATCCA ACAAAGGTG 360
GCTGATGCCA TCAAGAAAGT GGGTGACGAA GAAAACTGTG CCTACATCAT GGAGGCCGGT 420
ATGATGCTTT ACACCGGAGC TACTGCTATT GACTTGACCG CAAAGGTAAA AGCGAAACTC 480
GGAATCAAG 489

30 (2) INFORMATION FOR SEQ ID NO:182
(1) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 2481 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
(ii) MOLECULE TYPE: DNA (genomic)
40 (iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
45 (A) ORGANISM: PORPHYROMONAS GINGIVALIS
(ix) FEATURE:
(A) NAME/KEY: misc feature
50 (B) LOCATION: 1...2481
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182

55 ATGAAGGAAG CTATTCCCGG AAAGAACAAG TATATAAAGC TCAACGGTAT ATACAGATTG 60
TCATTCATTC TGCTATGCTG CCTGCTATGC TCTCAGGCAG CTATGGCACA AGCGCTCAGG 120
GTATCGGGCT ATGTGCTCGA CCGTGGGGAA AAGCCGATCC CGTTCGCGG AGTCAAAGTG 180
CGTGGTACGG GGACAGGCGC AACGACGAAT CTCAAAGGAT ACTACGAGTT TCGGATGAAG 240
GCCACGACGG ACAGCATCAC GATCGAGTTC AGCTCCATGG GGTACCAAGG GGTAAGTCGC 300
60 AGCTTTCCGT CTCTGACCAA GGACACTCGG CTGAATGTTT GTTTGGCAGA GGCCGAGATG 360
GAGCTTTGGA GCGTGACGGT ACAGGCCACA AAACGCAGAC TCAACACGAT GGAGCGCGTC 420
AATACCCGAG ACCTTCGTGT CAATGCAGGG CCTACGGGAG GGGTGGAAAT GCTCATCAGT 480
ACCTACGCAG GAGTAACGCA GAACAATGAA CTAAGCTCGC AATACTCGGT TCGCGGAGGA 540
AGCTACGATG AGAATATGGT CTATGTAAAC GGAGTGGAGG TTTATCGCCC GCTGCTGGTT 600
CGCTCTGCAC AGCAGGAAGG TCTGAGCTTC GTCAATCCGG ATCTGACACA ATCGGTACAG 660
65 TTCTCCGCGG GAGGGTTCAC GCGCGACTAT GCGGACAAGA TGCTCTCGGT ACTGGATATT 720
CGCTACRAGC AACCGCAGGA GAAGGAAGGA GCGGTACTCC TCGGGATGCT ACAATCGAGT 780
GCCTACTACT GCAGCAGTGC CGGAGCCTTC AGCCAAATCA CCGGTGTACG CTACAGAGT 840
GCCAAATCGC TCTTGGGCAC TACGGACAAG AAAGCCGAAT ACGATCCGAT CTATGCGGAC 900
70 GGACAGACAT TCATGACGTA CCGTTTCAGC CCCAAGCTGT CCGTTAGTTT CCTCGGCAAT 960
ATTTCCGCAA CTCGTACAA GTTTGTCCCT CAGACCGGTG AGACGAGCTT CGGTACACTG 1020
AGCGATGCCA AAAAGTTGAA GATCTTTTTC GACGGTCAGG AACAGATGOS TTTCTGACC 1080
TACTTCGGTG CCTTCAGCAT GAACCTTCGTG CCGGACGACA AACAGCGGCA TACGTTTACG 1140
CTTTCGGCCT TCAACAGTAA CGAACGGGAG ACCTACGATA TTCAGGGAGA ATACTTTCTG 1200
AACGATGTGC AGCTGGGGGC GGACGGAACT GCTTCGATGG CTTCCGGGCTC AGAGAACTCC 1260
75 AACCGCTTGS GCATCGGGCG CAATCAGCAG CATGCGCGCA ACAGGCTGAG CTACCGCGTG 1320

124/ 490

AGTCGTGGCA TAGCGGCCGA CAGGCTTACG TGGAAAGGCT ACGGTAAGTC TGTCCCCAAG 1860
ACGGTGACAG CCAAAATTCG CGAACGGCAC GATTTCCTGA AGGAAGGCGA TGTGCTCACC 1920
GAGGAATTGG TAGCACCTTT GACCGAGGAG CAGCAGTCAG TCTGCGACCA ACTGAACCGT 1980
CGTACCGAGT TCCGTGTGAT CGAAGAAGAG TTGCGT 2016

5

(2) INFORMATION FOR SEQ ID NO:184

10

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

15

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

20

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

25

- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...2124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184

30 ATGAAAAAGT TTTCTCTCGC GCTACTATCG ATTGGTATTT CAGCGCAGGC TTTGCCCCAAG 60
ACGGACAACG TCCCGACAGA TTCGCTACGA GTACACAATC TTCAGACCGT CACGGTCTAT 120
TCTACACGCA CGGCCGTACC TCTGAAAAAG ATACCGGCCA AGATGGAAGT CATCTCATCG 180
CGCAACATCA AGCAGTCCGG CTTTAAACAAC ATGACCGACA TCCTCAAGAC GCAAAGTTGG 240
CTCGATGTCA TACAATACCC GGGCTTTAGT TCGAACATCG GTATCCGGCG TTTCAAGCCC 300
35 TCCGCGCAAGT ATGTAACCGT ATTGGTAAAC GGCATCCCTG CGGGAACGGA CAATATCTCT 360
ACGCTCAACA CGAGCAACAT CGAACAAATC GAGATCCCTA AAGGCCCGGT CTCTTCCATC 420
TAGCGCACCA ATGCCATGGG CGGTGTGGTG AACATCATCA CCCACAAATC CAAGGACAAG 480
ATCCATGGCA ACGTTTCTCT CTTCGGCGGT AGCTACCAGA CCATGGCCGG ATCATTCAAC 540
40 TTGGGTGGCC GCTTCGAGGA TATTTTCTCA TTCGATCTTA GTCTGGGCTT GGACAAGCAG 600
AACAAAGGACT ATAAGACCGG ATCAACAAT TCCCTATCCC TGAGCAAACT GGAAGAAGCT 660
ATAGTAGATG TAAATGCTAC CAAAAACRAG AAAATGAAGG GGAGCGACTA TACTGTAGCA 720
ACGGGACGCT TGCGTTTCGG TATCGACTTC ACGCCCGAAT GGTCCCTGAA TCTGTATCAA 780
AACGTATTCC TCGGAGATGC GATCCCCGTA GGAGGATCTA TATGGGGCGT TTACGGAGAA 840
45 TCCAAAAAAA ATCTGAATCG TTCTTCGACC TCTTTCGAGC TGCTCGGCAG ACATGGCTGC 900
CACACGCTTC AATTCTCCCC CTACTTCAAC ATAGAGAAAT CGGAGAACTA TAACAATGCC 960
GATCCACCCG GTTTCATCAA CTACAAAGC GACTACTACA CCTATGCTCC CTTACTCCAG 1020
GACAAAGATT CTTTGGAGG ACRAAATATC GTACTCGGTG TCGACAGCCG AAACATGACG 1080
ATGGAGTCAG AAAGATTCTA GCAGGCAGGA GTGAATACAA AGCCATACAA CCCCAGATAT 1140
50 GCCACAAACA ATATCGGTTT GTTCGGACAG GCCAATTCTT ACCTGCTGAA CGATGCTCTA 1200
TCGATATCTG CCGGTGCACG TGCCGACTTC ATGTTCTTTG ACCTGAAAGC GAACGAGTAT 1260
CTCAACAATG AAGCCAAACA GGAAGCTCAT AACGTAATCA ATCGGAATGT CGGAATCAAA 1320
TATGAGTTTG TGAAGGCCCT TACAGCTCAT GGTACATTCT GTAGTGCAIT CAGTGTCTCC 1380
GATGCTTTC CCAAAAGCAG CCAATACGTA GGCCCGTTCG GCACGACCAT AGGCAATCCT 1440
GACCTGAAAC CCGAAAGTC CATGACCTGG GACTTCGGTA TCGGATACAG CAATGCACGC 1500
55 TCGGGGATCC AAGCGAGGT AACCTTAACC TATTTCCACA CCGACCAACA AGATCTGATC 1560
TTGTCCAGCC CTGACTATGC TAATAATATC ACCACATACA TCAATGCCGA CAAGGCTCGT 1620
ATGAGCGGTA TCGAGGCCCT TTTGTCTTAT GACTTCGGCA GCCTCTTTGC CAACAAGTTC 1680
TCTCTCCGCG CATTTGCGAA TGCCACGATC ATGCTCAATT CCGAGATGAA GAAAGCCAG 1740
ACCGATGCCG CTTGGAGCGA AATGTACTAC GTTCGCCAAGC AGAACATCAC CTTCCGTATC 1800
60 ATCGAGCATA ACTGGTATGC TTACTACCCC GAAGTTCGCC CCGAACTCCA GCAACTGCTT 1860
GCAGCAGAAG AGCCTGAATT GGCTGCTCAG GGACTGCTCC GTCATCCGCA AGCAATGGTG 1920
TTCAATGCCT CTGCTTACTA CCAATGAAC AAGTATCTCA CCTTCGGTGT GAACTTGAAC 2040
AACATCTTGG ATGAGCTTTA TACGGAGAAA GACGGCTACC ACATGCCCGG ACGTAACATC 2100
65 ATGGGTAAGG TTATGGTCAA CTTT 2124

(2) INFORMATION FOR SEQ ID NO:185

70

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

75

(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
5 (iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
10 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1386
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185
15
ATGAACAGGT TTTCAAATCA TTGGCCCTGC ATCCTCGTGG GTTTGTACT CTGGTTTGTA 60
TCGGCGAGTC GGACTGTGGC ACAAACGCGC TCCGAAACGA CGGTATCGTA CGATACGGAT 120
ACCGCCGTAC TCTCCGAAGC CGATGTGCTT CGGATCGCTC TTAGTGAGAA TGCCACAGTG 180
AAAGTGGCCG ATATGGATGT GCGCAACAGC GAATATGCAC GTAGGGCAGC ACGTGCCGAT 240
CTCTTCCCGA AAGTAGACCT CAATGGCGTT TACAGCCATA CCTAAAGAA GCAGGTCTTA 300
TATATAGATA TGCCCGGTTT CAGCAGTAGC GAAGGTATCG AAATGGGGCG TACACACAAT 360
ACGCAAGGAG GGGTGAACGT CTCCATGCCA TTGGTGTCCG CACAGCTTTG GAAAAGCATT 420
GCCATGACCG GAGAACAGCT CGATCTGGCT CTGGAGAAAG CTGCGAGCTC CGGAATCGAT 480
TTGGTGGCAG AGGTGAAGAA GGCTTACCTC AGTGTATTGT TGGCCGAGGA CTCTTATGSC 540
GTATTCAAGC GCAGCTATGA CAATGCTCTG GCCAATTATA AGAACATATC CGACAAGTTC 600
GATCGTGGAC TTGTGGCCGA GTATGATAAG ATTGAGGCCA ATGTACAGGT ACGCAACATC 660
GAGCCTAACC TCTTGCAAGC GCAGAACTCC GTAGCCCTTG CTCTCTGGCA GCTCAAGGTC 720
CTGATGAGCA TGGAAAGTGA AACTCCGATC AGACTCTCCG GTTCATTGTC CGACTATAAA 780
GAACAAGTCT ATACCGGCTA TTTTGGCCGC GATACGGCTA TTTCCAACAA CTCCTCCCTG 840
30 CGTCAGCTCG ATATACAGCG TCGTCTGGCT GTCACTGCAG ACAAGCTGAA CAAGTACAGC 900
TTCCTGCCTA CACTCAATCT GGGAGGGCAG TACACCTATT CGCTCAACAG CAACGACATC 960
AAATCTGCG GCGAGGGACA ACGCTGGACG CCTTCTCCA CCATATCGCT CAGCCTGTAC 1020
ATTCTATAT TCAATGGAGG CAAACGCTG TACAACGTGA AGCAAAGTGC TTTATCGATC 1080
CGTCAGATCG ATCTGCAACG ACGCCACATA GAGCAATCCA TCCGAATGGG AATCAAGAAC 1140
35 CAAATGACC GTCTGCGTAC CTGTATGCAG AGATTTGTGG CCTCGGAAGA GGCTGTCCGA 1200
AGTGCAGAAA AGGGCTATCA GATAGCAGAG AAACGCTATC AGACAGGCGA AGGCACTCTC 1260
GTGAGTCTCA ACGATGCCGA TGTGGCTCTT TTGCAGGCTC GACTCAATTA TAATCAGGCC 1320
ATATTGCACT TTATGACCGC AAAGGCCGAA TTGGACAAGA TGAACGGCAT GGGGATTCCC 1380
40 CAACAA 1386
(2) INFORMATION FOR SEQ ID NO:186
45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1476 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
50 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
55 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1476
60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:186
65 ATGTGGGGGG ACAGCCATGG AGTGGGCGCG AACCAAGTGC GCCGACGCT GGTGAAGGTA 60
GCCTTAAGTG AATCCCTTCC TCCGGGTGCA AAACAGATTC GTATCGGATT CTCTCTCCG 120
AAAGAAACCG AGGAAAAAGT CACCGCCCTA TATCTCCTTG TGAGTGATTG TTTAGCGGTG 180
CGCGACTTGC CGGACTACAA AGGGCGAGTC TCTTACGATA GCTTCCCGAT CTCAAAGGAA 240
GATCGTACCA CAGCCCTTTC TGCGGATTCC GTAGCCGGAC GCCGCTTCTT TTATTGCTG 300
70 GCGGATATAG GGCCTGTTGC TTCTTTTCC CGATCCGATA CGCTGACTGC CCGTGTGGAA 360
GAGGTGGCTG TCGATGGCCG CCTTTGCGG TTGAAAGAGC TGTGCGCTGC CTCCCGTCGT 420
CTGTATAGGG GGTATGAGGC CCTCTTTGTA CCGGSGATG GCGGATCGCG GAACATTCGT 480
ATCCCGGCCA TTTTGAAGAC GCCTAATGGA ACATCATAG CGATGGCCGA CAGACGAAAA 540
TATAATCAGA CGGATCTGCC GGAGGATATA GATATAGTCA TGCGGCGCAG TACGGACGGA 600
75 GGGAAATCGT GGAGCGATCC CAGGATTATC GTACAGGGAG AGGGGCGCAA TCATGGCTTT 660

126/ 490

5 GGGGATGTAG CCGTGGTGCA AACCCAAGCA GGAAAGCTCC TGATGATCTT TGTGGGTGGA 720
GTAGGCCTGT GGCAGTCTAC CCCCAGTCGT CCTCAGCGCA CTTATATATC GGAAAGTCGG 780
GACGAAGGAC TGACTTGGTC GCCTCCTCGG GATATAACCC ATTTCACTCT CGGCAAGGAT 840
TGTCGCGATC CGGGACGCGAG TCGCTGGTTG GCCTCCTTTT GTGCTTCGGG ACAAGGGCTT 900
GTGCTGCCAT CCGGTGCTAT CACGTTTG TGCTGCCATCC GCGAATCAGG GCAGGAGTAC 960
GTCCTGAACA ACTATGTCCT CTATAGCGAC GATGAGGCG ATACATGGCA GCTTTCGGAC 1020
TGTGCATACC GCCGTGGCGA TGAGGCAAAAG CTTTCATTGA TGCCCGATGG CAGGGTACTG 1080
ATGAGCATAAC GCAATCAGGG ACGGCGAGAG AGCCGACAGC GTTTCCTCGC TCTCTCCTCC 1140
GACGATGGCC TTACTTGGGA GAGAGCCAAG CAGTTCGAGG GCATCCATGA CCCCCTGTGT 1200
10 AATGGAGCTA TGCTTCAAGT GAAAGGAAC GGAAGGGATC AAGTGCTGCA CTCCTGCTCT 1260
CTCGGCCCGG ATGGGCGTCG CGATGGAGCT GTCTATCTCT TCATCATGT CTCGGCCCGC 1320
TGGTCCGCTC CCGTTGTGT CAATTCAGGA TCGAGTCCCT ACTCGGATAT GACTCTGCTG 1380
CGGGATGGAA CGATCGGTTA TTTCGTCGAA GAGGGCGATG AGATCTCATT GGTTCATT 1440
15 CGGTTCTGTC TTAGCATCT CTTCGATGTC CGCAA 1476

(2) INFORMATION FOR SEQ ID NO:187

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 735 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 25 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 30 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 35 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...735
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:187

40 ATGAAAAAAG AAAAATTG GATTGCGATC GTCGCCGTT TGGCTTTCGT ATTGGGCCTT 60
TATGCTCTTG GCCGAGTGT CGCTCAGCTA CGCCGCTCTC AGCCTTCGGT GACTGTGACC 120
GGTATGGCCG AGCGTAATTT CAAATCCGAT CTGATCGTTT GGACTGCTTC GTACCAGCTC 180
CAGATGATGG ATCTCGAATC GGCCTACAAG GCTTTGAAGG AAAAACAGAT ATTGGTAGCA 240
GACTATTTGA AAAACAAGCA GCTGCCGAT TCGTCTTATA TCTTCTCAAG CGTAGCCATC 300
45 TCTAAAGAA ACAACTACTA TTACGATCCT CGGCAGGAAC AAAACGTCAG GACCTTTGCC 360
GGGTATCTGC TCAGCCAGAC AGTTACGGTG ACCTCAGAGG ACATCGAACA TGTGGAGAAA 420
ATATCTCCGG ATATAACGGA GCTGATCAAT CAGGGGGTAG AGATTACCTC CGACCGTCCG 480
GCCTATTACT ACACCAAGCT CAATGATCTG AAGGTGGAGA TGCTGGCAA TGCCTCCGAA 540
50 GACGCTTCA ATCTGTCTTC GGTCAATGCG GAGGGGAGCG GTTCTCCGT GGGTAAGATG 600
CTATCTTCTT CGATGGGCGT GTTCCAGATA GTGGGGCTCA ACTCGAACGA AGATTATAGC 660
TGGGGAGGTT CGTTCAATAC GTCTTCCAAG ATGAAGACGG CAAGCATAAC GGTAAAGGCT 720
TCTTTCGCTT TGAAG 735

55 (2) INFORMATION FOR SEQ ID NO:188

- 60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 828 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- 65 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 70 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
75 (B) LOCATION 1...828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188

5 ATGAAAAA CAATTGCAAT TATCGCCTCA GCCCTCTTGG CTTTAGGAGC CGTCGGCTGT 60
AAGAAAAATG CTGACACTAC CGCTGTCAGT GAAAAGGATA GCATAGCCTT GTCCATGGGT 120
ATTTTGTACG GACAGGATT TGCATATCAG TTCGAAATGT CCGCTTGTCA AGGCCAGCCG 180
ATTGATTCGG TAGCTTTCTT GGACGGTTTC AAATATGGTA TCGATACGAC GCGCTTCTCG 240
TACAATCTGG GAGCCATCTA TGCTTCCAAT ATAGCTCGTC AGCTGGCTCA TGATTCCATC 300
GATATCGACA AGTTCTATGC AGCCATGCGT GCGGCTCTTC TTAAAGACAC CGTATCTATC 360
GCCATGAAGC CTGCAGATGC ACAGGCTTTC ATGCAACGAA TCCAAGCCAA AAAGCAGCGA 420
10 GAAAAAATA TGAAGCAGTT TGGCCAGAAC ATCGAAAAAG GTAATGAATA CATCGATACC 480
TTTAAAAAAG AAGATGGTGT AACTGTTACG ACAACTGGTC TGGCATACAA GACTCTTCAG 540
GAAGGTACGG GAGCTACTCC CTCTTGGGCC GATACTGTAC GTGTCAAGTA TGTGGGTACT 600
CTGGTCGATG GTAAAGAGTT CGACAAAAAC GAAGAAGGAA TCGAATTTGC CGTTACCGGT 660
GTGATTAAAG GCTGGACGGA GATGCTCCAA CTCATGAAGG TCGGTACAGAA AGTTGCGGTG 720
15 GTAATCCAC AGGAGCTGGC TTATGGGGAG ACCGGCAACT ATACCATCGA ACCGTTCTCT 780
ACCCTCAGCT TCGAGATGGA ACTTATCGGG ATCAAGCCCG GAAAAAAG 828

(2) INFORMATION FOR SEQ ID NO:189

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2325 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
(D) TOPOLOGY: circular
(ii) MOLECULE TYPE: DNA (genomic)
30 (iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
35 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION: 1...2325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189

40 ATGAAGTAT TACGGCAAGT ATTCCTCCCC ATCCTTTTGG TCCTACTGAC AGGTGCCTGC 60
TCCACCACAA AGAATCTGCC GGAAGGCGAA CAGCTGTATA TCGGAATGGG CAAGACACAG 120
ATACTCCGGC AGGACAAGAG CCACGCGGCG CAACAGGCTC TGACCGAAGT GGAGAGTACA 180
45 CTGAAAGTTA CACCAATGG AGCTATTTTC GGCAGTGCAA GTGCCTCCTT ACCCAAGATA 240
CCATTGCGGC TATGGCTATA CAACAGCTTC GTGGGGGATT CCCTGTGCAT TTGGAATGG 300
ATATTGACA AGTTTGACGC CAAGCCGGTT TTCATCAGTC AGGTCAAATC CGATAGCCGG 360
GCTAAGGTGG CGAGCAACAT CCTCCGCGAA CAGGGGTACT TCGATGTCAA AGTAAAAAGC 420
50 AGTGTGACCA CTCTGAAAAA GGAATCGCTC AAAGCCAAAA TCTCCTATAC GGTGGATATG 480
GCCTCTCCTT ATCATTACGA CAGCATCATT CCTTACCGA TCAGCACTTT CCGCGACAGC 540
ATTCTGGCTT ACAGGCAGAC TCCGTCTTTG ATCAGGAAAG GAGACCAGTT CAATTTGGCA 600
AAGTGCACG AAGAGCGTCA GACCATCAGT GCCCTGCTGA GAGACAATGG TTACTACTAC 660
TTCCGCCCAC AGGATATTAT CTACGAAGCC GATACCTCC TCGTAAGAGG TGCCGTATGC 720
55 CTGCGAGCCA AGCTCTCGGA AGATACTCCA CCCCAGCCA TGGCCCGCTG GAGGATAGGG 780
AAACGGACAG CAGTCTTGCT CGGAATGAAC GGAGAAAGCC CGACAGACTC GCTCGAAGTG 840
GAGGATATGA AAGTCCTTTA CTATCGTAAA ATGCCGGTTC GCGCCAGAT TTTGGCCAAA 900
CGCTTTCCTT TCTTCTCGGG CAATCTGTAT CGGCAGAAAG ACCATGAGAT GACACGCAAA 960
60 TCCTTGGCTC GTTTGGGAGC CTCTCCGTT ATCGATCTCA ATTTTTCCTA ACGCGATTCC 1020
ATTTCGCGCC TTTTGGATGT GCGACTGCTA ACCACCTCG ACAAACTTG GATGCATCA 1080
TTAGAGACCT TGTTACAGAG CAAAGCAAT GACTTCATCG GTCCCGGACT GAATTTTGCT 1140
CTTCTCTGGC GCAATGTATT CGGCGGAGGA GAAAATCTTT CTGGAATAT CGGTGGATCG 1200
TATGAGTGGG AGACCGGCAA TCGTCCCGAA AATAGCAGCA ATCGGCTGAT CGATATAAAT 1260
TCGTACAAAC TGAATACGGC CGTGAACCTC TCGTTTCCCT CGATTGTATT TCCCGTCTG 1320
55 CTGGATAAAT ACTATTACTA CCCCACGACT ACGACTTTTC AGGCTTCTGC CACCGCGCTG 1380
AACAGGGCAC ACTACTTTAG CATGTACTCT TTGGGCTTTT CGACCACCTA CGAATTTAG 1440
CCCTCCAGAG AACACCGGCA TGCTATTTTC CCGCTCAAGC TCAACTACAA CCTCCTGGGG 1500
CATCAGACAG AAATTTTCCA GGCCATTACG GCGAACAATC CCGCCCTGCT GCTCAGCCT 1560
CAGAGTCAGT TCCTTGCTCA AATGGGGTAT ATCTATACG TCAACAAATC CGTTTCAGAG 1620
70 AAAAGTCCCT ATCATCTTTG GATGCAATTC GGAATATCCG AGGCAGGCAA TCTCCTGAAT 1680
CTGATCTATC TGGCAGCCGG CAAGAAGTAC AGCGACACCA AGAATTTCTG CCGCGTCCCC 1740
TTCTCTCAGT TCATCAAAGC CACGGGAGAA CTGCGCTATT CCTATACCAT AGACCGCAAT 1800
CAGTCACTGG CAACCGTTT CGGCACGGC GTGATATATA GCTATGGCAA TATGCGAGTG 1860
GCACCTTATA GCGAGCAGTT CTATGTAGGC GGTGCCAATA GTATCAGAGC TTTACCGTC 1920
75 CGTAGCATCG GCGCCGAGC GTTCAATCCG GATTCGACA ATCAGTATTC CTATTGGAT 1980
CAGGTGGGCG AATTCAAACT CGAAGCCAAC GTGGAATAA GAGGCAAGCT TTTCGGGAT 2040

WO 99/29870

PCT/AU98/01023

129/ 490

(U) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

- 5 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
10 (iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
15 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...2601
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191

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20 ATGAGAAAAA GAATTCTACA ACTTTTCCTG ACCGCATTGC TGCTGGCATT AGGCTCCTCT      60
   CTGCCCCATAG CACAAACAGT GGTGACCGGT AAGGTGATCG ATTCAGAAAC GTCCGAACCG      120
   CTATCGGGTG TATCGTAAG CACCGGTGAG GGAGCATCCC TCCGGGGTGT AACCCACCGAT      180
   ATGGATGGTG GCTTCGGATT CGAAGTACCG GCCAAATCTG TCTTGACTTT CCGTTGCGTA      240
   GGTATGCTA CCGTAACCTG CTCTATAGGC AGAGGTCTC AAGAAGACCT CGGTAOGATT      300
   CTCCTCGATC CCAGGCCAT CGGCTTGGAT GAGATTGAGG TAATAGCCTC TGTGGTGCCC      360
   AAAGACCGTA TGACGCCGCT ACCCGTTTCC AATATCCGTG TGGCTGATAT TCAGGCAGCA      420
   TCGTTGAATG TCGAATTTC CGAAGCTGTT AATCCACTC CTTTACCTA TACGACAAAA      480
   GGAAGCGGAG GTTTCGGTGA TGGTCGTACC AATGTGCGTG GATTCCGAC TTACAACTTC      540
   GGTGTACTCA TCAACGGAGT TCCTGTCAAT GGTATGGAAG ACGGGAAAGT ATATTGGAGC      600
   AATTGGAGTG GTCTGATGAA TCAAGCCAGT ACCATTGAGA TTCAGCGCGG ACTCGGAGCC      660
   TCCAAGCTCG GTATCAGCTC GGTAGGTGGT ACGATGAACA TTATCAGGAA GACTACGGAC      720
   GCCAACACCG GAGGTTCCGC TTATGTCCGT ATGGGTAATG ATGGATTGCA CAAAGAATCG      780
   TTCTCCATTT CTACGGGTAT GAACGACGGT TGGGCTATCA CCATTGCAGG CTCGCATATG      840
   ACGGGTCTGG GTTATGTGAA GGGGCTGAAG GGACGTGCA TCTCTTACTT CTTCAACGTT      900
   TCGAAGAAGT TCAATGAACG TCATACCCTC TCTCTTACCG GATTCCGTGC ACCCAATGG      960
   CACAACCAAC GTTCTCCAA ATATTCTGTA GCGGACTATG ACAAATACGG CATCCGTCAC      1020
   AATCAATCCT TCGGCTATCT GCGAGGCGAA CTGACTCCTA CGGCTTATGC TTACAATACG      1080
   TACCACAAGC CCCAGTTCTC GCTGAACCA CTCTGGAAGA TGGATGAAA TACCTCTCTT      1140
   TATACCGCAN CCTACGCATC TTTGGCTACC GGTGGAGGTC GTCGCGCTTA TGGAAAGAAC      1200
   AGTAAGTGGG TATTGATCAA CTACAACACC GGACAACCT ATGAACAAAC AAAGGTGACT      1260
   CCCGATGGAC TTATCGACTA CGATGCGSTA CTGGCTGCCA ATGCTGCGCC GAGCAATGGC      1320
   TCGGAAGCAA TTTTGGCCCT TGGCTCCAAC TCTCACAAGT GGTTCGGTCT ACTCTCTTCA      1380
   TTCAAGAACA AACTTAATAG TTCGCTGACT TTGACAGCCG GATACGATGG GCGTTACTAC      1440
   CGTGGCGACC ACTATGACAA GATCACCGAT CTGCTCGGCG GTAGCTACTA CATAGAGGAT      1500
   CCCAAGACAA AGCTCGCATA CCATGCGGAA GGTGAGCAAC TGAAGTGGG TGACATTGTA      1560
   AATCGGGACT ACACAGGCGA AATCATGTGG CACGCGCTCT TCGCACAGAT GGAGCATTCG      1620
   TCCGAATGGA TCGATGCATT CGTATCAGGA TCTATCAACT ACGAATATA CCGCAATCAC      1680
   AACTATGGCG GTAGCAAGTC CACCGGCTAC CTGCCCGGCG TATGCGCGTG GAAAAGCTTC      1740
   CTTCGGTGA GTGGCAAGGC AGTCTGAGC TACAAGTTCG CACAGGGACA CAATGTATTG      1800
   GCCAATGGCG GTTCTCTTAC ACGTGACCA CTCTTTGGCA ATATCTATGC TGGGGGGGCT      1860
   ATCATTCCCA ATGACAAAGC CAATATGGAA AAGGTGCTTA CAGGAGAGGT CGGCTATGGA      1920
   TTCAGGAATC ACAAACCTT CGAGTTCAAT ATCAACGGAT ACTATACGAA GTGGATGGAT      1980
   CGCGTGACCT CGAAGAGAT CCGAAACGAG TATGTTTATC TCAATGGCGT TGATGCTGTT      2040
   CACTGTGGGG TAGAGGCTGA GGTGAGCTAT CGTCTATTG CTCAGATCGA CCTTCGCGGT      2100
   GCCGGCAATG AGACAGGGCA GGAATAAACC TATATCAAGG GTTACACTTC TTACGACGAA      2160
   GCACAGATGA CCGCTGCTGT ATCGGCAGAC ATAGAGCTGT TCAAGGGTTT CCATGTGATA      2220
   GGTAAGTACA ACTTCCTTGG CAAGAATCTAT GCAGGATTCA ACCCGGCAAC CGGTAATGCA      2280
   CAGCAGTACG AAGCGGATGG CAAAGAAATC GTGGAATCAT GGAAGTTGCC CGATGTAGGT      2340
   CTGTTGATC TGTCTGCATC CTACAATTTT AAGCTTGGTT CACTCAGCAC CACATTCTAT      2400
   TTCAACATG ACAAAGTAGC CGACAAGCGA TATGTGAGCG ATGCCGACGA CAATATCATC      2460
   GGTAAAGAAC ACGATGAGGC TTCGGCTCTC GTATGGTACG GTTTCGGCCG CACTTGGTCT      2520
   ACCGGTATTC GTGTAACCTT C
2601

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- 65 (2) INFORMATION FOR SEQ ID NO:192
(1) SEQUENCE CHARACTERISTICS:
70 (A) LENGTH: 1293 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
75 (ii) MOLECULE TYPE: DNA (genomic)

130 / 490

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
10 (B) LOCATION 1...1293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192

15	ATGAAGTTT CAATCCGCT TTTCTCTGC ATCATCTTC TCCTCTCTGC ATTTATCCTG	60
	CCTGCTCTCG GACAAAAATC CAAGCAGGTA CAGCGACTTG AGAAGCAACG TAAGGAGGCC	120
	CTCAAAGCCA TCGAAAAAAC CGATCGCGAA CTACGAAATA CCAAGAAAGA CAAGCAAGAC	180
	AAACAAAAGC ATCTCAACCT CCTGAACAAG CAGGTTGCTC AACGCAAGCA GATGGTACAA	240
	CTCTTGAGCA ATGAGGTCAA AGAGTTGCAA TCCGACATTG ATTCCATGAC GGGTGTATGT	300
20	CATCAGCTCT CTGTAGAAGA GAAAGCCCGA TCCGATGAAT ATGCCAAGC TCTACAGTCT	360
	ATGCAAAAGC GGAAACGCTC GTTGGATCGC ATCCTTTTCA TTTCTCTGCG CAAGAGCTTT	420
	GACGAAGGCA TGCGACGGAT GCGTTTCTTG GAACAATACG CTTCTGCATA CAAGCTGGCA	480
	TCTGTCCGGC TGCGCGATAC ACGTAGCAAG TTGGAGACTG AACGTGCGAC TGTAGAAGAC	540
	GCCAAAAAGG AGAAAGGACA TCTCTTAGTC ATCAGAGAAG AGGAAAAAAA GAAACTCGAA	600
25	GGACAGCAG CCGAGCAACG TCGGCAGGTG CAGGCTTTGG GAGCCAAACA AAAAGACTTG	660
	GAAGCGCAGC TGCGAAAGCA GAAAAAGCAA GCCGAAGCTC TGAACAGAAA GATCGAGAAA	720
	CASATTGCCA AGGAAATAGA ACCTGCCGAA CGTCGTGCTC GAGAAGAACG TGAACGGTTG	780
	GCACGCGAAG CCAAGCCCAA GGGTAAGCGG GTTCTTGCGG AACCGSAACG GAAGCGGAG	840
	ACCAAAGGCG GCTATGCTAT GGATGCCCTC GAGCGTGCTC TCTCGGGCAG CTTTGACAG	900
30	AACAAAGGTC GCCTGCCCGG CCCGTTTCGC GGCAGATACC GAATCGTAAG CGACTTTGGC	960
	GTAGCAACAG ACAGTGAGCT GAAAAAGTA CAAGTTAATA ATGGAGGTAT CGACATCGCT	1020
	ATACCGGTTT ATAATTGCGC CGTAATGGTT CGTCACGGA ACTATATCAC GGTATTGCG	1080
	AATCTGAGCA AAGTGTATGT AAATTCGGGC ACTCGTGTTA AAACGGGTCA GGCTCTTGGT	1140
	CGTGCCCTATA CGGATCCTTC CAACAACCG ACCATTATTC ACTTCGAAAT CTGGAAAGAA	1200
35	CGCAGCAAAC AAAACCCAAAG ACTATGGTTA CGA	1260
		1293

(2) INFORMATION FOR SEQ ID NO:193

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 999 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
45 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

50 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

55 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193

60	ATGAAAAAGT ATTTGTTATA TGCCTCGTTG CTAACGAGTG TTTTGCTCTT TTCTGTTCA	60
	AAGAACAATC CTAACGAGCC GGTGGAAGAC AGATCCATCG AAATTTCTAT AAGGAGTAGT	120
	GATTTACCCA AACCGGTGA GGCAGTAGCG TATGAAAGGA ATCAAGGAAG TGCTGCCGAA	180
65	AGGCTCATTA CCAATCTTTA CCTCTTGTTG TTCGATCAGT CAGGGGCGAA TCCGGCGAAA	240
	TACTATATTA CCGGTAACAC TTTCAACCGA GGGACCTGGC TTCTGACGA TATGAAGTG	300
	AAGTTGGATA TGACACAATC CGAGGCCGGA GAGCGCAAG TATATGTCTG AGCCAATGTT	360
	GATAATGCGG TTAACACGGC TCTTGATGCT GTCGTAACG AAAGCGATTG GCAGACTGTA	420
	AAGAGGACGA CTGCAATGCC GTGGTCGACC GATATAGCCT CTCCTTTCCT GATGTCCGGA	480
70	AACAAGACAC ACGACTTCTT GGCCAATCGT CTTTGGACA ATGTGCCCTT TGTGCGTGCC	540
	ATTGCCAAGG TGGAGCTGAA TATCTCGCTG AGTGAGAAAT TTCAGATTGT GCCGATAATT	600
	GTCATCGTGA GTTTGAGTGA GTTCAAGTTC AGATACGTA ACITCGACAA GGAGACCTAC	660
	GTAGTGAGGC CAACGACCAA GCCGGACAAT CTCATTAGTT CTGCTAATGG TGTGCGCTT	720
	CAGATTACAG ATTGAGCTGT ATGGGGTGCT TCCTTAAATA CTTCTCTGCG TCCGGATGCG	780
75	GGCACAGGTT ATACATTGSA TGCAAATGGC AAGGTAACGG CACTACGGAT TGTACCTAT	840
	CTGAATGAGC GCGATAGCAA ACGGGCTACG GTAGAGGTCT CATTGCTCTG TGTGGATGAT	900

GGCACCCTTC CTCCTCCGGA ATTCGGTCCG GAGCTTTATC GTTTGCCTTT GCCGGACVAG 960
ATCCTGCGCA ATCATTGGTA CAAGTATGAA GTCGAGATT 999

5 (2) INFORMATION FOR SEQ ID NO:194

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 945 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

10

(ii) MOLECULE TYPE: DNA (genomic)

15

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

20

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...945

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194

ATGATCAGAA CGATACTTTC ACGATATGTA TCCTCGAACT TTTGGAGTCG GGGAGCTACC 60
TTTTTTTTCA CGATTITCCC GGCCITCCTC CTCGCCGCTA CTCCTTTGCC GGCTTGTGGA 120
GGGGTACTG CTCAGGCTC CGATCGTACG CTGGCTGTGA CCATCGAGCC ACAGAAATAC 180
TTCATCGAST CCATTGCCGA TAAGTCGGTG CAGGTGGTGG CATTGGTACC GGCCGGCAGC 240
AATCCGGAGG AATACGACCC TTCGCCCTACC GTGATGAAGC GTTTGTCCGA AGCAGATGCC 300
TACTTCTATA TAGGAGGACT GGGGTTCGAG CAAAGAAATC TCGCTGCCAT TCGGGACAAT 360
AACCCTAAGC TCCCTCTTTT CGAAATGGGC AAAGCCTTGG CGGATGCCCG AAGTGCAGAT 420
CTCCACGGCT CCTGCACAGA TCATTCTCAT ACAGACCTGC ATGCCCATGA TCCGCACTAT 480
TGGAGCAGTG TGGTAGGGGC AAAGGCATC AGTCGTGCTG CATACGAGCG GCTTGTGGAG 540
CTTTATCCGA ACGAGAAAGA CAAATGGGAC AAAGGGCAGC ACCGTCTCAA CGGACGTATC 600
GACAGCGTGA AGAGACTCGT CGATACCATG TTTGCCAATG GCARAGCAGA CAAAGCCTTC 660
GTCATATATC ACCCATCGCT CAGCTTTTTC GCCCAAGAGT TCGGCCTGCG GCAGATCGTC 720
ATAGAGGAAG ATGGGAAAGA GCCTACGGCT GCCCACCTTC GTCGTGTGAT CGATCAGGCA 780
CGTGCCGATG GTGTGAGAAAT CGTATTTATC CAACCGAAT TTGAACGCG TCAGGCGGAG 840
GACATCGCAC GCGAGATCGG TGCTCGTCCG GTAAGGATCA ATCCTCTGCG CAGCTCGTGG 900
GAGGAGGAAA TTTTACATAT TGCTCGCGCT TTGGCTCATG AACGG 945

45

(2) INFORMATION FOR SEQ ID NO:195

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2544 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

50

(ii) MOLECULE TYPE: DNA (genomic)

55

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

60

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...2544

65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195

ATGATCGGAA AAAAAATCTT TTTTATCTTG CTGGCGCTCA TTGGGTTTCA TGGGCTGAAC 60
GCAGCGACAG AACTGAGTT CAAGTACCCG ACCGATGCCA ATATCATCGG TCACGTCAAA 120
GACAGCAAGA CGGGTGAACA CCTTGTGGT ATCACTATTG CTATCAAAGG CACTACCTTT 180
GGTACATCTA CAGATGCAAC CGGGCACTAC TATCTTCTTA ACTTGGGTCC GGGTGAGATC 240
ACTTTGATTA TGCGTGGCAT GGGCTATAAG AGCCAGGAGC GCGTAGTCCG CSTAGAAAAG 300
GACAGACTA TCGAGGTGAA TTTGGAAGCA GAAGAGGATG CCATCAATCT GGACGAAGTC 360
GTGATTTCGG CCAACCGCGA ACTGACGCTT CGCGCTCTTG CTCCTACTCT GTTAAATGTA 420

75

	TTGAACGAAA	AAGTCTTCTC	GCAAGTCAAT	GCTTCTAACC	TGGCTCAAGG	CTTGTCATTG	480
	CAGCCGGGAC	TTCCGTGTAGA	GAACAACGTG	CAGAACTGTG	GTTTCAATCA	AGTTCGTATC	540
	AATGGACTGG	ATGGTGGTTA	TGCACAGATC	CTCATCGACA	GCCGTCCCAT	CATGAGTGCC	600
5	CTTGCCGGTG	TTTACGGTCT	GGAGCAGATC	CCTGCCAATA	TCATCGAAGC	TGTGGAGGTA	660
	GTACGTGGTG	GAGGATCGGC	CTTGACGGT	TCTTCTGCTA	TTGCCGGAGT	GGTGAATATC	720
	ATCACCAAGG	AACCTTCTCA	CAATTCTTTC	ACATTCAATG	AACTCTGTAG	CTTTACCGGT	780
	TTACGCAAGC	TGGATAACAA	CACGAACTTC	AATGCCTCCA	TCGTACGCGA	TGACAACCGT	840
	GCCGGTGCCA	TGGTATTGCG	GCAGGCTCGT	TACCGCAACC	ATTGGGATGC	TAACAATGAC	900
10	GGTTATTCCG	AATTGGGTAA	AATAGATGCC	CGCTCGCTGG	GAGCGCATTC	TTATTTGCGC	960
	TTGAGCGACT	ACAGCAAATT	GACGGGAGAG	TTTCACACGA	TCAGTGAATT	CCGCCGTGGT	1020
	GGCGATCGTA	TGGATTGGCC	TCCTCACGTA	GTGGGTGTAG	CTGAACAAAC	TGACCATAGC	1080
	GTATTTAGCG	GAACCTTGAA	ATACGATCTC	TTCTCTTCCA	ACTATAAACA	CCACTTCCAG	1140
	GCTTATACTT	CCGGACAGAT	CGTAAATCGC	AAGAGCTATT	ACGGAGGTAT	CGGAGAGATT	1200
15	GACGTCAATG	GCCACCCCGG	TGGTACGGAA	GGCTACCCCTA	TCCCTCAAGA	TCAATACGGC	1260
	AATAATTATG	SCGTGACCAA	AGGCAAGACA	TATATGGGCG	GTATCCAGTA	CAGCTACGAC	1320
	TTGGACAAAT	TCCTCCTCAT	GCCTTCGCAA	CTTTTGTTCG	GAGCCGAATA	TACGCGTAT	1380
	GAATCAATG	ACGTGATGCC	CATCCTTTCA	TGGCAGACCG	GCGAGGATGC	CAATGGGAAT	1440
	ACCATTCCCG	TCTATCCCGA	ATTGGATCAG	AAATATCAACA	ACTACAGCCT	ATTCCGGTCAG	1500
20	AACGAATGGA	AAAATGACAG	ATGGAGCATC	CTTGTTGGCG	CTCGCTTGGG	CAAGCATAGC	1560
	GAAGTCAAGG	ATATGATTCT	GAGTCCCTCG	ACCACACTGC	GTTTCAACGT	GAATCCGGAC	1620
	ATCAACCTGC	GCGCTACATA	TGCAAAAGGG	TTCCGCGCAC	CGCAGGTATT	CGATGAAGAC	1680
	TTGACAGTAG	GGGTGTAGG	CGGTGAGGCA	CAGAAAGTAT	TCAACGATCC	GAACCTCAAG	1740
	CCTGAAATTT	CTCATGCATT	CAGTTTGAGT	GCCGATATGT	ATCATCGTTT	CGGTAACTGC	1800
25	CAGACCAACT	TCCTTGTGGA	AGGCTTCTAT	ACTCGTTTGC	TGGATGTATT	CACCAACGAG	1860
	GAGCAGCCTG	ATCAGACGGA	TGGCATCAAA	CGCTACACGC	GTATCAACGG	TAGCGGAGCC	1920
	AAAGTATTCC	GTCTCAATCT	GGAAGGTAAG	GTGCGATACA	AGTCCCTCCA	GCTCCAAGCC	1980
	GSTCTTACCC	TGGCCAGCAA	CAAATACGAC	GAAGCACAGG	AGTGGGGTCT	GAATACGGTG	2040
	AAAGACACCA	ACGGAGCTTT	TGTTACCGAG	GCCAATGCAA	ATGGACAACA	GGAATACAAG	2100
30	ALCGAATCCA	TGACGGATAC	GCAGATCACC	CGTACCCCCA	GCGTATACGG	TTATTTTACT	2160
	TTGGCCTTCA	ATCCTGCTCA	CTCATGGAAC	ATAGCCCTTA	CGGGAGCATA	TACCGGTCAG	2220
	ATGTATGTAC	CCCACGCTAT	CGAATATGGT	GTGAAGTCTG	CCGAACCTGGA	TATTATGCAG	2280
	AACAATCCTG	AGATTACCGA	CGAAACCGGA	AAGGCTCCCC	GTATTGTATG	GCTGAAGAG	2340
	ACACCTGCAT	TCTTCGATTT	GGGCTTGAAA	GTGGGTATG	ACTTCCACGT	ATTCCAGGCT	2400
35	ACTGAGGTTG	AACTCTATGT	AGGTATGAAC	AATATCTTCA	ACTCTTTCCA	GAAGGACTTC	2460
	GATCGTGGAG	CTGCACGTGA	CAGCGGATAT	ATCTATGGTC	CTACGCAGCC	GCGTACAGGC	2520
	TACATGGGCT	TGGTAGTGAA	GTTC				2544

(2) INFORMATION FOR SEQ ID NO:196

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 606 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196

	ATGACAGTAA	AGCGGCGCAGT	GCGAATAGCA	CTTCTCAGCG	TGATAGGCAT	TCTTTTTC	60
	TCACCTTCTC	TTGTTCCGGG	GCAAAAGTCTT	TTCAGCACCG	AACATGTCTT	GCAACTATAC	120
	AACAAGATAC	TCTATGGAGA	GTCCGCGCGG	GATACCGTCG	CAGAGAAAAC	GGCAGGTGAG	180
65	TCGGCATTTT	CTTTTATAGA	CAAACTCATC	AATCTCGGCC	GCACTTTTCT	CGGCAAAACA	240
	TATCGCTATC	GCGGTCCCTT	CCCATGGCGG	ATGGACTGCT	CGGGCTATGT	GTCTTACCTC	300
	TACTCAAAAT	TGCACATCAA	ACTCCACAGT	GGTGGCGGAG	CACAGAGCCA	ATATACGAAT	360
	CCTATCGAGC	GCGAGGATGT	TGCTCCGGGC	GACCTCCTTT	TTTTCAAAGG	CCGCAATGCA	420
70	CGCAGCAACC	GTATCGGGCA	TGTAGCTTTG	GTCGTATCTG	TGGATGAAGA	TGATATTACC	480
	ATGATGCACA	GCCGCAATTC	GCGAGCGATC	GTATCGAAAA	AACTCAATCG	CAGTGCATAC	540
	TTCTCCCGTC	GCTTGGTGGG	CTATGGCAGG	GTACCCGGAG	CCAAGAGAGT	GATCCACGGA	600
	AAAAAT						606

(2) INFORMATION FOR SEQ ID NO:197

133 / 490

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1365 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197

ATGAACCGGA	CAATCCTCCT	GACGGCACTG	ACCGTCCTAT	CTTCGCTCTC	CTTGCTTCGT	60
GCACAAAATG	AATCCGAAGC	ATCAACCAAT	CCGATGTCAG	GCCTCTCCCT	GGAAGACTGT	120
ATCCGGATAG	CCAAGGAGCG	CAACCTGAAT	CTGCGCAGAC	AGGAGATCGA	ACAAAGAAAC	180
CGAATCATTA	GTCTCGATGC	AGCAACGACAC	AGTTTCCTGC	CCTCGGTCAA	TGCAGGCATC	240
GGACACAAC	ATAGCTTCGG	ACGTTTCGAA	GACAAAACGG	GAGTAACCGT	AGATCGCTCC	300
TCGATGAATA	CCAATCTCAG	CATCGGAGCT	TCGGTGGGAA	TATTCAGCGG	CACACGTCGT	360
CTGCAGGACC	TCAAGCAGCA	AAAGTACAAC	GTGGAGGATG	GTATAGCCCG	ACTTCAAAAA	420
GCCTCGTGAAG	ACCTCAGCCT	GCAAAATCGCG	GCCTCTCTATA	TCAATTTCGT	CTTCCGTCAG	480
GAAATGACTC	GTACGGCAGA	AACACAGTTG	GCACTGATTC	GCGAGCAACG	CAATCGCACG	540
GCCGAAATGG	TTCGCGTAGG	TAAATGGGCA	GAGGGTAAGG	TCCTCGACAT	AAATGCCCCAG	600
ATGGCCCAAG	ACGAACAAC	TCTCGTACAA	TATCGTTCCG	AGGAGGAGCT	GGCTCGTCTG	660
GACTTGGGGC	AAGCCCTCGA	ACTGGAGCAC	CCCCAAAGCA	TTGCAGTCAA	GGCTCCCGAC	720
ACAGACGTTT	TCGTAGCAGA	AAGGTTGGGA	TCTCTCCTTG	CTCCCGAAGA	GATCTATCGC	780
ACGGCTCTCG	GCTTGAAACC	GGCACTGCAT	TCCAGCGAGC	TGCAAAATAGC	TTCCGGCAGC	840
GAAGGTCTGG	CCTCGGCTCG	TGCGGCATAC	TTCCCGACGC	TCAGCCTCTC	TGCCGGATAC	900
AGCAACGGTT	ACTTCCGCGA	CCTCGGCAAG	GAGTATGCGG	CCATCAACCC	CTCCTTCTCC	960
GAACAGTGA	AGAACAACGG	CAGCTACAGT	ATCGGACTCT	CTTTGAATAT	CCCCATCTTC	1020
TCTGCCATGC	AAACGCAAGA	TCGCGTTCCG	AGCAGTCGCC	TGCAAAATAGC	CTCAAGCGAG	1080
CTTCGACTCC	TGCAAGAGAA	AAAAGCCCTC	TATAAAGAGA	TCAGGCAAGC	ATACAGCAAT	1140
GCCGTGGGCG	CGGATAAGGC	CATCGCAGCA	GCCGAAAACA	GCAAGGCCGC	TACGCTCAAG	1200
GCATACGAAT	ACGCTCGCGA	CAGCTTCGAG	GCAAGGCCGT	TGTCTGCCCTA	CGAATATGCC	1260
GAGGCCAAAA	CAAAATACGC	CCTCAGCCAA	GTGGAAGAAC	TTCTGTGCCAA	GTATGACTTC	1320
ATATACAAAG	CCAAAGTTT	GGATTCTAT	CAGGCAAG	ACTTC		1365

(2) INFORMATION FOR SEQ ID NO:198

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1332 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1332

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198

ATGCGTTTCC	AACATTATCT	CATCTGTACG	GCTGCCGTAG	CGGCTTTGGC	TGCGAATCCC	60
CTTACGGGCC	AATCGAATAT	GACCTCGAA	GAGTGCATAG	ACTATGCACG	CCGGCAGCT	120
TCGGCCGTGG	CGCTGTCCCG	TGCGGAAC	GAGCAGTCCA	AGGCCGATTA	CCTTCAGGCC	180
GTCCGCAATT	TTCTGCCCGG	TGTATCGGCC	GGAACCGGTG	CTTCGTGGAA	TTTCGGACGC	240
GGATTGGATG	CCGAGACGAA	TACCTACACC	GACATCAACA	GCTTCAACAA	TTCTGACAGC	300

	ATACATGCCA	CGATGACCC	TTTCGACGGT	TTGCAGAGTG	TCTATCGACT	GCGSATGGCG	360
	CATGCCACGG	GGGAGGCTTC	GCGCCTCTCC	GTTCGCGAGC	AGCAGGAGCT	GGCAGCTCTC	420
	GGCACCACGG	AGGCCTACTA	CGAOCCTCGT	TATGCGCGCC	AAATGCAAGA	GCTGGCCATG	480
5	CAGAAGTACG	AGGAGAGCAG	CCGCCTCCAC	CGGCAGACGG	CTCGAATGGA	AGAGCTGGGG	540
	ATGAAGATGC	GTCCCGATGT	CCTCGAGATG	CAGTCGCGAA	TGGCCGGTGA	CCGTTTGGCC	600
	CTGACTCAAG	CGGACATCA	GTGCATCATC	GCTCTGATCC	GGCTCAAAGA	AAAAATGAAC	660
	TTCCCATCG	ATGACGAAC	CGTCGTAGAC	GATATGCCGG	CTGACAGTCT	CTCCGCCGAC	720
	ATGGCCGAAT	CGGACAGCTC	GGCCGGCGTC	TTCGCCCGTG	CTGCCATCA	TCATCCCGTC	780
10	CTCCTCCGTG	CCAAACTCGA	CGAGCAGGCT	GCCACCGACC	GTTCGCGAGC	CGCGCGAGGT	840
	GCATTCTG	CGAGTGTGTC	GGTATCCGGA	GGATGGAACA	CGGGATTCTC	ACCGTTTGTG	900
	AATGGATCGG	ACTATACGCC	CTTCAGCGAG	CAGTTTCGGA	ACCGTCGGGG	GGAAATACGTC	960
	AGCTGGAATC	TGAGTATCCC	CATCTTTTCG	GGATPCAGCC	TTGTGAGCCA	TCTGCGTCAG	1020
	GCGCGTGCCG	AACGCGAGGG	GGCAATCGTC	CGACGGGGCG	AAGCGGAGCG	CAGGCTCTAC	1080
15	AGCGAGATCG	CCCAAGCCAT	GGCCGACCGG	GATGCCGCTC	TGGCTTCCCTA	CCGCCAGGCG	1140
	AAGGAGCATA	CGGACGCCAT	GCAAAACCGT	TACGAAGCCG	TCTTGCAGCG	TTATGAGGAG	1200
	GGCCTGAATA	CGGCCATCGA	CCTGACCACT	CAGGCCAATC	GGCTCCTGGA	TGCCCGTGTG	1260
	CAGCGACTGA	GAGCGGCCAT	GACCTACCGG	CTCAAATGCA	AACTCATAGC	CTATTACGGC	1320
	TGCCTTTCGG	AC					1332
20	(2) INFORMATION FOR SEQ ID NO:199						
	(i) SEQUENCE CHARACTERISTICS:						
25	(A) LENGTH: 2820 base pairs						
	(B) TYPE: nucleic acid						
	(C) STRANDEDNESS: double						
	(D) TOPOLOGY: circular						
30	(ii) MOLECULE TYPE: DNA (genomic)						
	(iii) HYPOTHETICAL: NO						
	(iv) AMPLI-SENSE: NO						
35	(vi) ORIGINAL SOURCE:						
	(A) ORGANISM: PORYPHYROMONAS GINGIVALIS						
	(ix) FEATURE:						
40	(A) NAME/KEY: misc feature						
	(B) LOCATION 1...2820						
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199						
45	ATGAACAAAT	TTTACAAATC	ACTTTTGCAG	TCAGGACTGG	CTGCCCTCGT	GTGATGGCA	60
	ACTGCACTGA	CGGCTTCTGC	ACACATTTTCG	TTCCGAGGGG	AACCCCTTGAG	TTTCTCTTCA	120
	AGATCCGCGG	GAACGCATTTC	ATTTCGACGAT	GCAATGACTA	TCCGCCTTAC	TCCGGATTTC	180
	AATCCCGAAG	ACCTGATCGC	ACAGAGCCGT	TGGCAATCGC	AAAGAGATGG	CCGCCCGCTC	240
	CGGATAGGAC	AAGTAATACC	GGTGGATGTG	GACTTTGCAT	CCAAGGCTTC	GCACATCTCT	300
50	TCCATCGGAG	ACGTAGATGT	ATATCCGCTG	CAATTCAGT	TGGAAGGAGC	CAAAGCCATT	360
	ACGCTTTATT	ACGATGCATT	CAATATCCG	GAGGCGCGAC	GCCTCTATAT	CTATACCCCC	420
	GACCATGAAA	TTGTGTTGGG	AGCATATACG	AACGCCACTC	ATCGCCGCAA	CGGAGCTTTT	480
	GCCACAGAGC	CGGTACCGGG	GAGTGAGCTT	ATTATGGATT	ATGAAGTGTC	TCCGCGAGGG	540
	ACTTTGCCCT	ACATCAAGAT	CTCCGCTGCG	GGTTATATAT	TCGACAAAGT	CGGCGGACGC	600
55	CCCGTACCGG	ATAACCAITA	CGGGATCCGT	GAGGACGATT	CCGATTCCGA	TTGCCGATC	660
	AACATCAATT	GTCCCTGAAGG	TGCAGACTGG	CAGGCAGAGA	AGAACCGTGT	GGTGCAAAATG	720
	ATCATGGTAA	AAGGACAGTA	TATCTCAATG	TGCTCAGGCA	ACCTGCTCAA	TAATACGAAA	780
	GGAGACTTTA	CTCCGCTGAT	CATTCTTGCC	GGACACTGTG	CTTCCATAAC	AAACPAATTTC	840
	GGTGTAAAGC	AATCCGAGTT	GGATAAGTGG	ATCTTCACTT	TCCACTATGA	MAAAAGAGGA	900
60	TGCAGCAATG	GTACATTGGC	CATCTTCCGT	CGCAACAGTA	TCATCGGAGC	TTCCATGAAG	960
	GCTTTCTCTC	CGATCAAAGG	TAAATCCGAT	GGTCTCTTGC	TGCAACTCAA	CGATGAAGTC	1020
	CCTCTGCGCT	ATCGTGTCTA	TTACAATGGA	TGGGACAGTA	CGCCCGATAT	TCCCTCGAGC	1080
	GGTGCCGGTA	TTATCATCC	GGCCGGAGAT	GCCATGAAGA	TTTCCATCCT	AAAGAAGACT	1140
	CCGGCTCTGA	ATACATGSGAT	CTCCTCCAAT	GGTTCCGGAG	GGACTGACGA	TCATCTCTAT	1200
65	TTCAAAATAG	ATCAAGGTGG	TACGGAAGGA	GGATCGTCCG	GTTCCTCTCT	CTTCAATCAG	1260
	AATAAGCAG	TGSTCCGGCAC	ACTGACCGGA	GGTGCCCGCA	ATTGTGGCGG	GACGGAGTTC	1320
	TACGGCAGAG	TGAACAGTCA	TTGGAACGAG	TATGCATCCG	ATGGCAATAC	GAGCCGATG	1380
	GACATCTATC	TGGATCCCCA	AAACAATGGC	CAGACGACCA	TCCTCAACGG	AACGTATCGT	1440
	GACGGTTATA	AGCCTTTGCC	CTCTGTGCC	CGGCTATTGT	TGCAGTCTAC	AGGCGATCAG	1500
70	GTGCAATTGA	ATTGGACGGC	TGTTCTCTGC	GATCAATATC	CATCATCTTA	TCAGGTCGAA	1560
	TACCAATAT	TCCGAATGG	AAAGGAAATA	GCTACGACAA	AGGAGTTGTC	CTATTCCGAT	1620
	GCCATCGACG	AAAGTATTAT	CGGTAGCGGT	ATCATTGCGAT	ACGAAGTAAG	CGCACGCTTC	1680
	ATTATCCCT	CGCGTGTGGA	TGGAGTGGAA	TCTTATAAGG	ATACGGACAA	GACTTCTGCC	1740
	GACCTTGCCA	TAGGAGACAT	TCAGACCAAG	CTGAAGCCCG	ACGTAAACCC	TCTCCCGGGA	1800
75	GGAGGAGTAT	CATTAGCTG	GAAAGTTCCT	TTCTTAAGCC	AGTTGGTTTC	CCGATTCCGA	1860
	GAAAGCCCCA	ATCCTGTGTT	CAAAACCTTT	GAAGTGCCCT	ATGTTTCTGC	CGCAGCCGCA	1920

135/ 490

	CAAAACCCCA	ATCCTCCCGT	TGGCGTAGTC	ATTGCAGACA	AGTTTATGGC	CGGTACATAT	1980
	CCCGAAAAGG	CTGCTATCGC	TGCCGTTTAT	GTAATGCCAT	CCGCTCCGGA	CTCTACTTTC	2040
	CACCTCTTCC	TCAAGAGCAA	CACAAACAGA	AGATTGCAGA	AGGTGACAAC	TCCCTCCGAT	2100
	TGGCAGGCCG	GAACATGGTT	GAGGATCAAT	TTGGATAAGC	CGTTCCCGGT	GAATAATGAC	2160
5	CATATGCTTT	TGCGCGGTAT	CAGAAATGCT	AATAAGTACA	AGCTCAATCG	TGCTATCCGT	2220
	TATGTAAGAA	ATCCGGATAA	CCTTTTCTCC	ATTACCGGTA	AGAAGATTTC	ATATAACAAC	2280
	GGAGTCTCTT	TCGAAGGCTA	CGGAATACCC	TCGCTCTTGG	GCTATATGGC	TATCAAATAT	2340
	CTGCTGGTAA	ATACCGATGC	TCCGAAGATC	GATATGTGCG	TTGTACAGGA	GCCTTATGCT	2400
	AAGGGAACGA	ATGTGGCTCC	ATTCCCGGAA	TTGGTCCGCA	TATATGTCTA	T'AAGAACGGA	2460
10	ACATTTATCG	GCACACAGGA	TCCATCCGTC	ACAACTTATT	CGGTTTCAGA	CGGAACAGAG	2520
	AGCGATGAAT	ACGAAATAAA	ACTGGTATAT	AAGGGATCGG	GCATTTCCGA	TGGCGTTGCT	2580
	CAGATTGAGA	ATAACAATGC	TGTCGTTGCA	TATCCGTCCT	TTGTAACAGA	TCGTTTCAGC	2640
	ATTAAGAACG	CTCATATGGT	TCACGCTGCC	GCCCTCTACT	CATTGGATGG	CAAGCAGGTT	2700
	CGTTCCTGGA	ACAACCTCCG	CAATGGCGTG	ACATTTCAGT	TTCAAGGACT	TACGGCCGGT	2760
15	ACTTATATGC	TCGTTATGCA	GACGGCAAAC	GGCCCTGTGA	GCCAAAAGAT	CGTGAAGCAG	2820

(2) INFORMATION FOR SEQ ID NO:200

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2010 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION: 1...2010
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:200

	ATGAAATATC	TTATCAGACT	CTTCTTATCA	TTGATGTTAC	TCTCTCTCTG	GACGGGCTGT	60
	ACACACGAGG	AGCTCTCTAT	TTGCGATGGC	GAGAATACGC	TTGTTTACG	CGTAGAGACC	120
	GGTAAAGCCC	CAAATGCTCG	TGCCACAGAA	CCCGGTCAAG	GCATATACAA	TGAGAATAAA	180
	GTACGCTCCA	TTTCTGTGCT	CTTCTATTTA	GAGGGACAAC	TTGTTGGCA	GGTGAAGTCT	240
45	ACAGACTATC	AAATCCATGA	AGGGGCTAT	ATCATTCCGG	TCAAAGAGCA	AATGOGACCA	300
	CTATTCAATG	GCAACAACAA	CTTCAGATC	TATGTAGTGG	CCAATCTCGA	TTTCAATGCT	360
	CCGGCCACAG	AAGCTGGGCT	TTCTCAATTT	GTGGTAGAGA	AATCTATTGA	AGTCTCTTCT	420
	ACGACAGCCC	CTGCCGATTT	CGTAATGCTT	GCATATGGCA	ATAAGCAGAT	CAATATGGCT	480
	ACGACAGGAG	GGAAACTGTT	GGGGGATTAT	AAACTCAAAC	GAGTGGCAGC	AAAGATTGCG	540
50	ATGATAAAAC	CCACCATCAA	TGTGCAAGGA	TATGAAGTGG	TCGGAAATAT	ACAGGCAAAAG	600
	TTTCGCAATT	CGGTAACGAA	GGGGTTCCTT	ACCACAGAAG	CTCAAGAGAT	CCCAGCTGCT	660
	GCATCTCTATA	AGACATCGGA	ATATCTTGAT	ATTGCAGAGT	CGGCACCTGC	CAATTCTATC	720
	CATTTCTATT	CTTACTATAA	CAATATGGACA	CTCTCCACAC	CGGAGAAGCG	ACCGGAATTC	780
	TTTCATCATGG	TCAAATTCAA	AAAGACAGGA	CAGCCGGACA	ACACAGCCAA	ACCGTACTAC	840
55	TACAGAGTGC	CCCTCGAATC	TCAGGACAAT	CAGGTCAAGA	GCAATGTCTT	CTATAATCTG	900
	AATGTGA AAA	TCGAAATCTT	GGGTTCTTTA	CAAGAGCCGG	AAGCTGTTTC	TGTAACCGGC	960
	ACACTCGCAA	TAGAAGAATG	GATTCTCCAT	CAGGATGCAT	TCAATCTGCC	TGCCACCAAT	1020
	TACTTGATAG	TGGAACAGCA	CGAAATCTTC	ATGAATAAGG	TGAACACATA	CTCGGTGAAA	1080
	TATCAAACCT	CGCAGAAACC	AATCAGCAAT	AGCATACAGT	CAGTTACCTT	TAGCTACGTC	1140
60	TCTTCTGATG	GCACTCAGCA	CAATGATCTT	GTAGCAAGTA	GTAGCGACCA	GTATCCTACG	1200
	ATTACAAGCG	ATAATACAAG	CATCATAATC	ACTTCCAAGA	TACCGGTTAA	TAACGTACCA	1260
	AAGAAGATCG	TTTTTGAGGT	AATTAATGGG	GTAGCCGGTT	TGAAGAGAGC	TGTCACAGTA	1320
	CTCCAATATC	CTGCACAATT	TATTGTCAAT	ACACTTGGCA	CAGCATCGGC	ATGGAGACCA	1380
	GACGGATCTT	TGGCTCCGGG	GCTTAACAAT	AAAGCGATTT	ACCATGTGCT	AGTACTGGTT	1440
65	CCACCCGAGA	ATTTATTGTA	AGATGGGACA	CAGACAATCA	TCGGTTATCC	CCCCACTGAA	1500
	ACAATTTCTT	ITCATAAGAA	AGAGAACAAT	ACCTATCCGA	TAGTATGGTC	TGACACAAAT	1560
	ACGACAAAAC	AGGAACCTGA	GACATCAAGA	ATGATTTCAC	CTTCTTTTGA	GTTAGCCTCC	1620
	CAACTTGGGG	CTACTCTCCC	GATGCCCTAT	CTCGAGTATT	GGCCAGGGAC	ATCATATCTC	1680
	CTTGACTATT	CGGGAACTA	TAATAATAAG	AGATACGCCT	TGTTTAATTG	CGCTTTTAC	1740
70	TGGGAGAAAA	GAAAGTTAA	TAACGAAGAA	ATTAATTCG	ATGACTGGCG	TTTGCCGACA	1800
	GAAGCTGAGA	TCAAATTGAT	AGATAAGCTG	CAACATAATG	AGCAGAGTGC	TGTCCAAGCT	1860
	ATCATGACAG	GGAATTATTA	TTGGGATAGT	TACTCTGCAA	ATGGGTCTTA	TAAATGCAA	1920
	GGAGGAGGGG	GCCAAGGAAA	TTCTCCAAA	GCCTATGTTC	GTTGCGTGCG	GGATGTGAAA	1980
75	AAGCCGATTC	GTGACAACAA	GTCAGGTAAG				2010

(2) INFORMATION FOR SEQ ID NO:201

5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 3846 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: circular	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(iii) HYPOTHETICAL: NO	
15	(iv) ANTI-SENSE: NO	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PORYPHYROMONAS GINGIVALIS	
20	(ix) FEATURE:	
	(A) NAME/KEY: misc_feature	
	(B) LOCATION 1...3846	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201	
25	ATGCGAAAAA TTTTGAGCTT TTTGATGATG TGCTCTCTGC ATTTAGGTCT ACAATCTCAG 60	
	ACTTGGCATG GAGATCCGGA CTCAGTGGCA GCCCTACCTT CTATCGGTAT TCAAGAGTCA 120	
	AGTTGTACCC GAATCACGTT CGAGGTGTGT TTCCCGGAT TTTATAGTGT GGAACAAACGA 180	
	GAAGSCAACCC AAGTCTTTCA GCACATTTCC ATGCCGGGTT GTGGCTCCTT TGGGAATCTG 240	
30	GGCGAAGCTG AATTGCCTGT TTTGAAAAAG ATGATAGCCG TTCCGGAATT TTCAACAGCT 300	
	AACGTTGCTG TAAAAATCAA AGAGACGGAG ACAITCGACA ATTATAATAT CTATCCTAAT 360	
	CCTACCTATG TCGTAGAGGA GTTGCTCTGAG GGGGGGACTT ATCTGGTAGA GGCTTTCGGG 420	
	ATAAACAAATG ACTATTATAG CCAAAATGTA AGCCTCCCTT CTACTCACTA TGCTATTCT 480	
	CAAGACGGGT ATTTTCGCTC ACAAGATTY ATCGAAGTTA CCCTGTATCC TTTTCGATAC 540	
	AACCTGTCC GACAAGAAAT TCTATTTGCA AAAAAATCG AGGTACAAAT AACTTTCGAT 600	
35	AATCCTCAGC CACCTTTACA AAAAAACACC GGCATATTTA ACAGAGTAGC CTCCTCTGCA 660	
	TTTATTAATT ATGAAGCTGA TGGCAAATCG GCGATAGAAA ATGATATGGT GTTCAGTCTG 720	
	GGTACAACAA CGTACATAAG CGGAAATGTT GCCAGCAACC TCCCTCAGAA CTGTGACTAC 780	
	TTGGTTAATT ACGATGATAT GTTCAACGTA AATCAACAAC CACACGACGA AATCAACCGG 840	
40	CTGTGCGAAC ATAGAGCCCT CTACAACGSC TTTGATGTAG CTGCTGTAAG TATAAAGGAC 900	
	TTCAATTCCT CAGTTTACAA CCAAAGCAAT GCGAAGAGGA CTTTAGATGG CAACTGGGA 1020	
	TACGTGCTAC TGATCGGAAA ACCATTGAGC AAATATTGGG CTGACACTGA TAATACAAAA 1080	
	GTCCCAACCT CTTTATTCCA TAATGTCTCC TTAATTCCAA GTCATCCAAC TTTTGGTTCC 1140	
45	ATATGCGGCT CCGACTATTT TTTTAGTTGT GTTTCGCCCC TTGATACTGT CGGCGATTGG 1200	
	TTTATCGGTC GATTTAGCGT CACCAATGCT CATGAATTGC ACAATCTGAT TGAAGAGACT 1260	
	ATCAACAAAG AAATCTCATA TAATCCTATT GCACACAAAA ATATTCTTTA CGCAGAAGGG 1320	
	AAAGGCTGCG ATGCTCCAAT CTTACGTTTA TTCTTAAAAG AAATCGCCTC TGGTTACACA 1380	
	GTCAACTCTA TCTTAAATC TAATCAGGTC TCTGCAATAG ACTCGATATT TGACTGCTG 1440	
50	AATAATGGTT CCCATCATT TTTTAAAC ACTCATGGAA TGCCGACTGT TTGGGGGATA 1500	
	GGGCAGGGAC TCGACGTCAA TACTCTAACA GCCGATTGA ACAATACATC TTCGCAAGGA 1560	
	TTATGTACGA GTCTATCATG TAGTTCGGCT GTAGCAGATT CAATATTAG ATCGCTTGA 1620	
	GAAGTCCTGA CCACATACGC ACCTAACAAG GGATTCTCGG CTTTCTTAGG AGGAAGCAGA 1680	
	GCCACCCAAT ATGCCGTTTA TTTAGAAGGC CCTGTCTCTC CGTCAGAAAT TTATGAATAT 1740	
55	TTACCTTATT CTTTATATCA CAATCTCTCG ACTGTGTGTT GCGAAATGTT GCTATCATCC 1800	
	ATTATCAATA CTAATTCTGT TGATACGTAT TCGAAATTCA ACTTCAATTT GCTTGGCGAC 1860	
	CCTGCACTAA ACATTATGGC TCATGGCATG GAGGTTAGTA ATTGTATTAC ACTACCAAAC 1920	
	AACACCATT TAAGCAGTCC GATAACAATA AAAAAATGGT GCTGCCTAAA AATACCGGAA 1980	
	AAAGGAGTTT TGCATTTTAC TAATAATGGC TCCATACAAG TCATGTCCCG AGGAACCTCG 2040	
60	GAAATAGGCA ATCAGGCTAA AATATCCGGA GAGACCGGTG CTAACCCAC CTTTATTACC 2100	
	GTTTACGCGG ATGGTCTTGC GATTAAACAG CAGGTAGAGA TAGACAATAT AGACCGACTT 2160	
	AACCTGTGTT CTACGCATTG GGTATGCCCC AAATTTCATT TTGACAGTGT GAAATTC AAC 2220	
	AGTGCCCCGC TGTATACAA GAATGTGATG GTGGAGATAA GCAATTGCGA ATTTACCAAT 2280	
65	CGAAGTGACA TTATTTCAAA GAATGTGAC CTAAGCGTTG AAAACAGTAT GTTTAGCAAT 2340	
	TCGGGGATAA CGGTATTCAA GCCTATGGCT ACAAGCTCCA TCACCGGATT ATCTACAAAA 2400	
	GCAAGATTA CCGACAATAC TTTTGTGCG ACAGGAACT TCGCTACCA TATCACAAAC 2460	
	ACGCCAGGCT TAACAGCAAC CTCCAATGCT GCCATCAAGT TAGACAATAT TCCTGAGTAT 2520	
	TACATTTCGG GTAATAAAAT AGTCAATTGC GATGAGGCTC TTGTACTAAA TAATAGTGGC 2580	
70	AACAGAACGA ACAGACTCCA CAATATCACA CGGAATGTGA TAAAAAATG TAGGATTGGG 2640	
	AGCAGCGTTT ATAATTCTTA TGGTATTAC AACCAGATA AGATCAGTAA CAATCATATA 2700	
	GGAGTACGTC TCCTCAACAA CAGTTGTTT TATTTCGATA ATGCTCCTGT AATCAATGAA 2760	
	GAAGATAAGC AGACGTTTAT TTCTAATAGG ACTTGGCAGC TCTATTTCATC AAACGGTACA 2820	
	TTCCCTCTCA ACTTCCATTA CAACAGCTTG CAGGGGGGAG ATACAGATAC ATGGATTAC 2880	
	AACGACAGCT ATACGAATCG CTATATTGAC GTTTCAAATA ATCACTGGGG CAACAATGAT 2940	
75	TGTTTGTATC CGAATCAGGT TTTCAATACG CCAGACTGT TCATTGGAT ACCTTTTGG 3000	
	GATGGATTGC CAAATGGGAG ATCGGGCAAT AGCTCTGCTG AAGCAGTAGA ATTCAAAAA 3060	

5	GCATTGGACT GTATTGGCAA TAGCGATTAT CTTTCGGCAA AAGTGGCTCT CAAGATGATG 3120
	GTGGAACCT ACCCGGAATC CGACTTTGCA ATAGCTGCTT TGAAGGAATT GTTCAGGATA 3180
	GAGAAATGT CAGGCAACGA TTACGAAGGC TTGAAAGAAT ATTTTCAGATC CAATCCAAACC 3240
	ATCATCTCTT CCCAGAACTT GTTCCCGACA GCTGATTTCC TGTCTGGCGG ATGCGATATT 3300
	GTGTGTGAAA ACTATCAGTC TGCCATCGAT TGGTACGAAA ATCGCTTGAA TAGTGAAATC 3360
	TCCTATCAGG ACAGTGT TTTT TGCAGTCATT GACCTTGGTG ACATTATTG GAATATGCAG 3420
	TTAGACTCAC TCAGAGGGAC TGGTATAGAT TTGAACATAC TTCTCTGTGA ACAAGGAAA 3480
	TCGCTCGAAA GCCATCAAAA TGTAAAAAAT TATTTGTTGT CAACTCTTCC CGAATCAACA 3540
10	GGTACTCTCC TGCTCCATT AGAATGCAAC AAATCAAGCC TTGATAAATC CAAGATAATC 3600
	TCATTTTGGC CCAATCCGGC GAAAGCTGTT GTAACAATAA TCTACTATAC CGATAACCCCT 3660
	TCCTGTTCTG TAATAAAAAAT ATATGGAATA AATGGAGCCT CGGCTGATAT AACC GGTTG 3720
	CCCAACATC TATCCGAAGG TTATTACAGC ATACAGTTCA ATACATCCAA CTTTGATCCC 3780
	GGTTTCTACC TGGTAACGCT AAATGTTGAT CAGAAAAATA TAGATACGGA AAAATTACGA 3840
15	ATCAAA 3846

(2) INFORMATION FOR SEQ ID NO:202

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
- (A) NAME/KEY: misc feature
- (B) LOCATION 1...3822
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:202

40	ATGATGTGCT CTCTGCATT AGGTCTACAA TCTCAGACTT GGCATGGAGA TCCGGACTCA 60
	GTGGCAGCCC TACCTTCTAT CGGTATTCAA GAGTCAAGTT GTACCCGAAT CACGTTTCGAG 120
	GTGTTTTTCC CCGGATTTTA TAGTGTGGAA AAACGAGAAG GCAACCAAGT CTTTCAGCGC 180
	ATTTCCATGC CGGGTTGTGG CTCGTTTGGG AATCTGGGCG AAGCTGAATT GCCTGTTTTG 240
45	AAAAAGATGA TAGCCGTTCC GGAATTTTCA ACAGCTAACG TTGCTGTAAA AATCAAGAG 300
	ACGGAGACAT TCGACAATTA TAATATCTAT CCTAATCCTA CCTATGTCGT AGAGGAGTTG 360
	CCTGAGGGGG GGACTTATCT GSTAGAGGCT TTCGCGATAA ACATGACTA TTATAGCCAA 420
	AATGTAAAGC TCCCTTCTAC TCATATGTC TATTCTCAAG ACGGGTATT TCGCTCACAA 480
	AGATTATGCG AAGTTACCCT GTATCCTTTT CSATACAACC CTGTCGACGA AGAAATTCTA 540
50	TTTGCAAAAA AAATCGAGGT TACAATAACT TTCGATAATC CTCAGCCACC TTACAAAAA 600
	AACACCGGCA TATTTAACAA AGTAGCCTCC TCTGCATTTA TTAATTATGA AGCTGATGGC 660
	AAATCGGCGA TAGAAAAATGA TATGGTGTTC AGTCGTGGTA CAACAACGTA CATAGCGGA 720
	AATGTIGCCA GCAACCTCCC TCAGAACTGT GACTACTTGG TTATTTACGA TGATATGTTT 780
	AACGTAATC AACCAACACA CGACGAAATC AAACGGCTGT GCGAACATAG AGCCTTCTAC 840
55	AACGGCTTGT ATGTAGCTGC TGTAAATATA AAGGACGTAT TGAATAGCTT CCCATCAAT 900
	GCCACCTCAT ACATCAACGA AACTAAACTG AAAAATTTCA TTCGCTCAGT TTACAACCAA 960
	AGCAATGCGA AGAGGACTTT AGATGGCAAA CTGGGATACG TGCTACTGAT CGGAAAAACA 1020
	TTGAGCAAT ATTTGGCTGA CACTGATAAT ACRAAAGTCC CAACCTCTTT TATTCTAAT 1080
	GTCTCCTTAA TTCCAAGTCA TCCAACTTTT GGTTCATAT GCGCTCCGA CTATTTTTT 1140
60	AGTTGTGTTT CGCCCTTGA TACTGTGGGC GATTGTTTA TCGGTGATT TAGCGTCACC 1200
	AATGCTCATG AATTGCACAA TCTGATTGAA AAGACTATCA ACRAAGAAAT CTCATATAAT 1260
	CCTATTGCAC ACRAAATAT TCTTACSCA GAAGGGAAGG GCTGCGATGC TCCAATCTTA 1320
	CGTTTATCTT TAAAGAAAT CGCCTCTGGT TACACAGTCA ACTCTATCTT AAAATCTAAT 1380
	CAGGCTCTGT CAATAGACTC GATATTGAC TGCTTGAATA ATGGTTCCCA TCATTTTTAT 1440
65	TTTAACAATC ATGGAATGCC GACTGTTTGG GGGATAGGGC AGGGAAGTCA CGTCAATACT 1500
	CTAACAGCCC GATTGAACAA TACATCTTGG CAGGGATTAT GTACGAGTCT ATCATGTAGT 1560
	TGCGCTGTAG CAGATTCAAC TATTAGATCG CTTGGAGAAG TCCGTAGCAC ATACGCACCT 1620
	AACAAGGGAT TCTCGCTTT CTTAGSAGGA AGCAGAGCCA CCCAATATSC CGTTTATTTA 1680
	GAAGGCCCTT GTOCTCGGTC AGAATTTTAT GAATATTIAC CTTATTCTTT ATATCACAAT 1740
70	CTCTCGACTG TTGTTGGCGA AATGTTGCTA TCATCCATTA TCAATACTAA TTCTGTTGAT 1800
	ACGTATTGCA AATTCAACTT CAATTTGCTT GGCAGACCTG CACTAAACAT TATGGCTCAT 1860
	GGCATGGAAG TTAGTAATTG TATTACACTA CCNACAACA CCATTATAAG CAGTCCGATA 1920
	ACAATAAAAA ATGTTGGCTG CCTAAAAATA CCGGAATAAG GAGTTTGTCA TTTTACTAAT 1980
	AATGGCTCCA TACAAGTCA GTCCGGAGGA ACTCTGGAAA TAGGCAATCA GGCTAAAAA 2040
75	TCCGGAGAGA CCGGTGCTAA CCCACCTTTT ATTACCGTTT ACGGCGAAGG TCTTGCGATT 2100
	AACAAGCAGG TAGAGATAGA CAATATAGAC CGACTTAACT TGTTTTCTAC GCATTCCGTC 2160

5 ATGCCCAAT TTTATTTGA CAGTGTGAAA TTCAACAGTG CCCCCTGTGA TACAACGAAC 2220
TGTATTTGG AGATAAGCAA TTGCGAATTT ACCAATCGAA GTGACATTAT TTCAAAGAAT 2280
TGTGACCTAA GCGTTGAAAA CAGTATGTTT AGCAGTTCTG GATTAACGGT ATTCAAGCCT 2340
ATGCTACAA GCTCCATCAC CGGATTATCT ACAAAGCAA AGATTACCGA CAATACTTTT 2400
TTTGGCAGAG GAAACTTCGC CTACCATATC ACAAACACGC CAGGCTTAAC AGCAACCTCC 2460
AATGCTGCCA TCAAGTTAGA CAATATTCCT GAGTATTACA TTTCGGTAA TAAATAGTC 2520
AATTGCGATG AGGCTCTTGT ACTAAATAAT AGTGGCAACA GAACGAACAG ACTCCACAAT 2580
ATCACACGGA ATGTGATAAA AAAGTGTAGG ATTGGGAGCA CGCTTTATTA TTCCTATGGT 2640
ATTTACAACC GAAATAAGAT CAGTAACAA CATATAGGAG TACGTCTCCT CAACAACAGT 2700
10 TGTATTTTATT TCGATAATGC TCCTGTAATC AATGAAGAAG ATAAGCAGAC GTTTATTCTT 2760
AATAGGACTT GGCAGCTCTA TTATCAAAAC GGTACATTCC CTCTCAACTT CCATTACAAC 2820
AGCTTGCAGG GGGGAGATAC AGATACATGG ATTACAACG ACACGTATAC GAATCGOTAT 2880
ATTGACGTTT CAAATAATCA CTGGGGCAAC AATGATTGT TTGATCCGAA TCAGGTTTTC 2940
AATACGCGAG ACTTGTTCAT TTGGATACCT TTTTGGGATG GATTGCCAAA TGGGAGATCG 3000
15 GGCAATAGCT CTGCTGAAGC AGTAGAATTC CAAACAGCAT TGGACTGTAT TGGCAATAGC 3060
GATTATCTTT CGGCAAAAGT GGCTCTCAAG ATGATGGTTG AAACCTACCC GGAATCCGAC 3120
TTTGCAATAG CTGCTTTGAA GGAATTTGTC AGGATAGAGA AAATGTCAGG CAACGATTAC 3180
GAAGGCTTGA AAGATTATT CAGATCCAA CCAACCATCA TCTCTTCCCA GAACCTGTTC 3240
CCGACAGCTG ATTTCTGTTC TGCGCGATGC GATATTGTGT GTGAAACTA TCACTCTGCC 3300
20 ATCGATTGGT ACGAAATCG CTGGAATAGT GAAATCTCCT ATCAGGACAG TSTTTTTCGA 3360
GTCAATGACC TTGCTGACAT TTATTGGAAT ATGCASTTAG ACTCACTCAG AGGGACTGGT 3420
ATAGATTGGA ACATACTTTC CTGTGAACAA AGGAAATCGC TCGAAACCCA TCAAAATGTA 3480
AAAAATTATT TGTGTCAAC TCTTCCCGAA TCAACAGGTA CTCTCTGCC TCCATTAGAA 3540
25 TGCAACAAAT CAAGCCTTGA TAAATCCAG ATAATCTCTA TTTCGCCCAA TCGGCGGAAA 3600
GCTGTTGTA CAAATATCTA CTATACGAT AACCTTCTCT GTTCTGTAAT AAAAATATAT 3660
GGAATAAATG GAGCCTCGGC TGATATAACC GGGTTGCCCA AACATCTATC CGAAGGTTAT 3720
TACAGCATA AGTTCAATAC ATCGAATTT SATCCCGGTT TCTACCTGGT AACGCTAAAT 3780
GTTGATCAGA AAATTATAGA TACGGAAAAA TTACGAATCA AA 3822

(2) INFORMATION FOR SEQ ID NO:203

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2775 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGINAL SOURCE:

- (A) ORGANISM: PORPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
(B) LOCATION 1...2775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203

55 ATGCTATCA TGATGAAAG TATTGTTTT AGAGCATTC TAACGATTT GCTCTGTGG 60
GCAGCGATCA CGAATCCGAC TGCTCAAGAG ATCTCAGGCA TGATGCAATC CTGTCTGGCT 120
GCTCGGCTC AACCGGATAC TATCTTATAT GAAAGTTTGG AGAATGGACC TGTTCCCAAT 180
GGCTGGCTTG AGATAGATGC TGATGCTGAT GGTGCCACTT GGGGAAGCCC ATCAGGCTCT 240
TTCTCTGAC CTACCGGACA CAATGGCCTT TGCACCTACT CCCATATACG TTCCGGTATC 300
TCAACAGCGG GCAACTATCT GATTACACCC AATATAGAAG GAGCCAAACG GGTCAAGTAC 360
60 TGGGTATGCC ATCAGTATAG TACCAATCCG GAACATTACG CAGTAATGGT ATCGACAACC 420
GGGACTGCCA TTGAAGACTT TGTTTTGTG TTTGATGATT CCATAACAGG GAAACCGACT 480
CCTCTTSTAT GGCCTAGACG AATCGTGGAC TTACCGGAAG GGACCAATA TATTGCATGG 540
CGACATTACA AAGTCACCGA CTCACACACA GAATCTTGA AATTGGATGA TGTCACTGTG 600
TATAGGTCGA TCGAAGGGCC CGAACCTGCT ACCACTTCA CAGTAATCAA TATTGGTCAG 660
65 AATGTTGGAC GATTGACTTG GAACTATCCG GAGGATTAAT AACCGGAAGG AAAGGGGAAT 720
GAAGAGTTGC AGCTTAGCGG CTACACATC TATGCGAACC GTACACTACT GGCACAAATA 780
AAAGATGTCT CCATAGTGA GTATGTGGAC AGCACTTACT CTTTGGGAGA CAATCCCTTG 840
CAAGTGGAGT ACTGCGTTAC AGCCGTTTAC GATGAAAGCA TAGAATCTTC GACCGTATGT 900
70 GGCACGCTGC ATACCCGAC GATGCCATC CTTTATGAAA ATTTTGAGAA TGGACCTGTT 960
CCCAATGTTT GGCTTGTGAT AGAGGCTGAT GGAGATGGAT TTAGCTGGGG ACATATTGT 1020
AATGCAATAG ACCTTTTTC CGGCCATAAT GGAGGCCATT GCTCCTTGTC GGCTTCTTAT 1080
GTTCCGGSTA TAGGCCCCGT GACTCCCGAC AACTATCTGA TTACCCCAAA GGTGGAAGGA 1140
GCCAAACGTG TCAAGTACTG GGTAAAGCAC CAGGATGCCA ATTGGGCAGC GGAACATTAC 1200
75 GCGGTGATGG CTTGACAAAC GGGGACTGCT GTCGAGATT TCGTCATATT GTTCGAAGAA 1260
ACCATGACAG CGAAGCCGAC CGGCGCATGG TATGAAAGAA CCATCAACTT ACCTGAAGGG 1320

	ACTAAATACA	TCGCATGGCG	GCATTACAAC	TGTACCGATA	TATATTICTT	GAAGTTGGAC	1380
	GATATCACTG	TATTCGGGAC	TCCTGCATCA	GAGCCCGAAC	CTGTTACCGA	TTTCGTTGTC	1440
	TCGCTTATTG	AAAACAACAA	GGGACGATTA	AAGTGGGAAT	ATCCTAACGG	CTACGAACCC	1500
5	GATAAGACTG	ATGATAAAGA	CCCATTGCAG	CTTGCCGGCT	ACAATATCTA	TGCAACCGGC	1560
	TCGCTCCTTG	TTACATACA	AGACCCGACT	GTTTTGGAST	ATATCGATGA	GACTTATTCT	1620
	TCACGAGACG	ATCAGGTGGA	AGTGGAAATAT	TGTGTCACTG	CCCTTTATAA	CGACAATATC	1680
	GAGTCCCAAT	CGGTTTGCGA	TAAGCTGATT	TATGATTCTC	AATCGGACAT	TATCTTATAT	1740
	GAAGGCTTTG	AGGCCGGAAG	TATTCCTGAA	GGCTGGTTGT	TGATTGATGC	TGATGGCGAC	1800
10	AATGTTAATT	GGGACTATTA	TCCTTGGAAT	ATGATGGAC	ATGACAGTGA	GAATGTATT	1860
	GCATCCGCTT	CGTACTTACC	GATGATTGGC	GTTTTAACTC	CGSATAACTA	TTTGGTTACA	1920
	CCCAGACTCG	AAGGAGCCAA	GCTGTGCAAG	TATTGGGTAA	GTGCGCAAGA	TGCTGTTTAT	1980
	TCGGCTGAGC	ATTATGCTGT	GATGGTTTCT	ACTACGGGAA	CTGCTGTGA	AGATTTTGTG	2040
	CTCTTGTTTG	AAGAGACAAI	GACCGCTAAG	GCTAACGGTG	CATGGTATGA	GCGAATATT	2100
15	ACATTGCGCTG	CAGGAACAAA	ATATAATTGCC	TGGCGGCATT	ATGATTGCAC	CGATATGTTT	2160
	TTCTTGCTCT	TGGATGACAT	TACGGTTTAT	CGTCTACTG	AGACTGTTCC	CGAGCCTGTT	2220
	ACTGATTTCC	TTGTCTCGCT	TATTGAGAAT	AACAAGGGTC	GCCTGAAATG	GAATTTATCT	2280
	ACGGGCTACG	AACCGGATAA	GACTGATGAT	AAAAAACCAT	TGCAGCTTAC	CGGCTACAA	2340
	ATCTATGCAA	ATGGCTCGCT	CCTTGTTTAC	ATACAGAGCC	CGACTGTTT	GGAGTATATC	2400
20	GATGAGACTT	ATTCTTCAGC	AGACGGTCAG	GTGGAAATGG	AATATTGTGT	CACTGCCGTT	2460
	TATAACGACA	ATATCGAGTC	CCAATCGGTT	TGCGATAAGC	TGAACATATC	TATCACATCC	2520
	TTGGATAATA	TTCAATCTGA	TACAAGCTTG	AAAAATATATC	CTAATCCGGC	ATCGTATGTC	2580
	GTAAGGATAG	AGGGATTGAG	TCGGAGCAAG	TCGACAATCG	AGTTGTATAA	TGCGCTGGGA	2640
	ATTTGCATAT	TAAGGGAAGA	GACTCATTCA	GAGAAAACGG	AAATCGATGT	TTACGCTCTC	2700
25	AATGACGGAG	TCTACTTGAT	TAAAGTAGTC	GGTGAAATA	AAACAACAAC	CGAAAGGTA	2760
	GAGATAAAGA	GGCCG					2775

(2) INFORMATION FOR SEQ ID NO:204

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2766 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 35 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 40 (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 45 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...2766
- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:204

	ATGATGAAAA	GTATTGTTTT	TAGAGCATT	CTAACGATT	TGCTCTCGTG	GGCAGCGATC	60
	ACGAATCCGA	CTGCTCAAGA	GATCTCAGGC	ATGAATGCAT	CCTGCTCGGC	TGCTCCGGCT	120
	CAACCCGATA	CTATCTTATA	TGAAAGTTTT	GAGAAATGGAC	CTGTTCCCAA	TGGCTGGCTT	180
	GACATAGATG	CTGATGCTGA	TGGTGCCACT	TGGGGAGGCC	CATCAGGCTC	TTTCTCTGTA	240
55	CCTTACGGAC	ACAAATGGCT	TTGCACCTAC	TCCCATATAC	GTTCGGGTAT	CTCAACAGCG	300
	GGCAACTATC	TGATTACACC	CAATATAGAA	GGAGCCAAAC	GGGTCAAGTA	CTGGGTATGC	360
	AATCAGTATA	GTACCAATCC	GGAAACATTAC	GCAGTAATGG	TATCGACAAC	GGGACTGCC	420
	ATTGAAGACT	TTGTTTTGTT	GTTTGATGAT	TCCATAACAG	GGAAACCGAC	TCCTCTTGTA	480
	TGGCGTAGAC	GAATCGTGGA	CITACCGGAA	GGGACCAAT	AAATTGGATG	ATGCTCACTG	540
60	AAAGTCACCG	ACTCACACAC	AGAATCTCTG	AAATTGGATG	ATGCTCACTG	GTATAGGTCG	600
	ATCGAAGGGC	CCGAACCTGC	TACCGACTTC	ACAGTAATCA	ATATTGGTCA	GAATGTGGGA	660
	CGATTGACTT	GGAACTATCC	GGAGGATTAT	CAACCCGGAAG	GAAAGGGGAA	TGAAGAGTTG	720
	CAGCTTAGCG	GCTACCAACAT	CTATGCGAAG	GGTACACTAC	TGGCACAAAT	AAAAGATGTC	780
	TCCATACTGG	AGTATGTGGA	CAGCACTTAC	TCTTTGCGAG	ACAATCCCTT	GCAAGTGGAG	840
65	TACTGCGTTA	CAGCCGTTTA	CGATGAAAGC	ATAGAATCTT	CGACCGTATG	TGGCACGCTG	900
	CATTACGCCA	CGGATGCCAT	CCTTTATGAA	AATTTTGAGA	ATGGACCTGT	TCCCAATGGT	960
	TGGCTTGTA	TAGACCTGSA	TGGAGATGGA	TTTAGCTGGG	GACACTAITT	GAATGCATAC	1020
	GACGCTTTTC	COGGCCATAA	TGGAGGCCAT	TGCTCCTTGT	CGGCTTCTTA	TGTTCCGGGT	1080
	ATAGCCCGGG	TGACTCCCGA	CAACTATCTG	ATTACCCCCA	AGGTTGAAGG	AGCCAAACGT	1140
70	GTCAAGTACT	GGGTAAGCAC	GCAGGATGCC	AATTGGGCAG	CGGAACATTA	CGCGGTGATG	1200
	GCTTCGACAA	CGGGGACTGC	TGTGCGAGAT	TTCGTATAT	TGTTGGAAGA	AACCATGACA	1260
	GCGAAGCCGA	CGGGCGCATG	GTATGAAAGA	ACCATCAACT	TACCTGAAGG	GACTAAATAC	1320
	ATCGCATGGC	GGCATTACAA	CTGTACCGAT	ATATATTCTT	TGAAGTTGGA	CGATATCACT	1380
75	GTATTCGGGA	CTCTGCTATC	AGAGCCCGAA	CCTGTTACCG	ATTTGCTTGT	CTCGCTTATT	1440
	GAAAAACAAC	AGGGACGATT	AAAGTGGAAAT	TATCTAACCG	GCTACGAACC	CGATAAGACT	1500

140/ 490

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GATGATAAAG ACCCATTTGCA GCTTGCCGGC TACAATATCT ATGCAAAACGG CTCGCTCCTT 1560
GTTACACATAC AAGACCCGAC TGTITTTGGAG TATATCGATG AGACTTATTC TTCACGAGAC 1620
GATCAGGTGG AAGTGGGAATA TTGTGTCAC TCCGTTTATA ACGACAATAT CGAGTCCCAA 1680
TCGGTTTGGC ATAAGCTGAT TTATGATTCT CAATCGGACA TTATCTTATA TGAAGGCTTT 1740
GAGGCGCGAA GTATTCCTGA AGGCTGGTTG TTGATTGATG CTGATGGCGA CAATGTTAAT 1800
TGGGACTATT ATCCTTGGAC TATGTATGGA CATGACAGTG AGAAGTGTAT TGCATCCOCT 1860
TCGTACTTAC CGATGATTGG CGTTTAACT CCGGATAACT ATTTGGTTAC AGCCAGACTC 1920
GAAGGAGCCA AGCTTGTCAG GTATTGGGTA AGTGCSCAAG ATGCTGTTTA TTCGGCTGAG 1980
CATTATGCTG TGATGGTTTC TACTACGGGA ACTGCTGTTG AAGATTITGT CCTCTTGTTT 2040
GCAGGAACAA AATATATTGC CTGGCGGCAT TATGATTGCA CCGATATGTT TTTCTTGCTC 2100
TTGGATGACA TTACGGTTTA TCGTCTACT GAGACTGTTT CCGAGCCTGT TACTGATTTC 2160
GTTGCTCCG TTATTGAGAA TAACAAGGT CGCCTGAAAT GGAATTATCC TAAOCCGTAC 2220
GAACCCGATA AGACTGATGA TAAAAACCA TTGCAGCTTA CCGGCTACAA CATCTATGCA 2280
AATGGCTCGC TCCTTGTTCA CATACAAGAC CCGACTGTTT TGGAGTATAT CGATGAGACT 2340
TATTCTTAC GAGACGGTCA GGTGGAAATG GAATATTGTG TCACTGCCGT TTATAACGAC 2400
AATATCGAGT CCCAATCGGT TTGCGATAAG CTGAACATA CTATCACATC CTGGGATAAT 2460
ATTCAATCTG ATACAAGCTT GAAAAATATAT CCTAATCCGG CATCGTATGT GGTAAAGGATA 2520
GAGGGATTGA GTCGGAGCAA GTGCAACATC GAGTTGTATA ATGCGCTGGG AATTGTCATA 2580
TTAAGGGAG AGACTCATTC AGAGAAAACG GAAATCGATG TTTCACTGCT CAATGACGGA 2640
GTCTACTTGA TTAAAGTAGT CGGTGGAAT AAAAAACAA CCGAAAAGGT AGAGATAAAG 2700
AGGCCG 2766

25 (2) INFORMATION FOR SEQ ID NO:205

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2763 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...2763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205

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ATGAAAAGTA TTGTTTTAG ASCATTCTA ACGATTTTGC TCTCGTGGGC AGCGATCAG 60
AATCCGACTG CTCAGAGAT CTCAGGCATG AATGCATCCT GTCTGGCTGC TCCGGCTCAA 120
CCGGATACTA TCTTATATGA AAGTTTTGAG AATGSACCTG TTCCCAATGG CTGGCTTGAG 180
ATAGATGCTG ATGCTGATGG TGCCACTTGG GGAAGCCCAT CAGGCTCTTT CTCTGTACCT 240
TACGGACACA ATGGCCCTTG CACCTACTCC CATATACGTT CCGGTATCTC AACAGCGGGC 300
AACTATCTGA TTACACCCAA TATAGAAGGA GCCAAACGGG TCAAGTACTG GGTATGCAAT 360
CAGTATAGTA CCAATCCGGA ACATTACGCA GTAATGGTAT CGACAACGGG GACTGCCATT 420
GAAGACTTTG TTTTGTGTTT TGATGATTCC ATAACAGGGA AACCGACTCC TCTTGATGG 480
CGTAGACGAA TCGTGGACTT ACCGGAAGGG ACCAAATATA TTGCATGGCG ACATTACAAA 540
GTCAUCCACT CACACACAGA ATTCTTGAAA TTGGATGATG TCACTGTGTA TAGGTCGATC 600
GAAGGCGCCG AACCTGCTAC CGACTTCACA GTAATCAATA TTGGTCAGAA TGTGGGACGA 660
TTGACTTGGG ACTATCCGGA GGATTATCAA CCGGAAGGAA AGGGGAATGA AGAGTTGCAG 720
CTTAGCGGCT ACAACATCTA TCGGACGGGT ACACACTCTG CACAAATAAA AGATGTCTCC 780
ATACTGGAGT ATGTGGACAG CACTTACTCT TTGCGAGACA ATCCCTTGCA AGTGGAGTAC 840
TGGTTTACAG CCGTTTACGA TGAAGCATA GAATCTTGA CGATGTGG CACGCTGCAT 900
TACGCCACGG ATGCCATCCT TTATGAAAT TTGAGAATG GACCTGTTCC CAATGGTTGG 960
CTTGTGATAG ACGCTGATGG AGATGGATT AGCTGGGGAC ACTATTGAA TGCATACGAC 1020
GCTTTTCCCG GCCATAATGG AGGCCATTGC TCCTTGTGCG CTTCCTTATG TCCGGGTATA 1080
GGCCCGGTGA CTCCCGACAA CTATCTGATT ACCCCCAAGG TTGAAGGAGC CAAACGTGTC 1140
AAGTACTGGG TAAGCACGCA GGATGCCAAT TGGGCAGCGG AACATTACGC GGTGATGGCT 1200
TCGACAAACG GSACTGCTGT CGGAGATTTC GTCATATTGT TCGAAGAAAC CATGACAGCG 1260
AAGCCGACCG GCGCATGGTA TGAAGAAGC ATCAACTTAC CTGAAGGAGC TAAATACATC 1320
GCATGGCGGC ATTACAACCT TACCGATATA TATTCTTGA AGTTGGACGA TATCACTGTA 1380
TTCCGGACTC CTGCATCAGA GCCCGAACCT GTTACCGATT TCGTTGTCTC GCTTATTGAA 1440
AACAACAAGG GACGATTAAA GTGSAATTAT CCTAACGGCT ACGAACCCGA TAAGACTGAT 1500
GATAAAGACC CATTGCAGCT TGCCGGCTAC AATATCTATG CAAACGGCTC GCTCCTTGT 1560
CACATACAG ACCCGACTGT TTTGGAGTAT ATCGATGAGA CTTATTCTTC ACGAGACGAT 1620
CAGGTGGAAG TGGAAATATT TGTCACGGCC GTTTATAACG ACATATCGA GTCCCAATCG 1680

142/ 490

(2) INFORMATION FOR SEQ ID NO:207

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1767 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 10 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 15 (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 20 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...1767

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207

25 ATGAAATATC AATTATATAC GGCCTGCATA ATGGCTCTCT CTGTATCATC CGTTTGCGGT 60
CAAACCCAC GAAATACAGA AACCAACCGC CCGGACACGC TGGCGAGGGA GCTTACTATC 120
GTTAATGACC AGACTGTGGA GATGGAGCAT GCGGATCCGC TTCCGGCTGC ATACAGGCC 180
ATCGAACCTC GATTAAACCC TTTCCTCCG GAATATAACA AGCGTACATT CGGATTTGTC 240
CCTGAAGTTT CCTCTTCAGG CAGGAACAAT CTTCGGAATA TCCTGCGGAC GGAAGGTCAT 300
30 ATGAAGCACC GGGGGTACCT GAATATCGGT ATCGGCCATA CGCTAAACCA GCGAATGGAT 360
GCCGGCTATC GTCTGATAGA TGCAGAGCAG GAGAGACTGA ATCTTTTCT CTCTATCGT 420
GGGATGAAT CGGCTTTCAA TACCGGTGAC TTCGACGCG ACAGAAAGGA TAGACGAATG 480
ATGGCAGGAG TGGACTACGA GCAGCGCAGG CCTTCCTTG TGCTTGCTAC CGGCTTGAT 540
TATTCGAACC ATTATTTCAA TAACTACGGA CGGGGAGCTA CCACCAATGT GGGCAGCATC 600
35 CCTCAGCTAT CGACACCTGT TACTCCTCAG ATGGACACG GGACCCACAA CGTCCGTGTA 660
TACTTGGGTG CAAAAAATGA TGTGATCGAT GCCAGGATCG ACTATCGTTT CTTCGGTTCT 720
ATTCCCTATC TGGGTACCGA TCGATGAAG GCTCTCACAG AACATACGCC TGAACGAAAC 780
GTGACGATGA TGAATGAGTT GTCCGATGAT ATTAAGCTCG GTGTGGAAGT TCGTACGGGA 840
GGATTTGTTT TTGCCAAAAA CAGCGAAATG ATTCAAACGG GCGTCTGTGC CGAAACCGAC 900
40 CGCAACCTGT ATTATGTGGA GGGCGCGCCC ACAATCGSAT TTGTGGGAGA CTCGGCAAT 960
ATGCATGGA ACATACAGGC CGGAGTAGGG ATTTCTTCCC ATTTGGGAGC CAAAGGGAGG 1020
TTGTTTTCCT GGCCTAAACT GGATGCTTCG CTTAGTATCT TCCCTTCATG GCGTGTGTAT 1080
GCGAAGCCTT TCGCGGTGT GATTGGAAT GGTCTGCGCG ATGTTATGCA AGAGGAGATG 1140
COCTACCTGA TGCCCAATAC GATTGTACTC CCTTCGCGCA ATGCTTTGAC CGCCCAATTA 1200
45 GGGGTGAAGG GGAATATAGC CGATGTGGTA CGTATGGAGG TTTATGGCGA CTTCTCCAAG 1260
CTGACAGGTG TGCCTTTCTA TACTCGACT CTACCTTAT ATAATCCATC CGACTTGTAT 1320
CAGTATATG TGAGTTTCTT GCCGATATAT GCGSACGGCA GCGCTGGCG CGCAGGTGGT 1380
AAGCTGGAAT ACTCTTATCG CGATATGCTC CGCTTCTGCG TAGACGCATC CTATGGCAAG 1440
50 TGGAAATTTG ATGGAGGACT TGTGCGCTCC ATGCAGCCCG ATCTTATATT GAAGGCAGAA 1500
GTAGGTGTTT ATCCATTGCG CCCATTGGAT GTCAGACTCC GGTATACACA GCTGAACGGA 1560
CGGTATCGST ATTCCTTCGG CTCGGCTGGC TCGGAAGCCT TGGGTATCGG TAATGTACAT 1620
CTTCTTAGTG CGGATGTTT ATACAAGCTG AAAAAGAAGT TGAGCCTTTA TCTCAAAATC 1680
GATAATATGC TGGCGGAAC GACAGAGCTT ATCGGTTATT ATCCTATGCA GCCGTTCAT 1740
55 TGTTCGCGG GTTTAGCTG GACTTTC 1767

(2) INFORMATION FOR SEQ ID NO:208

- 60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1038 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 65 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 70 (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 75 (ix) FEATURE:
(A) NAME/KEY: misc_feature

(B) LOCATION 1...1038

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:208

5 ATGATGGAAT AATGTATCTT TGCTCACTAT CCACATAACC TTGTGTTTAT GATTGCAAG 60
CATTTCCGTA TCATTTTGGG ATTTCTTTCT CTTGTGTTT CGGCAGGTGC TCAACAAGAG 120
AAGCAGGTGT TTCATTTTCT GAACCTTCCG GCTACTGCAC AGGCTTTGGC TGCCGGAGGC 180
AAAGCTATCA CCATCGTAGA CGACAATCCC GGACTGGGCTT TTGAGAATCC GGCTCTGCTC 240
GGATATGAAT CCGGTGGCCG CGCCTTTCTT TCCATTTAT ATTATATGAG TGGTTCCGAT 300
10 ATGGGCAATG CCGTGTATGC CTCGTCCGTC GGAGAGCGTG GCATGTGGGG TGTGGCATG 360
CGTTTCCTGA ACTACGGGTC TATGCAAGGA TACGATCAGA ATGCGATTGC CACCGGCTCT 420
TTTASTGCTT CGSATATAGC TGTACAAGGA TTTTACAGCC ATGAAGTATG CAACCACTTC 480
CGCGGTGGAG TCAGCCTAAA AGCATTGTAT TCTTCTATCG AGACGTATAG TTCTTTGGC 540
CTTGGTGTGG ATGTCCGTAT CAGTTATTAC GACGATGACA AAGGATATTC CCGTTCCGCT 600
15 TGGGATTTC AGCTCCGGCT TTCCCGCAGT TTTATCAATG CTCGGTTTCG CTGTCACATC 660
ACGTTGTTC ATCTGAATCC GCACTATTTC AAGCGTCTTG TACCACGCGA TCTGTCCAAG 720
ATGCATAAAGT TCCTCCGACA CTCTCCGATA GGAGCAGAAT TTACTCCTTC CGAGAGGTTT 780
TGGGTCCGGC TGGGATATAC GCCACAGATT GCACAGGATT TCGAGGTGGA AGCCGCAAC 840
20 AAATGGGGAG GTCTTCCGGC CGGCGTCCGT TTCACITCAG GTGTAGTACG TGTAGGCGTA 900
TCTGCTGCCA CCTATCATCC TGCAGCTCTT TCGTTCAATG GTTCGGTAGG TATCCGTTTG 960
GACGATAAGA GCATCTTC 1020
1038

25 (2) INFORMATION FOR SEQ ID NO:209

(1) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 1035 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

35 (111) HYPOTHETICAL: NO

(1v) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

40 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(1x) FEATURE:

45 (A) NAME/KEY: misc feature
(B) LOCATION 1...1035

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:209

ATGGAATAAT GTATCTTTGC TCACTATCCA CATAACCTTG TGTTTATGAT TCGCAAGCAT 60
50 TTCGGTATCA TTTTGGGAT TCCTTCTCTT GTGTTTTCGG CAGGTGCTCA ACAAGAGAAG 120
CAGGTGTTTC ATTTTCTGAA CCTTCCGGCT ACTGCACAGG CTTTGGCTGC CGGAGGCAAA 180
GCTATACCA TCGTAGACGA CAATCCCGGA CTGGCTTTTG AGAATCCGGC TCTGCTCGGA 240
TATGAATCCG GTGGCCGCGC CTTTCTTCC TATTATATAT ATATGAGTGG TTCCGATATG 300
GGCAATGCCT GTTATGCCTC GTCCGTCCGA GAGCGTGGCA TGTGGGGTGT TGGCATGCGT 360
55 TTCTGAACT ACGGGTCTAT GCAAGGATAC GATCAGAATG CGATTGCCAC CGGCTCTTTT 420
AGTGCCTTCG ATATAGCTGT ACAAGGATTT TACAGCCATG AACTGAGCAA CCACTTCCGC 480
GGTGGAGTCA GCCTAAAAGC ATTGTATTCT TCTATCGAGA CGTATAGTTC CTTTGGCCTT 540
GGTGTGGATG TCGGTATCAG TTATTACGAC GATGACAAAG GATATTCGCG TTCCGCTCTG 600
TTCAAGAAAG TAGGGGCGCA ACTGAAAGGC TATAATGAAG AACGGGAACC GCTCGATTG3 660
GATTTCACGC TCGGCTTTTC CCGCAGTTT ATCAATGCTC CGTTTCGCTT GCACATCAGG 720
60 TTGTTCAATC TGAATCCGCA CTATTTCAAG CGTCTGTAC CACGGGATCT GTCCAAGATG 780
CAAAAGTTCC TCCGACACTT CTCGATAGGA GCAGAAATTA CTCCTCCGGA GAGTTTGG 840
GTCCGGCTGG GATATACGCC ACAGATTGCA CAGGATTTTG AGGTGGAAGG CGGCAACAAA 900
TGGGGAGGTC TTTCCGGCCG CGTCCGTTTC ACTTCAGGTC TAGTACGTGT AGGCGTATCT 960
65 GCTGCCACCT ATCATCTGCG AGCTCTTTCG TTCATGTGTT CCGTAGGTAT CCGTTTGGAC 1020
GATAAGAGCA TCTTC 1035

(2) INFORMATION FOR SEQ ID NO:210

70 (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 990 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
75 (D) TOPOLOGY: circular

144/ 490

(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
5 (iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
10 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...990
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210
15
ATGATTGCGA AGCATTTCGG TATCATTTTG GGATTTCCTT CTCTTGTTGT TTCGGCAGGT 60
GCTCAACAAG AGAAGCAGGT GTTTCATTTT CTGAACCTTC CGGCTACTGC ACAGGCTTTG 120
GCTGCCGGAG GCAAAGCTAT CACCATCGTA GACGACAATC CCGGACTGGC TTTTGAGAAT 180
20 CCGGCTCTGC TCGGATATGA ATCCGGTGGC CGCGCCTTC TTTCCTATT ATATTATATG 240
AGTGGTTGCG ATATGGGCAA TGCTGTAT GCTCTGTCGG TCGGAGAGCG TGGCATGTGG 300
GGTGTGGCA TGGCTTTCTT GAACTACGGG TCTATGCAAG GATACGATCA GAATGCGATT 360
GCCACCGGCT CTTTACTGTC TTCCGATATA GCTGTACAAG GATTTTACAG CCATGAACTG 420
AGCAACCACT TCCGCGGTGG AGTCAGCTTA AAAGCATTGT ATTCTTCTAT CGAGACGTAT 480
AGTTCCCTTG GCCTTGGTGT GGATGTGGGT ATCAGTTATT ACGACGATGA CAAAGGATAT 540
25 TCCGCTTCGG CTCTGTCAA GAACGTAGGG GCGCAACTGA AAGGCTATAA TGAAGAACGG 500
GAACCGCTCG ATTGGGATTT CCAGCTCGGC TTTTCCGCA GTTTTATCAA TGCTCCGTTT 560
CGCTTGCACTA TCACGTTGTT CAATCTGAAT CCGCACTATT TCAAGCGTCT TGTACCAAGC 600
GATCTGTCCA AGATGCAAAA GTTCTCCGCA CACTTCTCGA TAGGAGCAGA ATTTACTCCT 660
TCCGAGAGGT TTTGGGTCGG GCTGGGATAT ACGCCACAGA TTGCACAGGA TTTGAGGTTG 720
30 GAAGGCGGCA ACAATGGGG AGGTCTTTCG GCGGGCGTGG GTTTCACCTC AGGTGTAGTA 780
CSTGTAGGCG TATCTGCTGC CACCTATCAT CCTGCAGTCT TTTGTTTAT GTGTTCCGTA 840
GGTATCCGTT TGGACGATAA GAGCATCTC 900
960
990
35 (2) INFORMATION FOR SEQ ID NO:211
(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 972 base pairs
40 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
(ii) MOLECULE TYPE: DNA (genomic)
45 (iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
50 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...972
55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:211
60
ATGTGCGCTG AACCCATAAT TGCTCCGATT TCATCCGAGT TGCTCGAGCA GGAGCTGACT 60
GCCGATCGTT TTCTGCGGAT GACAAACAAA GCGGCAATG AGATCTATGT TTTTACGGCC 120
GAAGAAGCTC CGCATTGCAT GAAAGAAGTA GCGCGACTGC GAGAAGAAGC CTTTCGGCAT 180
TATGGCGGAG GTACTGGCAA GCGGATCGAT ATAGACGAGT TCGACACCAT GCCCGGAGC 240
TACAACAGCG TGATCGTATG GGATCCGCAA AACAAAGGCTA TACTCGGAGG CTACCCCTTT 300
ATCTATGGGC GGGACGTTGC TTTTCGATCC GATGGCAAGC CTTTGCTGGC AACGGCAGAG 360
65 ATGTTTCGCT TCAGTGATGC TTTTTCGAC GATTATCTCC CTTACACAGT CGAATTGGGA 420
CGTTCTGTCG TGTGCTCCA GTACCAATCG ACACGGATGG GCACAAAGGC CATTTTGTG 480
CTGGACATTC TTTGGGACGG TATCGGAGCA CTCCTGTAG TCAATCCAGA GGCACCTAT 540
TTCTATGCGA AGGTGACCAT GTACAAAGAC TATGATCGGC GAGCTCGCAA TCTGATCCTG 600
TATTTTCTTC GCAAGCACTT CTCCGATCCG GAAGGCTTGG TCAAGCCTAT TCATCCCTA 660
70 CCGATAGAGA TCAGTGCGGA GGACGAAGCC TTGTTCTCCT CATCCGACTT TGACACCAAT 720
TACAAGACTC TCAATATAGA AGTGCGCAAG CTGGGTATCA ATATCCCTCC TCTCGTGAGT 780
GCATATATAG CTTTGTCTCC GGAGATGCGT GTTTTCGGCA CTGCAGTGA TGAATCTTTC 840
GGAGAGGTGG AGGAAACCGG CATATTCAAT GCTGTGGGTA AGATCCTGGA AGAGAAAAA 900
CAACGGCACA TAGAGAGCTT CATCTCAGC CGGAACGAAA AAAAAGGTCT CGACAGTAGC 960
75 AATGCGCGAT CA 972

(2) INFORMATION FOR SEQ ID NO:212

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1641 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 10 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 15 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 20 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1641

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212

25 ATGAAACCA TTGTAAGATA CAGCCGCTT CCGGTCGCTC TCTTCTTTG CCTTTTGGGA 60
GCTGTGCACT TGTCTGTGGA GGCGCAGATG CPCAATACTC CTTTCGAGCT GTCGGATCAG 120
ATCGTCTCTG TCCCCACCGA AAGGCAATAC AGGGAGATTT GTGTGCAAC GAAAGAAAAA 180
AGGGGGGCGG ATCTTTTCCC GTTGAGCGAT AAGCTGCGCG ATTCGGCCTA TGTTCGTTTC 240
GGCTCGGCGT ATGGCGATAT TGGGGGCGAC TATCTTCCGT ACAACGGCAA TAACTACTCC 300
TCGCTCTCGC TCGAATCGGG TGGTCGCATC AGTGTCCGTA ACTATGGCAC ATTGCAGGGC 360
AGTGCTTCCT ACTCAGGTGG CATGCACAAA CGCATCGGCT GGAATGCTCT GCGCAACGCC 420
GAAGCTTACT ATCCCTATTT GGTGTCCGAT TCGACCGGCG GAGACTATCA TTTCGAAGAC 480
TATCGGCTTG CCGGCTACTA TTCTTTTCGC GCGGCGCGCT TGCCCTTCGG TATAGGCTTC 540
TCATACAGGG GCGAAGTTGC TTATCGGCTG ACCGATCCGC GTACGACCAA TACGACCGGT 600
GCATTGGAGC TTCTTTGTGC TACCTCTTTG ACGCTGCCTC GAGAGAACAG GCTATCGCTT 660
TCGGCTCGGT ATCTCTATCA TAGACAACAC CTCACACAGI ACAACTGGCG TCCCGGGCAG 720
CAGGACAAAT TCTTCGTGAG CTACGGTTTC GGTCAAGTGG ATGTGAGCAA CAGCCCTATC 780
TGTTTCGGTA TCTCCAGAAT GAACTACGTC AACGGATGGA AGCTTAGCTC CCGTCTGGAT 840
ACCCGTAGGG GCGATGCCAT CGGTCTCGAC TACAGCGGCT ACTTCTCGA TACCGAAGAG 900
40 AGTCTGCTCA TCAATCTCTT TGCTTTGCTT TACAATCGCC TGCGACTCTA TGGTAGCTGG 960
CATCTGTCGG ACTTCGATTT TTCTTTTCA GCCACTATG CTCTGCGCCA AGGGATAGAG 1020
CGGATATACG AACACTACAA GCCGGATGAT AATTATCATA TCTACGACCT CCGTATCTTG 1080
GCCATTGCGC SCTGGTATAT GCTCAATGAG TTTTCTGCCC AAGCCCAAGC CTCCTACCGT 1140
45 ATTCGCACGG ATAGAGGTTG TGCCCTGACA GTGAGTGCCG GTAGTGATTT CTACGGCTAT 1200
GATGATAGCT ATCGCAAGCA TGGACATCAT ACCATGAGCG GAATGCTACG TCCTTTTGCC 1260
GGTATAGCCT ATGACCATGC CGGATCCAAA TTGGATTTTG GACTTTCGCT TTCGGCTGCT 1320
TATCGAATGG TGCTGACGCA TTCGTATAAG ATTGTTACCA TCCAGAAAGA GCAGCTCGAC 1380
TATCAGCTGG CCTATTGCCC CTATGCCTAT CGTAATAGAG AAGGCGTGGA GGTGCGTTCC 1440
50 TCTCTGTAGC CTCGATTCC GATGCAGAAT ACCCACCSCC TGATGACAGA GCTGCGGTTG 1500
TATGGCGACC TGATGAAAG AAAGGACGGT ATAGCCTATG GCAAAACGCC CGGTGTCTATC 1560
TCACATATCC TGTCCGATCC GCAAGCCGAA CGAACGTCCG GCCATACCAT CGGGGCTATC 1620
TGCAATATCT CCTACCTCTT C 1641

55 (2) INFORMATION FOR SEQ ID NO:213

- 60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2250 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 65 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 70 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
(A) NAME/KEY: misc feature
75 (B) LOCATION 1...2250

146/490

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:213

5 ATGAAAAAAC TTCACATGAT TGCCGCTTAA GCCGTCCTGC CTTTCTGCCT GACGGCACAA 60
GCACCCGCTCT CCAACAGCGA GATAGATAGT CTTAGCAATG TGCAGCTCCA GACCGTACAG 120
GTCTAGTCTA CTGCGGCCAC GGCGAAAAACC CCTGTCGCTT ACACCAAAGT TCGCAAGGCC 180
GAACTTTCCA AGTCCAAATTA TGGTCGTGAC ATCCCTATC TGCTGATGCT GACTCCCTCC 240
GTGGTAGCCA CCAGCGATGC CGGTACGGGT ATCGGATATT CGGCTTTGCG CGTGGGTGGC 300
ACCGATGCCA ATCGCATCAA CATAACTACC AATGGAGTAC CCCTCAACGA CTCCGAATCT 360
CAGTCCGCTCT TTTGGGTGAA TATGCCCGAC TTCGCTCTT CCATCGAAGA CCTTCAGGTG 420
10 CAGCGAGGTG TGGGTACTTC CACCAATGGT GCCGGAGCTT TTGGGGCAAG TGTCATATG 480
CGTACGGATA ATTTGGGACT GGCTCCTTAT GGCCGTGTGCG ATTTGAGCGG AGGTTCTGTT 540
GGCACAATTCC GCCGATCGGT CAAACTCGGT AGCGGACGCA TCGGTGCGCA TTGGGCGAGT 600
GATGCCCGCC TGTCCAAAT CGGTTCTGGAC GGCTACGTGG ATAGAGGAAG CGTGGATCTG 660
AAATCCTATT TCGCACAGGT GGGCTATTTC GGTAGCAACA CGCTCTCAG GTTCATCACT 720
15 TTCGGAGGAA AAGAAGTTC GGGTATCGCA TGGAAACGTC TTTCCAAGGA GGATGAAGCC 780
AAATATGGCC GCGGATACAA CAGTGCCGT CTTATGTACG TGGACGCGCA AGGAGTACCG 840
CACTACTACC ACAATACCGA CAATTACGAG CAGCGTCACT ACCATGCCAT CATGACGCAC 900
AGGTTCTCTC CTTCCGTTAT CTTCAACCTC ACGGCACACT ACACGGCCGG ATATGGCTAT 960
ACGGAGGAAT ATCGTACCGS ACGTAACTA AAGGAATATG CACTGCAGCC CTATGTGGAA 1020
20 AACAGTGTGA CGGTGAAGAA AACGGATCTC ATCCGTCAGA AGTATCTGGA CAATGACTTC 1080
GGAGGACTCA TCGGTTGCT TAAGTGGCAC ACCGGTGCA TGGGATTGCA GTTCGGGGCC 1140
TCGGGCAATA TCTATAAAGG AGACCACTTC GGCGGTATCA CTTACATCAA AAGTACAAT 1200
CAGCCCTTAG CTCCCGACTT CGAATATTAT CGGAACAGGG CAGACAAAAG AGAAGGTGCA 1260
GCCTTTGCCA AAGCCAACTG CGGATCACT CGGAACTGA ACATGTATGC CGACCTCCAG 1320
25 TATCGTACCA TCGGTACAC GATAACCGC ATCAGGACG AATATGATGA GGTACAGGGA 1380
AGATGCGAGC ACATCGATTG GGACAAGACC TTCCGCTTCC TCATCCGAA GGCCGGTCTT 1440
ACCTATAGTT TCGACGATGC TCATCTGCC TATGCTTCTG TTGCGGTAGC ACACCGCGAG 1500
CCTAACAGAA CCAATTACAC CGAAGCGGA ATAGGACAGT ATCTACGCC TGAGCGACTG 1560
ATCGACTATG AGCTGGGCTA CCGCTATGCT TCGCCCTCTT TGTGCGCCGG AGTAGGTCTC 1620
30 TATTATATGC AATACAAGGA CCAACTCGTG CTGGATGGCC GTTTGAGCGA TGTGGGACAG 1680
ATGCTCACAA GCAACGTCCC CGACAGCTAC CGTATGGGAC TGGAGCTGAC TCTCGTTGG 1740
CAGATCCTTC CTGTTTGGCT GCGTTGGGAT GCTTCTTTCA CTATGAGTCG CAACAAAATC 1800
GACCGCTACG TACAAATATC ATCCGTATAT GATGCGGACT ACAACTGGCT CGAACTCAG 1860
GAGGAGACCC TCGAAAGCAC GGAATAGGCC TACTCGCCCA ATGTCATGCG CGGACGATG 1920
35 CTTACCTCT CTGATGCCGG TTTCGAAATG GCTTGGAGCA GCCGCTTCGT CAGCAAGCAA 1980
TATCTGGACA ATACACAGCG CAGCGATCGC ATGCTTCTCT CCTATTGGGT GAACGACCTC 2040
CGCTCCGGCT ATGTGCTGCC GGTTCACCTT GTTAAGAGAG TGGCACTGGG CGTACAGCTC 2100
AATAATCTCT TCAACCTCAT GTATGCGTCC AATGCCTACA TCTACGATGC CGGTTACGTA 2160
40 CAGGCATCCG GAGAACTAAG TGCAATGCCC GATCTGCGTT ATTATCTCA GGCCGGATTT 2220
AATGCACTGG GTAGTCTGAC AATCGATTTC 2250

(2) INFORMATION FOR SEQ ID NO:214

45 (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1482 base pairs
(B) TYPE: nucleic acid
(C) STRAINEDNESS: double
(D) TOPOLOGY: circular
50 (11) MOLECULE TYPE: DNA (genomic)
(111) HYPOTHETICAL: NO
55 (1v) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
60 (1x) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1482

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:214

65 ATGAAAAGAA GGTTCCTATC GCTGTTACTG CTGTACATAC TCTCTTCCAT CAGCCTTTCT 60
GCTCAGCGGT TTCGATGGT GCAGGGAATC GAGTTGGATA CCGATTCCGT TTTCTCTCTG 120
CCCAAGCGTC CTTGGCGCGC CATCGGTAAA ACGATAGGCG TCAATCTGGC CGTATGGGGC 180
70 TTGATCAAT TCATCATGAA CGAGGACTIT GCAGACATCA GTTGGCAGAC TATCAAGAGC 240
AATTTCCAAA CAGGCTTTGG CTGGGACAAAT GACAAGTTTG TCACCAACCT CTTGCGACAT 300
CCTTATCAAG GATGCTCTA TTTCAATGCA GCGAGGTGCA ACCGTTTGA GCTTCAGGCAC 360
TCTGCTCCGT TTGCTTCTT TGGCAGTCTC ATGTGGGAGC TGCTTATGGA AAACGAGCCA 420
CCGAGTATCA ACGACCTCTG TGCCACCACC ATAGGCGGTA TAGCTTTGGG GGAGATGGGG 480
CAGAGGCTGT CCGACCTGCT CATCGCAAT CGTACCACAG GGTGGGAACG TATGGGGCGC 540
75 GAGGTGGCTA TCGCTCTGAT CAATCCGATG CGCTTTCTCA ACCGTCTGAC ACCAGGAGAG 600

147/490

GTGACTTCTG TCGGGAGTCG CAGCGGACAG ATATTTTCAGT CTGTCCCAT AAACATAGTC 660
GTGATGCGG GCTTTCGCTT TTTGGCAGAC AAGCGGCATG CCGGAACCGG TGCCACGSGT 720
CTGACCCCTGA ATCTGAGATT CGACTAGGGC GATCCATTCC GAAGCGGAGAC TTTCTCTCCA 780
TACGATTCTT TCCAATTCAA AGCCGGATTG AGTTTCTCCG AATCGCAACC TCTGCTGAGC 840
5 CAGATCAATC TGATCGGAAT CCTAAGCGGA TGCCAACTGC TCGCACACGA ACGAACGGTT 900
TTGGTGGGAG GTCTCTTTCA GCACTTCGAC TACTACAATT CGGAAAAACG AATAAGCAAA 960
AATTCGGAGG AGGTACTCGT CACCCCATAC CGTATCTCGC AAGTGGCAGC TCTGGGAGGC 1020
GGTCTTATCT TCCAGCACCA CGGAAAAATT CGACGAGTC CTCTGGAGCT ATATGCCGAG 1080
10 ACCTACCTGA ATGTCGTCCC GATGGGAGCC AGTCTGTCCG ATCACTACAA CGTGGACAAT 1140
CGGGACTATA ACCTCGGCAG CGGATTGAGC GGCAAGCTAT ACCTTGGTGC TACGTACAAT 1200
GATCTGTGGA GCTGGCTCTT GGGAGTCGAA AGCTATCGGC TCTACACATG GATCGGGTAT 1260
GAAGAGCCGC ACCAGAAAAA TACCGATGTC AGCTCTTTTA TGGTGCAGGG GGACGAAAGC 1320
AAGGCCGCC TACTGGTGAC GAGTTCCGAG TTCGCATTTC ATCCTGGCCC CTGGCATGTA 1380
GCCATCGTCG CTCGCCGTTT CATCCGCAA ACAGCCTATC AATTCTACCC TAACGTATCA 1440
15 TTCGATACCG GCGACATACA GCTGCGTGTC GGATTTCAT TC 1482

(2) INFORMATION FOR SEQ ID NO:215

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 882 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 25 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 30 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 35 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...882
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:215

ATGAAACGAC TGATTGTTTT TCTGGCAATG GGTGGCTTGC TGTTCACCCT TGCGAAGCGA 60
CAAGAAGCAA AACTGTCATC TGCACTCCC AAAAAGGACT GGACTATAAA AGGTGTGACC 120
GGACTAAATG OCTCTCAGAC TTCTCTGACC AACTGGGCTG CCGGTGGAGA AAACACGGTG 180
GCACGTAAAC TCTATTGAA CATAGATGCC AACTACCTGA AAGATAAATG GAGTTGGGAC 240
45 AACGGTTTTG GTACAGACTT CGGTCTGACC TACACAACAG CCAACAAGTG GAACAAAAGT 300
GTAGACAGA TCGAAGCTTT CACGAAGGCC GGCATATGAGA TCGGCAACCA TTGGTACGGA 360
AGTGGCGTTT TCACTTTCTT CTCACAGTAT GCCAAAGGAT ATGAGAAGCC CTCGGATCAC 420
TTGACAGGAG TCAAGCATAT CTCTAATTC TTGCTCTCTG CATATCTCAC TCTCGGTATT 480
GGTGGCGGACT ATAAGCCCAA TGAGAAGTTC TCTCTTACC TCTCTCTTAC AACGGGCAAG 540
50 CTGACTGTAG TAGCAGACGA CTACCTCTCA AGTTTGGGAG OCTTCGGGGT GAAAGTTGGT 600
GAAAGACAA TGTTCGAATC TGGTGCTTTG GTAGTGGGTT CGGCCAATAT AAATCTGATG 660
GAGAATGTCA ATTTGATAAC CAAGGCTTCA TTCTTCTCGG CTTATACGCA CGACTTTGGC 720
AACATTGACA TCAATTGGGA GGCTATGCTG GCCATGAAGA TCAACAAGTT CCTACGGGT 780
ACGATAGCCA CCAATCTTAT CTACGACGAT GATGTGAAGA TCAACGATGG CCGGAAATC 840
55 CAGTTCAAAG AAGTTGTGGG CGTGGGTGTT GCGTACACTT TC 882

(2) INFORMATION FOR SEQ ID NO:216

- 60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 612 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 65 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 70 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 75 (ix) FEATURE:

148/490

(A) NAME/KEY: misc_feature
(B) LOCATION 1...612

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216

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ATGAAGAAAA TGATTTTGGC AGCTACTATG CTGCTCGCAA CAATCGGTTT TGCAAATGCT
CAGAGTCGTC CTGCTCTTAG ACTGSATGCT AACTTTGTCG GTAGTAACTT AATGCAAAAA
GTGSCAAACA CGAGCGTGAA CAATAAGATG ATCGTAGGCT TACGTGTTGG TGCTGCTGCT
GAGTTCCGCTC TTAGCAATGA TGGATTCTAT CTCGCCCCCG GATTGGCCTA TACGATGAGA
GGTGCTAAGA TGGAACTACT AAGTGAACG ACAACTCGCT TGCATTATCT GCAATACCG
GTGAATGCCG GTATGAGATT TAGCTTTGCT GACAACATGG CTATTTTCATT GGAAGCAGGT
CCCTATTTCS CATATGGTGT CGCCGGAACG ATTAAGACTA AAGTTGCAGG CGTTACGGCT
TCTGTAGATG CCTTTGGTGA TAACGGATAT AACCGTTTCG ACTTGGGCTT GGGCTTGTCI
GCTGCCCTGA GCTACGACCG TTATTACGTA CAAATTGGAT ATGAGCATGG ATTGCTTAAT
ATGTTGAAGG ATGCTCCGGA TAAGACTTCT TTGCGTAATC ATGACTTCTT TGTGGGTCTC
GGTGTTCGCT TC

(2) INFORMATION FOR SEQ ID NO:217

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 729 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217

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ATGAAAAGGA TTTTACTGT AGCCCTTGTG CTACTTGCTT CGGTCACTAT GGCCATCGGA
CAAAGCCGCC CGGCACITCG CGTAGATGCC AACTTCGTAG GCAGCAATCA GAGCATGAAA
AGAGACGGAT ATGTGTGGA CACCAAAATG AATGTGGGCC TGCGGGTCGG TGCCGCTGCC
GAATTCTATG TCGGATCAAG AGGATTCTAC TTGGCTCCGG GTCTGAACTA TACGATGAAG
GGCTCCAAAA CGGAATGGA TATACCCGAA ATGGTTCCCTG GTACCTATAT TACGATGGTT
TCCACTCGCT TGCACTATCT GCAACTGCCG ATCAATGCCG GCATGCGGTT CGACCTGATG
AATGACATGG CGGTTTCGAT CGAAGCGGGT CCTTTCCTTG CATACGGTAT ATATGGTACA
TATCGGCAGA AGTTGGAAGG ATGGAAGCCG AACAACTACA GCACAGAGTT TTTTGGCCCA
ACGCTTGGTG GCCCAACAAA TATCCGCTGG GACATCGGGG CAAACATAAT AGCCGCATTC
CACTATAAGC GTTATTATAT ACAGATAGGC TATGAACATG GATTGTGGA TATTGTGTCA
GGTGGAGGTT CTGATATTCC CCGACTGAAC GACAATAGGC AATCCTCTTC GACGACCGCT
CTAAGAGAAA AGGGAATATA CGAATACGCT TATAATCGTG ACTTCTTCGT GGGCATAGGT
TACCGCTTT

(2) INFORMATION FOR SEQ ID NO:218

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 621 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature

149/490

(B) LOCATION 1...621

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:218

5	ATGAAAAGAA TCCTGCTGCT TCCTGTTGTA TTATTATATG GAATTGCAGG CCGATTGGCT	60
	GCACAAGACG TTATCAGACC ATGGTCATTG CAGGTCGGAG CGGGATACTC CGATACGGAG	120
	AACATCCCGG GAGGATTACG CTATGGTTTC TATTTGGGAA AGCGTATGGG GAGCTTTCTG	180
	GAAGTGGGGC TGTCATGTA CACTCCACA CGTCAACAG CCAACAATGC AGACTCCTTT	240
	GCATCGAAGC AAGGAGACGG ATCTTTTCAG GTAAATATGT CTCTCCGAA TGAGAAGTGG	300
10	TCATTCTTCG ATGCAGGCAG TGCCAACTGC TATATGATCG TCGTCGGAGT CAATCCTCTC	360
	CATCTGTTTT GGCAGAAATAG CCGGCACAAT TTGTTTCTGG CAGTACAAGC CGGCCTGTCC	420
	AATAAGCACA ATATTCATTT CATCTATGGA GACAAGGGAG CCAAAGTCAG TATCTACACC	480
	AATTGGAATA CCTACATCGG TTACGGAGCA CGTGTAGCCT ACGAATATCA AATTCAATAA	540
15	AACGTGGGGG CGGGTGCCGC TGTAATGTAC GACCACGGCA ATAAGATGCT TACGGCCATG	600
	GCCACGCTCT CCACTCATTT T	621

(2) INFORMATION FOR SEQ ID NO:219

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 2853 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
25	(D) TOPOLOGY: circular
	(ii) MOLECULE TYPE: DNA (genomic)
	(iii) HYPOTHETICAL: NO
30	(iv) ANTI-SENSE: NO
	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
35	(ix) FEATURE:
	(A) NAME/KEY: misc_feature
	(B) LOCATION: 1...2853

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219

40	ATGAGAGTAT CCGATCTCTG TTCCAGACTT TCATGGTTAT TACCGTAAT CCTTGTGGGA	60
	TTGCTCTGTG CTACTTTGGT CGCTGCGGAA CGTCTATGG CCGGAGCAGT CCGATTGCAC	120
	CACCGTCGGC ATGCTGCGCT GTCTGATTCT ACAGCGAAAG ACACGGTGCC TCTCGCAAAA	180
	CCTATTCCCTG ACAGTGCCTT TCGAGATTCC CTTCCTGCGS ATTCCACCGG ATCGATGCGG	240
45	CAAGATAGCG TGTATGACGA TGAATTCGAA TTGGAAGATA TAGTGGAGTA CGAAGCTGCC	300
	GATTCCATCG TTTTGCTCGG ACAGAATCGT GCCTATCTTT TCGGCAAGAG CTATGTGAGC	360
	TATCAAAAGA GTGCTTGGGA GGCAAACTTC ATGTATCTCA ATACCGACAG CAGTACGGTT	420
	TATAGTCGCT ATGTCTCTGA TACCGCGCGT TATCCGATGG CCTTTCCTGT TTTCAAGGAT	480
50	GGAGAGCAGT CGTTGGAAGC CAAGAATCTT ACCTACAAC TCGGCAAGGA GAAGGGGATT	540
	ATCAGCGGAG TGATCAGCGA GCAGGGCGAA GGCTATCTGA CTGCGCGTAA GACCAAGAAG	600
	ATGCCCGACA ATATCATGTT TATGCAAGGA GGGCGTTATA CGACCTGCGA CAATCAGAT	660
	CATCCTCACT TCTATATCAA TCTTTCCAAG GCAAAGGTGC ATCCGGAGAA AGACATCGTC	720
	ACAGGTCCGG TCAATCTGGT TATCGCGAT ATGCGCGTGC CGATAGGTCT TCCTTTGGC	780
55	TATTTTCCCT TTTCCAACAA ATACTCTTCC GGTATATTGA TGCCACGTA CGGAGAGGAC	840
	AATCGCTATG GATTTTATTT GAGGAATGGT GGATATTATT TTGCTTCAG CGACTATATC	900
	GAITTTGGCAT TCGGTGGGGA GATCTTTTCC AAAGGGTCAT GGGGCATTTC AGCCCAATCG	960
	AAATATAAGA AGAGGTATAA GTACAACGGC TCGTTGGAAG CCAATTATCT GGTATCGAAG	1020
	TCGGGGGACA AATACGTGCC CGGAGACTAC AGCAAGACCA CCACTCTGAA TATCCGATGG	1080
60	ACACACAGTC AGGATCCGAA GGCCAATCCT TTGCAACGCT TGTCGGCCAA TGTCATTTT	1140
	GCTACGACAC GAAGTTCGGC CGTGAGCTAT TCGGCGAAGT TTCCGGGTAC TCCTTTTTCG	1200
	ATTACGGGTA GCATGGATAT CAGCCAGAAC ATGCCGCGATA CGACGGTGAG CCTTACCTTG	1260
	CCGAATCTTT CGATTAATAT GTCCACGCGT TATCCTTTCA AGCGGAAGAC CCGTGTAGGA	1320
	CGGGAGCGAT GGTACGAGAA STTGAGTGTG GGCTATTCGG GTCAGCTTCG CAATAGTATC	1380
65	TTGACAAAAG AGAAAGATT TCTCCAGAGC AATCTCGTGC GCGATTGGAA GAATGCTATG	1440
	CGTCATTCCG TACCGATCAG TTTGACTGTC CCTTTGTTGG ATTATATCAA TCTGACTATG	1500
	GGGGTTAACT ACAATGAGTG GTGGTACAGC AAAGGCATAC GGAAGTCGTG GAATGAGGAT	1560
	AAGAAACAT TCCTGCCTTC GGACACGACC TATAAATTCC GCAGACTGTA CGATTACAGT	1620
70	CTGTGCGGAG GCTTATCTAC CACATTGTAC GGTATGTTCA AGCCTTGGAA ACCTTTTTC	1680
	TTCCGAGGCA ATCTCATTAT GATCCGTGAT CGCTTCAGC CCACTGTGAG TTTCTCCTAT	1740
	ATGCCGGACT TCACGAAAGC CCGATATGGC TTTTGGGAGC TTCTTGAGCA TACGGATCAG	1800
	AACGGCAAGC TGCATACGCT GCTCTACICT CCTTATTTCC AGCAGATATT CGGTGCTCCC	1860
	TCCATGGGCA ATGCAGGATC TGTCAATTTT TCTTTTGACA ACAACTTAGA GGCCAAGATC	1920
	AAATCCAAT CCGATTGAC AGGGATCAAG AAGATCAGCC TGATAGATCA GTTCACATGG	1980
75	TCTACATCTT ATAATATGTT TGCCGATTCC ATCCGATGGA GCAATATCTC GGCTTCGCTG	2040
		2100

150/490

	GCACTTCGCC	TCTCCAAGAG	CTTTACCTTG	CGCTTGTCGG	GTCTGTTCGA	TCCCTATTTG	2160
	ACGAAGTATT	ATCAGGGAGA	AGATGGGAAG	ATCATTCCCT	ATAAGAGCAA	CGACCTGCCG	2220
	ATTTTAAACG	GCAAGGGATT	GGCAGCCTG	ATCAGTACGG	GTACTTCTTT	CAGCTATACG	2280
5	CTCAACAAAG	AGTCGCTCAG	CGGATTGATA	GCTCTTTTCA	GTGGCAAAAA	GGAGCGGAGA	2340
	GATGAAAAGA	AAAACACAGG	GGCTACTCCT	CATGAAGGAG	ACGATGCTGC	CGATATACTT	2400
	GAGGGAGGAA	GACCGCAAAA	TGAAAGTGGG	GGGTGCTCC	TCGAGCGCAA	CCGTGAGGCG	2460
	GGAGCAGTGG	ATCAGGATGG	TTACTTCGCA	TATTGATCC	CATGGAGCCT	GTCTTCGAC	2520
	TATAGTTGGA	ATATTGCTAC	CGACTACAAT	AGGTACAATG	TCAATAAGAT	GGAGCACTAC	2580
10	TACCGGGTAA	CGCAGAATCT	GAGCTTTCGG	GGCAATATCC	AGCCTACACC	GAAGTGGAGC	2640
	TTCGGATTCA	ATGCGAACTA	CAATTTTCGAC	TTGAAGAAAA	TAACATCGCT	TACCTGCAAC	2700
	GTCACTCGCG	ACATGCACTG	CTGGGCTATC	TCGGCCAGTT	TCATCCCTAT	AGGAGCATAC	2760
	AAGTCCTATA	ATTTCGTCAT	ATCGGTGAAG	AGTTCACCT	TGCAGGATCT	GAAGTATCAG	2820
	CAGAGCAATC	GTCCCATCAC	GAATACTTGG	TAT			2853
15	(2) INFORMATION FOR SEQ ID NO:220						
	(i) SEQUENCE CHARACTERISTICS:						
20	(A) LENGTH: 3678 base pairs						
	(B) TYPE: nucleic acid						
	(C) STRANDEDNESS: double						
	(D) TOPOLOGY: circular						
25	(ii) MOLECULE TYPE: DNA (genomic)						
	(iii) HYPOTHETICAL: NO						
	(iv) ANTI-SENSE: NO						
30	(vi) ORIGINAL SOURCE:						
	(A) ORGANISM: PORYPHYROMONAS GINGIVALIS						
	(ix) FEATURE:						
35	(A) NAME/KEY: misc feature						
	(B) LOCATION 1...3678						
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220						
40	ATGATGAAAC	GATATACAAT	AAATCTTGCA	GTTTTCTTT	TATCTGAC	GGTATTACC	60
	TTTCAAAATA	AAGTCGCC	TTATGAAAGA	TTTGCAGATG	TAGAGAAGCC	TTGGATTGAG	120
	AAACATTCAA	TGGATTCTAA	ATTGGTGCCCT	GCAAATAAGG	GTAACTTAAT	TCAAGCTGAA	180
	ATTGTATACC	AATCTGTTTC	TGAACATAGT	GACTTAGTTA	TTTCACTGT	GAACGAAATA	240
	AGGCTGCAA	ATCGTTTCCC	TTGCGATAGG	AAGTCTTTTT	TTGCAGAAAA	TCTACGGGCA	300
45	TCTCCCCCGG	TAGTTCCCGT	TGCCGTGAC	AAGTATGCGG	TACCGGTTGC	CAATCCAATG	360
	GATCCTGAAA	ATCCCAATGC	CTGGGATGTG	ACGCTAAAAA	TCACTACTAA	AGCGGTAACA	420
	GTACCTCTCG	ATGTGGTGAT	GGTTATCGAC	CAGTCTTCGT	CAATGGGAGG	GCAAAACATT	480
	GCCAGATTAA	AGTCTGCCAT	TGCATCGGGA	CAGCGTTTTG	TGAAAAAAT	GTGCTAAG	540
	GGGACGGCTA	CAGAAGGGGT	GCSTATCGCT	CTGTGAGTT	ATGACCATGA	GCCTCATCGC	600
50	TTATCTGATT	TTACCAAGA	CAGTCTTTT	CTCTGTCAA	AAATCCGGGC	TTTGACTCCT	660
	ATTGGGGGAA	CACATACCCA	GGGGGGGCTT	AAAATGGCGA	GAACATTAT	GGCCACTTCT	720
	ACTGCTGTGG	ATAAGCATAT	CATATTGATG	TCTGACGGGT	TAGCGACGGA	GCAGTATCCT	780
	GTAAAAAATG	TAACTACTGC	AGACTTCATT	GGCAAACTG	GAAATGCGAA	TGATCCCAT	840
	GATTGGTTA	TACAAGGAGC	AATTAATTTT	CCTACAAAT	ATGTTTCCAA	CAATCCATCT	900
55	ACACCTCTTA	CCCAAAATTA	TCCAACATCAT	TCTTCTAAAG	TTGGACGGAG	AAATCTGCGG	960
	GAATCCAAAT	TCGATTATAG	TAACTCTGAGT	GCAAGGATTA	CTTTGATGG	TGTTGTGGG	1020
	GCATTGGTCT	ATGAACCGAG	GTTCCTCAT	CCCTATTATT	ATTATTTCCC	TTGTAACGCT	1080
	GCTATCAATG	AGGCTCAGTT	TGCGAAAAAC	TCTGGTTATA	CAATCCATAC	TATTGGCTAT	1140
	GACCTGGGAG	ATTTTGCCCT	GGCCAACAAT	TCGTTGAATC	TAACCGCTAC	AGACGAGAAAT	1200
60	CACCTCTTTA	CGGCGACACC	GGCCAATTTA	GCTGCAGCGT	TTGATAATAT	TGCCCAAAT	1260
	ATTAATATAG	GTATACAGAG	GGGGGAGGTG	ACGGACTTTG	TAGCTCCTGG	TTTCATCGTT	1320
	AAAAATCTGA	CGCAATCGGG	AGATGTTACT	CATTGCTAA	ATGTTTCAA	TGGAACGGTG	1380
	CACATGATG	TCTCTACTAA	AAAACTGACA	TGGACTACTG	GTACTATCCT	GAGCTCATCA	1440
	GAAGCTACCA	TAACCTATCG	TATTTATGCC	GATTGGGATT	ATATACAGAA	CAATGATATT	1500
65	CCGGTAATA	CTACTTCTGC	TATCGGCCCG	GATCTGGTG	GATTGATAC	CAATACCGAG	1560
	GCAAAATTA	CCTATACCAA	TTCCAATGGC	GAACCGAATC	ACAGTTAAT	TTTCCCACGT	1620
	CCGACGGTTA	AGTTAGGTTA	TGGTGTATT	AAGCGGCACT	ATGATTGGT	AAATAAAGAC	1680
	GGTCAACCCA	TACAGGCAAA	TGGAACAGTT	GTCACTTCCC	TAAGCGAGGC	TCATGTTCTA	1740
	CAGTCACAA	ATTTCTTTT	GCCCTCAGGT	GGAGGTGATA	TTGTTCCCAA	ATGGATAAAG	1800
70	TTGGACAAA	CGACCGAAGC	ATTACAGTAC	TATTCCGTAC	CGCCGACTAA	CACGGTCATC	1860
	ACTACTGCCG	ATGGTAAACG	TTATCGTTTT	GTCCGAAGTCC	CAGGCTCCAC	CGCGAATCCG	1920
	GGCCAAATCG	GTATCAGTTG	GAAAAAACCG	GCAGGAAACG	CTTACTTCGC	TTACAAGCTC	1980
	CTCAATTATT	GGATGGGAGG	AACAACAGAC	CAACAGAGTG	AATGGGATGT	GACGTCCCAAT	2040
	TGGACAGGAG	CCCAAGTACC	GCTCACAGGA	GAAGATGTAG	AGTTTGCAAC	GACGAAAAAT	2100
75	TTCCGTTCTC	CGCGGTGTCG	CGATTGTCAT	GTCCCGACAA	CCAAOCCCAA	AATTATCGGT	2160
	AACCTTATCA	ATAATTCGGA	CAAGGATTTA	GTTGTTACCA	CAAGCAGTCA	ATTGACGATC	2220

WO 99/29870

PCT/AU98/01023

151 / 490

	AACGGCGTGG	TTGAGGATAA	CAATCCGAAT	GTCGGTACGA	TGTCGTGAA	GTCGTGAAA	2280
	GACAAATCCTA	CGGGGACATT	GCTTTTGGCC	AATCCGGGCT	ATAATCAAAA	TGTAGGGGGG	2340
	ACCGTCGAGT	TTTACAATCA	GGGATATGAT	TGTGCCGATT	GTGGTATGTA	TGCGAGGAGC	2400
	TGGCAGTATT	TCGGTATCCC	TGTCAATGAA	TCAGGTTTTC	CAATTAATGA	TGTGGGCGGA	2460
5	AACGAGACCG	TCAACCAATG	GGTTGAGCCT	TTCAATGGCG	ATAAGTGGCG	GCCAGCACCT	2520
	TATGCACCTG	ATACAGAGCT	TCAAAAATTC	AAGGGCTACC	AGATCACGAA	TGACGTGCAG	2580
	GCACAGCCTA	CGGAGATTTA	CAGCTTCAAG	GGTATGATT	GTGTGTCCGA	TGCCTTCCTG	2640
	AATCTGACAC	GCACGTCCGG	TGTCAACTAC	TCGGGCGCCA	ACTTGATCGG	CAACTCATAC	2700
	ACTGGAGCCA	TCGACATCAA	GCAGGGTATT	GTCTTCCCGC	CGGAAGTCGA	GCAGACGGTG	2760
10	TATCTGTTCA	ACACGGGAAC	ACGCGACCAG	TGGCGTAAGC	TTAATGGAAG	CACGGTTTCA	2820
	GGCTATCGAG	CCGGTCAGTA	CCTCTCTGTA	CCTAAGAATA	CAGCGGGTCA	GGACAATCTT	2880
	CCGGATCGTA	TTCCATCGAT	GCATTCTTTC	TTGGTGAAGA	TGCAGAACGG	AGCGTCTTGT	2940
	ACGTTGCAHA	TCTTGTACGA	TAAGCTGCTC	AAGAACACGA	CTGTAAACAA	CGGTAATGGT	3000
	ACGCAGATCA	CATGGCGATC	CGGCAACTCC	GGATCGGCGA	ATATGCCGTC	ACTTGTGATG	3060
15	GATGTTCTTG	GTAACGAGTC	GGCCGACCGT	TTGTGGATCT	TTACCGATGG	GGGTCTTTCT	3120
	TTCGGATTTC	CAACCGGCTG	GGATGGTCCG	AAGCTGACTG	AAAAAGGTTT	GTCACAACTT	3180
	TATGCGATGT	CTGACATCGG	TAATGATAAA	TTCCAGGTTG	CAGGGGTTC	GGAGTTGAAT	3240
	AACCTGCTGA	TCGGCTTCGA	TGCGGATAAG	GATGGTCAAT	ACACGTTGGA	GTTTGTCTTT	3300
	TCGGATCATT	TTGCGAAAGG	GGCTGTTTAC	CTGCACGATC	TTCACTCAGG	AGCCAAACAC	3360
20	CGTATTACGA	ATTCTACGTC	GTATTCATTC	GATGCCAAGC	GGGGAGATTG	CGGGGCTCGT	3420
	TTCCGCTTGT	CATATGGATG	TGATGAGAAC	GTAGATGATT	CGCATGTGCT	GAGTACAAAT	3480
	GGCCGTGAAA	TTATAATTCT	GAATCAGAT	GCTCTTGACT	GCACGTGAAC	CTTATTCACA	3540
	ATAGAAGGTA	AGCTTCTTCG	CCGCTTGAAA	GTATTAGCTG	GTATAGAGA	AGTCATGAAA	3600
	GTGCAGACCG	GAGGGGCCCTA	TATTGTGCAT	CTTCAAAATG	CTTTCATAA	TGATGTGCAT	3660
25	AAGGTGCTTG	TTGAGTAT					3678

(2) INFORMATION FOR SEQ ID NO:221

30	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 3675 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
35	(D) TOPOLOGY: circular
	(ii) MOLECULE TYPE: DNA (genomic)
	(iii) HYPOTHETICAL: NO
40	(iv) ANTI-SENSE: NO
	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
45	(ix) FEATURE:
	(A) NAME/KEY: misc_feature
	(B) LOCATION 1...3675
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221

	ATGAAACGAT	ATACAATAAT	TCTTGCAATT	TTTCTTTTAT	TCTGCACGGT	ATTACCTT	60
	CAATAAAAG	CTCGCCCTTA	TGAAAGATT	GCAGATGTAG	AGAAGCCTTG	GATTGAGAAA	120
	CATTCAATGG	ATTCTAAAT	GGTGCCTGCA	AATAAGGGTA	ACTTAATTCA	AGCTGAAATT	180
	GTATACCAAT	CTGTTTCTGA	ACATAGTGAC	TTAGTTATTT	CACCTGTGAA	CGAAATAAGG	240
55	CCTGCAAAATC	GTTTCCCTTC	GCATACGAAG	TCITTTTITG	CAGAAAATCT	ACGGGCATCT	300
	CCCCCGTAG	TTCCCGTTGC	CGTCGACAAG	TATGCGGTAC	CGGTTGCCAA	TCCAATGGAT	360
	CCTGAAATC	CCAATGCCTG	GGATGTGACG	CTAAAAATCA	CTACTAAAGC	GGTAACAGTA	420
	CCTGTCGATG	TGGTGATGGT	TATOSACCAG	TCTTCGTCAA	TGGGAGGGCA	AAACATTGCC	480
	ASATTAAGT	CTGCCATTGC	ATCGGGACAG	CGTTTGTGA	AAAAAATGTT	GCCTAAGGGG	540
60	ACGGCTACAG	AAGGGGTGCG	TATCGCTCTT	GTGAGTTATG	ACCATGAGCC	TCACTGCTTA	600
	TCTGATTTTA	CCAAAGACAC	TGCTTTTCTC	TGTCAAAAAA	TCCGGGCTTT	GACTCCTATT	660
	TGGGGAACAC	ATACCCAGGG	GGGGCTTAAA	ATGGCGAGAA	ACATTATGGC	CACCTCTACT	720
	GCTGTGSATA	AGCATATCAT	ATTGATGTCT	GACGGGTTAG	CGACGGAGCA	GTATCCTGTT	780
	AAAAATGTAA	CTACTGCAGA	CTTCATTGGC	AAAACCTGGA	ATGCGAATGA	TCCCATTGAT	840
65	TTGGTTATAC	AAGGAGCAAT	TAATTTCCCT	ACAAAATTATG	TTTCCAACAA	TCCATCTACA	900
	CCTCTTACCC	CAAAATTATC	AATCTATTCT	TCTAAAGTTG	GACGGAGAAA	TCTGCCGGAA	960
	TCCAAATTGG	ATTATAGTAA	TCTGAGTGCA	AGGATTACTT	TTGATCGTGT	TGCTGGCGCA	1020
	TTGGTCTATG	AACCGAGGTT	TCTCATCCCT	TATTATTATT	ATTTCCCTTG	TAACGCTGCT	1080
	ATCAATGAGG	CTCAGTTTGC	GAAAAACTCT	GGTTATACAA	TCCATACTAT	TGGCTATGAC	1140
70	CTGGGAGATT	TGCGCTTGGC	CAACAATTCG	TTGAAACTAA	CCGCTACAGA	CSAGAATCNC	1200
	TTCTTTACGG	CGACACCGGC	CAATTTAGCT	GCACGCTTTC	ATAATATTGC	CCAAACTATT	1260
	AATATAGGTA	TACAGAGGGG	GGAGGTGACG	GACTTTGTAG	CTCCTGGTTT	CATCGTTAAA	1320
	AATCTGACGC	AATCGGGAGA	TGTTACTCAT	TTGCTAAATG	TTTCAAAATG	AACGGTGAC	1380
	TATGATGTCT	CTACTAAAAA	ACTGACATGG	ACTACTGGTA	CTATCCTGAG	CTCATCAGAA	1440
75	GCTACCATAA	CTTATCGTAT	TTATGCGGAT	TTGATTATA	TACAGAACAA	TGATATTCCG	1500

152/ 490

5 GTAAATACCTA CTTCTGCTAT CGGCCCGGAT CTTGGTGGAT TCGATACCAA TACCGAGGCA 1560
AAATTGACCT ATACCAATTC CAATGGCGAA CCGAATCAGC AGTTAATTTT CCCACGTCGG 1620
ACGGTTAAGT TAGGTTATGG TGTATTAAAG CGGCACCTATG TATTGGTAAA TAAAGACGGT 1680
CAACCCATAC AGGCAAAATGG AACAGTTGTC AGTTCCCTAA GCGAGGGCTCA TGTCTACAG 1740
TCACAAGATT TCTTTTGGCC CTCAGGTGGA GGTCAATTTG TTCCCAATG GATAAAGTTG 1800
GACAAAACGA CCGAAGCATT ACAGTACTAT TCCGTACOSC CGACTAACAC GGTCACTACT 1860
ACTGCCGATG GTAAACGTTA TCGTTTGTG GAAGTCCGAG GCTCCACGCC GAATCCGGGC 1920
CAATTCGGTA TCAGTTGGAA AAAACCGGCA GGAACGCTT ACTTCGCTTA CAAGCTCCTC 1980
AATTATTGGA TGGGAGGAAC AACAGACCAA CAGAGTGAAT GGGATGTGAC GTCCAATTGG 2040
ACAGGAGGCC AAGTACCGCT CACAGGAGAA GATGTAGAT TTGCAACGAC AGAAATTTT 2100
GGTTCTCCGG CGGTAGCCGA TTTGCATGTC CCGACAACCA ACCCCAAAT TATCGGTAAC 2160
CTTATCAATA ATTCGACAA GGAITTAGTT GTTACCACAA GCAGTCAATT GACGATCAAC 2220
GGCGTGGTTG AGGATAACAA TCCGAATGTC GGTACGATCG TCGTGAAGTC GTCGAAAGAC 2280
AATCCTACGG GGCATTTGCT TTTTGCCAAT CCGGGCTATA ATCAAAATGT AGGGGGGACC 2340
15 STCGAGTTTT ACNATCAGGG ATATGATTGT GCCGATTGTG GTATGTATCG CAGGAGCTGG 2400
CAGTATTTCG GTATCCCTGT CAATGAATCA GGTTTTCCAA TTAATGATGT GGGCGGAAAC 2460
GAGACCGTCA ACCAATGGGT TGAGCCTTTC AATGGCGATA AGTGGCGGCC AGCACCTTAT 2520
GCACCTGATA CAGAGCTTCA AAAATTCAAG GGCTACCAGA TCACGAATGA CGTGCAGGCA 2580
CAGCCTACGG GAGTTTACAG CTTCAGGGT ATGATTGTG TGTGGCATGC CTTCCTGAAT 2640
20 CTGACACGCA CGTCCGGTGT CAACTACTCG GGCGCCAATC TGATCGGCAA CTCATACACT 2700
GGAGCCATCG ACATCAAGCA GGGTATTGTC TTCCCGCCGG AAGTCGAGCA GACGGTGTAT 2760
CTGTTCAACA CCGGAACACG CGACCACTGG CGTAAGCTTA ATGGAAGCAC GGTTCAGGC 2820
TATCGAGCCG GTCACTACCT CTCGTGACCT AAGAATACAG CCGGTGAGGA CAATCTTCCG 2880
GATCGATTTC CATCGATGCA TTCCTTCTTG GTGAAGATGC AGAACGGAGC GTCTGTACG 2940
25 TTGCAATCT TGTACGATA GCTGCTCAAG AACACGACTG TAAACAAACG TAATGGTAGC 3000
CAGATCACAT GGCATCCGG CAACTCCGSA TCGGCGAATA TGCCGTCCTT TGTGATGGAT 3060
CTTCTTGCTA ACGAGTCGGC CGACCGTTG TGGATCTTTA CCGATGGGGG TCTTTCTTTC 3120
GGATTGACA ACGGCTGGGA TGGTCGCAAG CTGACTGAAA AAGGTTTGTG ACAACTTTAT 3180
CGGATGCTG ACATCCGTAA TGATAAATTC CAGGTTGCAG GGGTTCCGGA GTTGAATAAC 3240
30 CTGCTGATCG GCTTCGATGC GGATAAGGAT GGTCAATACA CGTTGGAGTT TGCTCTTTCG 3300
GATCATTTTG CGAAAGGGGC TGTTTACCTG CACGATCTTC AGTCAGGAGC CAAACACCGT 3360
ATTACGAATT CTACGTGCTA TTCATTGCTG GCCAAGCGGG GAGATTCCGG GGCCTGTTTC 3420
CGCTTGTCAT ATGATGTGA TGAGAACGTA GATGATTCGC ATGTCGTGAG TACAAATGGC 3480
CGTGAATTA TAATTCGAA TCAAGATGCT CTGACTGCA CTGTAACCTT ATTACATAA 3540
35 GAAGGTAAGC TTCTTCGCCG CTGAAAGTA TTAGCTGGTC ATAGAGAAGT CATGAAAGTG 3600
GAGACCGGAG GGGCTATAT TGTGCATCTT CAAATGCTT TCACATAATGA TGTGCATAAG 3660
GTGCTTGTTG AGTAT 3675

40 (2) INFORMATION FOR SEQ ID NO:222

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1275 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
(B) LOCATION 1...1275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222

65 ATGGAAGTGA AGAAAAACAC AGTGGTGCTA CGCCTTCTGA TTTGGTTCGT GGCCATTCTT 60
CTCTTCCACT CCTCACGGCT GTGGGGACAG GAAGGGGAGG GAGTGGCCG ATACAGATTC 120
AAAGGATTTC TGGATACCTA CCATGCCGTA CGCAGCTCTT CTCCTTTTGA TTTATGAGC 180
TCGCGTACGA GAGTGAGAGG TGAGCTGGAG AGGTCGTTCC GTAATTCGAA AGTAGCCGTA 240
TCGGTCAATG CCACCTACAA TGCTCTACTG AAAGACGAGA CCGGCTTACG TTTACGTGAA 300
GCCTTCTTCC AGCATCAGGA AGAGCATTGG GGGTTGCGCC TCGGACGACA GATTGTCTAT 360
TGGGGGCGCT CGAACGGTGT GCGCATCAGC GATCTGATCT CCCCGATGGA TATGACCGAG 420
70 TTTCTGGCAC AGGATTACGA TGATATTGCT ATGCCGGTCA ATGCATTGGG TTTCTCTGTC 480
TTCAACGAAT CGATGAAAGT GGAAGTCGTG GTACTGCGTG TATTGAGGGG GTACCGCTG 540
CCTGTGGATC CTGCAATCC TTGGAATATC TTCTCCCTTT CGCCCATTCG TCAGGGGATG 600
AATATCTCTT GGAAAGAAGA AGCCGGCAAA CCGGCTTCA AGGTTGCCAA TATCGAGTAC 660
GSTGCCGATG GGAGCACTAC GCTCTCCGGT ATCGACTTCC CTTTGGCTGC ATTGCATACA 720
75 TGGAAACAAG TGCCCGTCAT CGAAGTACAG GGCATTGTGC CGACGGAAAT CATCGTTAGC 780

153/490

5 CCGCTGCTATT ATCGTATGGG ATTTGTCGGC GCGGACCTCT CCGTACCGGT CGGACAGTTT 840
GTTTTCAGGG GAGAGGCTGC GTTCAATATC GACAAACACT TCACCTATAA GAGTCATGCC 900
GAGCAAGAGG GTTTCCTAAC AATCAATTGG TTGGCCGGAG CCGATTGGTA TGCTCCCGGT 960
GAATGGATGA TCTCAGGACA ATTCTCAATG GAAAGCATAT TCAGGTATAG GGATTTTCATC 1020
TCCCAAAGAC AACATTCTAC CCGTATTACT CTCATGTTT CCAAGAAATT CTTCGGCAGT 1080
ACACTCCAAC TTTCGGACTT CACCTACTAC GACCTTACGG GCAAGGATG GTTCAGTCGC 1140
TTTGAGCTG ACTATGCCCTT GAACGATCAG ATACATCTGA TGGCCGGATA TGAATGGTTC 1200
AGTAGTAAGG GCAGCGGTAT ATTCGATCGC TACAAAGACA ATTCGGAAT CTGGTTCAAA 1260
10 GCGGCTACA GCTTC 1275

(2) INFORMATION FOR SEQ ID NO:223

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
20 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
25 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
30 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223

35 ATGTCTCTCT GTGAGGTGGC TTATTTTCA CTAAAGCCGA TCGATCTGCA GAACATCCGC 60
GAACGGAATC ACTCTTCCGA CATCGCGCTT TCCAATTAT TAGACAATTC GAATCAGCTA 120
TTAGCTACTA TTCTGATCGG GAATAATGTG ATTAATGTAG CCATCGTTAT CCTTCCCAAT 180
TATGCCATCG AGCAGACATT CGTTTCTCT TCTCCGATCA TTGGATTCT GATCCAGACG 240
ATACTCCTGA CCCTGTTCT TTTGCTGTTT GGAGAGATTC TGCCGAAAGT GTATGCGCGG 300
40 AAGAATCCGC TGCAATACTC GCGCTTTCT GCTGCAGCTA TGTCGGTTAT CTATAAGATA 360
TTGTCAACGT TTTCAAAATT GCTGGTCAAA AGTACCGGCA TCGTTACCAG AGGTATCAGC 420
AAGAAGAAAT ACGATATGTC CGTGGATGAG CTCTCGAAAG CCGTAGCCCT CACCACTACG 480
GAGGAGAGAG CCGAGGAGAA AGAAATGATT AACGAAATCA TCAAATTCTA TAATAAGACA 540
GCCTGCGAAA TCATGGTTCC GCGTATCGAT ATTGTGGATG TGGATCTGAG CTGGCCATT 600
45 CTTAAGATGC TTGACTTCGT TGTTCTGTC GGTATTCCA GACTTCCCGT TTCAGAGGGG 660
TCAGAGACA ATATCAAAGG GGTGATTAC ATCAAAGATC TAATCCACA CATGGATAAA 720
GGCGATGAAT TCGACTGGCA TCCTCTGATT CGTAAAGCAT ATTTGTCCC CGAAAACAAG 780
CGCATAGATG ATTTGCTCGA GGAGTTCAGA GCCAATAAGG TGCATGTCTC CATCGTTGTG 840
GATGAGTTCG GTGGCACTTG CCGACTGATC ACAATGGAGG ACATATTGGA AGAGATCGTC 900
50 GCGGAGATTA CGGACGAGTA CGATGAGGAA GAACTCCCT TTAAGGTTT GGGGGATGGC 960
AGTTATCTTT TCGAAGGAAA AACGCTCTCT TCCGATGTTT GACACTATCT TGACCTTCCG 1020
GAAATGCTT TCGGTGAATT GGGGGACGAG GTAGATACGC TAAGTGGGCT CTTCCTGGAA 1080
ATCAAGCAGG AACTCCCCCA TGTGGCGGAT ACAGCAGTGT ACGAGCCATT CCGCTTCAA 1140
GTGACCCAAA TGGACAAGCG CCGAATCATC GAAATCAAGA TTTTCCCTTT CGAGCGCACT 1200
55 TGGGAGGTG AA 1212

(2) INFORMATION FOR SEQ ID NO:224

60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 780 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
65 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
70 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
75 (ix) FEATURE:

154/ 490

(A) NAME/KEY: misc feature
(B) LOCATION 1...780

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:224

5
ATGAAACIAT TACTTTATCT CCTATTGGTC TTGTGACTC TATCCCCGAT GTATTGCGAA 60
ATGCTCTTCT CAGAGAATCT CACANTGAAT ATAGACAGCA CCAAACCCAT ACAAGGAACG 120
ATATTGCCCG TACTGGATT T CAAAACCGAA AAGGAAAATG TGTTCACCTT CAAAAATACT 180
GCCANTCTCA ATCTGCTGAT AAAGCACGGT CAAGTAATCA ACTTAATTAA TAAGCTTGAG 240
10 TTTTCTACCT ATGGCAATAA AGTAACCGTA AGTGGAGGAT ATGTACACAC CGAATACCGC 300
TAITTTGTTGC ATCATGTTTT TGAGGTTTAT CCTTATGTCG AGTCGCAATG GGCAGAAAGT 360
ACAGGAATGA AATATAAGGT TTCTACGGGA TTACAGTCGC GTTATCGGCT GGTAAATAGT 420
GATAACTGTC TCATGTTTGC AACATTGGGG GTATTTTTCG AATTGGAATA GTGGGAACAG 480
CCAGCCACTA GCCTCTTTGC AGGAACGTAT GCATACAGCC GAAGTATCAA AAGCCACCTG 540
15 TCTATCAGTT TCAGACATCG GTTGGGTGAA CATTTGGGAAT TTACAACCTAC GGCTATTAC 600
CAGGCAAAAG CTGACAGTTA TTITAAGAAG GCACGTTTTG GAGGAGCTAT CGACCTCAAA 660
TACCATATCA CACCTACGAT AGGAATACGC GGGGCTATC GGATCATCTA CGATACTGCC 720
CCTATTGTAC CTGTGCGGAA AGATTACAAC ACCGTTGATG TTGGTATCGA TATTTCGTTT 780

(2) INFORMATION FOR SEQ ID NO:225

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 2502 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORPHYROMONAS GINGIVALIS

(ix) FEATURE:

40 (A) NAME/KEY: misc feature
(B) LOCATION 1...2502

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:225

45 ATGAAACGAA TCGTTTTATC ATCTTTCTCG TTCGTTCTGT CCATACCTTC TTTGATGGCA 60
CAGAACAAATA CCCTCGATGT ACACATATCC GGTACGATCA AGGATGCCTC CTCGGGGGAA 120
CCAGTGCCCT ATGCCACTGT AAGCATCCGG CTGACAGGAG CAGATACCAC ACAGGTGTTT 180
CGACAAAGTA CTGACGGCAA CGGCTACTTC GTCATAGGCC TGCCGGCAGC TCCCTCCTAT 240
CACCTGACAG CTTCGTTCTG AGGTATGAAA ACCCATAGCA TGCAGATTAG TCGGGGAAAT 300
50 GGACAGCAGC ACATCAAATC CATCGACATT TCTCTCGAAT CCGAGGACAA ACAACTCTCC 360
ACCGTCACCG TATCGGCAGC AGCAACCTGC TCGAAATGCT GCGCAACGTT 420
AATATGAAG ATGACCCCGC AGCCAAGACG AACCAACCTGC TCGAAATGCT GCGCAACGTT 480
CCTTTGGTAA CGGTGGATGG TCAGGGCAAT ATCCAGGTGA AAGGATCTTC CAACTTCAAA 540
ATCCACCTCA ATGGCAGGCC CTCGACCATG GTGAGCAGCA ACCCGAAGGA GGTCTTTCGC 600
55 TCCATTCTCG CCCATACGAT CAAACGGGTG GAGGTCTATCA CCGATCCGGG TGTAAAGTAC 660
GATGCGGAAG GCACAAGTGC CATCTGGAC ATCGTCACGG AAGAAGGTAA GAAGCTGGAA 720
GGATATTTCG GTTCCATCAC GGCAGTGTG ACACAACAATC CCACAGCCAA CGGTAGTATC 780
TTTCTGACG CAAAGTCCGG CAAAGTCCGG CTGACTACCA ACTATAACTA CTACGGTGGC 840
AAAAACAAG GCTCTCGCTA CTTTACCGAA CGTACTACAT CCATGCTCCA AACGATAGAA 900
60 GAAGGCAAG GGCAGAAAC CTTTGGCGGA CACTTCGGA ATGCCCTCCT CTCATTTCGAG 960
ATAGATTTCG TCAATCTCTT TACGGTGGGC GGCATGTAC GCCTTTGGA GATGACCACC 1020
GACCGGAACA GCGTAGAAAA AAGCTTTGCC GGCAGCAACC TCATGTCCTA CATAGACAGA 1080
AAACTCAAAA CACAGATGGA TGCCGGATCA TACGAGCTCA ATGCCGACTA TCAGCACAGC 1140
ACTCGCTGCG CGGGCGAATT GCTCACCCTT TCCTACCGCT TCACTCACAA TCCTAATAAT 1200
65 AGCGAGACCT TCATTGACCA ATGGAAGCGC GATCCGCTCA ACACAGCTAA TACGATCCAG 1260
TACGCGGGCC AGCACTCCAA ATCCGATGGG GGCATGGACG AACATACGGC ACAAGTGGAC 1320
TATACACGTC CCTTAGGACA AGCAGATTCT TTGGAAGCAG GGTGTAAGTA CATCTATCGT 1380
CATGCCACGA GCGATCCTCT CTATGAGATA CGACCATCCG AAGATGCTCC GTGGCAGCCC 1440
GGCTCTCTAT ATGCACAGAA TCCGTCGAAC GGAAGTTCG GCCACGATCA ATACATCGGA 1500
70 GAGGCTATG CCGGCTACAA CTATCGTAAG GATCAGTATT CTTTGAACAC CGGCTCCGA 1560
GTGGAAAGCA CGAGCTGAA AGCACTCTTT CCGCAAAACG CAGCAGCAGA TTTTCCAC 1620
AACTCGTTGG ACTGGGTGCC ACAGCTCAGC CTCGGCTATA CCCCCTCGCC CATGAAGCAG 1680
CTTAAGCTGG CCTATAACTT CCGAATCCAA CGTCCCTGCA TCGGCCAACT GAATCCCTAC 1740
CGGTACAGA CCAACGATTA TCAAGTACAG TATGGTAATC CCGACCTAAA GTCGGAGAAG 1800
CGTACCAAG CTCGCTCTCT CATATAATCA TACGGAGCCA AGGTATGCT TACAGCATCG 1860
75 CTCGACTACG ACTTCTGCAA CAACGCCATC CAGAATTACA CTTTCTCCGA CCGGCCAAT 1920

155 / 490

5 CCCAATCTCT TCCACCAGAC CTATGGCAAT ATCGGACGAG AGCATTCTTT CAGCTTGAAT 1980
ACCTATGCCA TGTACACGCC GGGCGTATGG GTCAGGATTA TGCTCAACGG AAATATCGAT 2040
CGCACATTCC AAAAGAGCGA AGCACTCGGC ATTGATGTCA ATTATGGTC CGGCATGGTA 2100
TACTCAGGCC TGAFTTTCAC CCTGCCGAAG GATTGGACTG TGAATCTCTT CGGAGGTTAT 2160
TATCATGGGG GAAGAAGCTA CCAGACGAAG TATGATGGCA ATGATTCTCA CAATATCGGT 2220
ATAGCCAAAC AGCTTTTCCA CAAAAATTG AGAGTCTGCG TGAGCGCMAA CAACATTCAT 2280
GCGAAGTATT CGACATGGAA GAGCCGGACC ATCGGCAATG GATTTACTAT TTATTGGGAA 2340
AATGCCGGTA TACAACGGAG TGTTCCCTC AGCCTCACCT ACAGCTTCGG TAAGATGAAT 2400
10 ACACAAGTGC GCAAGGTAGA GCSTACGATC GTCAACGACG ACCTCAAGCA AACCTCATCC 2460
CAAGGACAGC AGGGTGGCGG ACAAGGAAAT CCTACCGGCA AT 2502

(2) INFORMATION FOR SEQ ID NO:226

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1197 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 20 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 25 (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 30 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226

35 ATGAGACTCT CTGCCATTCT TATCGCTTTG ATTGTGATGC TGCCTGCTGT GCTTAGCGGG 60
CAGCATTATT ATTCCATGGC GGGAGAGCGA CTGGAGACGG ACAGCATTCG TCCGAACGAA 120
CTCTCGGCAT CGATCCGAAG TGCGCTTTTC TTTCGGACAA ATGAATACAA TGCACGTTCCG 180
GTCAAAGGTT ATACGTTGCC GGGTGACGGG GTTTCGGCTT TTGCCCTCTA CTGCGTGCCG 240
40 GCAGCACATG GTGTGAAGCT TTCGCTCGGA GTATCTACCC TGAACACTCG GGGGGCAAGT 300
CGCTATCCGG CCGGTATCGC TTATTCGGAT TTACCTTATT GGAACGACTA TAACGACTAT 360
GTACGCTTGC GTATCCTGCC TTATGTACAG GCCATGCTGA AGCCGACGGC CACGACTGCT 420
CTCATGCTGG GCATATAGC CGGTGGTACG GCTCACGGAC TGATCGAACC GATCTACAAT 480
CCTGAGTTGG ATTTGACGGC TGATCCTGAA GCCGGTGTGC AATTTCGGGG TGATTGGACA 540
45 CGTTTCCGAA TGGATGTTTG GGTCAATTGG ATGAGCATGA TTTTCAAAAA TGACAATCAT 600
CAGGASTCGT TTGTCTTTGG CTGTGCCACT ACTTCGAAAT TGTTATCGGG TGAAGGCAAA 660
TGGCGACTCG AACTGCCCTT GCAGGCTATT GCCACGCATC GCGGCGGGGA ATACAACCTG 720
GGCGAGCAGS ATACCGTSCA TACATGGGTC AATGGAGCTG TCGGACTTAA GCTTTCGTAT 780
50 CGCCCTCGTA CCGACAAAC CATGCAGATT TGGGGATCTG CTTATGGTGT GGCAGCCTTG 840
TCAAGCGGAG GATACTTCCC TTACGAAAGA GGGTGGGGCG GTTATCTTTC TCTCGGAATG 900
GACTTGGAGC ACTTCGCTTT TCGTACCGAC TATTGGTACG GCAGGCATTA CGTTTCTCCC 960
TTTGTGCAC CTTTCGCCAA TTCCCTGACG TATGACAAAC AGCCTCTTAC GAACGGTTGG 1020
GGCGATTATA TTCGTCTCTA TGCCGACTAT TCGTGGCGCA TGGCAGGAAG TGTTTCGTTG 1080
GCGGCTGTTG CTCGGGTATG GTTCCAGCCT TCGGATCGTT TTGCGATGAG CCACGCCTTG 1140
55 GAAGTACGCA TCGGTATCGA TCCCAAAATC CCAATAGCTT TTCTGAAAGG CAATCAT 1197

(2) INFORMATION FOR SEQ ID NO:227

- 60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1146 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 65 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 70 (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 75 (ix) FEATURE:

(A) NAME/KEY: misc feature
(B) LOCATION 1...1146

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:227

5
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20
25
ATGAACAAAT CGCTATTATC ATTGGCATGC CTCATCCTGT GCGGTATGCC GGCCATCGCC 60
CAACAGACAG GACCGGCCGA ACGCAGCGGC GAGCCTTCTC TGGCCGAAAG TGTATTGGT 120
CTGGAGCAGA AGCAGAAAAA GCTGAAGGTG TACTTAGGCA TACAGTCGTT CTACGACCAG 180
CCGCTTGTCC ATGACGAATC CCATATCGGA CACTTCAAGG TACAGGAGCT GCGGATGTCT 240
GCTCATGGCG AACTGAACCG CCACCTCAGC TTGACTGGC GACAACGTCT CAACCGTGCC 300
GCCGACGGCA CTTCGTTTGC CGACAATCTC TCCAATGCCA TCGACATCGC AGGTGTGGAC 360
TGGCACCCGA ACGACAAGGT GTCTTTCTTC TTCCGACGTC AGTACGCGCG TTTCGGAGGG 420
ATAGAATACG ACATGAACCC CGTAGAGATC TACCAGTACA GCGACCTTGT GGATTACATG 480
ACCTGCTATA CTTCGGGCGT GAACTTCGCA TGGAACTTCC ACCCCGAACA GCAGCTGCAG 540
CTACAGGTAC TCAATGCTTA CAACAACCGC TTCGCCGACC GCTACCAAGT GACACCCGAT 600
GTCCGTACCG CCACGAGCTA CCGGCTCCTC TACTCGGCAC AGTGGAAACG TACCCTCCTC 660
GGAGGAGCAC TGCATATGCG TTACGCCGTG TCGATGGCTC ATCAGGCCCA AGAGCGTAAT 720
ATGTGGTACT TCACTGCGGG CAACCTGTTC AATCCGGGCA AACGGATCAA CGGATACCTC 780
GACCTCACCT ACTCGATCGA GGGATTGGAC GACAAAGGCA TTATGACTGC TCGCTACGGC 840
AAGGGCAAGA CCCTCACGGA CGTCAAGTAC TATGCTCTGG TATCGAAGTG GAACTTCGCG 900
ATTTTCGATC AGGTCAATCT CTTCCTCAAA GGCATGTACG AGAACGGCTA TGCCTCGCC 960
CAATACGGCG AGAGCAGCCA CACGCGCCAC TCCTACGGCT ATATGGGAGG GGTGGAATAT 1020
TACCCTACGG AGACCAACTT CCGTCTGTTC GTACCTACA TAGGACGGCA TTACCGGTAC 1080
AGTGGGACCG AGACGGAAAG CACCAATGCT CTTCGCGCCG GTCTGATCTA TCAGATACCT 1140
TTCTTA 1146

(2) INFORMATION FOR SEQ ID NO:228

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 666 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
35 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
40 (iv) ANTI-SENSE: NO
(v) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
45 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...666

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:228

50
55
60
65
ATGAACATT TGTTTAAGTC GACATTAGTA CTCTTTGTG CTCTTTCTTT TTCCGGTACC 60
TATACCTTTG CACAAGAAAA TAATACAGAA AAGTCACGAT TTGATTTTTC TGTTAGGCTG 120
GGACAGGGAT ATATTGCAGG TTCAACTACC AACCTGATGT ATGGGTATAC ATCTGCTAAC 180
GATAGACTTT TGCTGGGTGC AATTATCTG GGCCTGACAC CAAGTAAGAA AGAAAATGCA 240
ACCGGCGTAG CATTTGTTTT CTATCNCCTC TCTCCGGGTT ATTATGCGA TATATCCGGC 300
AAAGAAAAAT CCTTGAATTA TGGGTTTTAC GTTGTGGGAG CATATAATAG AATAGCCATT 360
CCTATACGCC CTATCAAAAA TTTTAATTTC ATCTTCTCTA CAGAAGTCGG AATGGCTTGG 420
ATGAGTCGTC ATGAGCAAAAT TTACAATTCT ACTTCGCAGA CTTGGGATAA GCAGCGCAAG 480
TCGAGGTCCG GACTGGATTT TGGTCTCGGG ATGCATCTGC AATHCCACAT TAATAAGACC 540
GTTTACTTTA TGGCAGGAAC CGATCTTACG TCTTGCATGT TCGGAAAAAG GATCAATGAC 600
TACCAGCAAA AGGATCGAAC CTTCATTGCA CTTATCGACA ACAGTATTGG CATAGGATTA 660
AACCTC 666

(2) INFORMATION FOR SEQ ID NO:229

70 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1173 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
(ii) MOLECULE TYPE: DNA (genomic)
75 (iii) HYPOTHETICAL: NO

157/ 490

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229

15	ATGATTATCA AGAAATGCT GAAAAATAAA TTGGCCCCCT TGGCCATACT GTTCCTTTT	60
	GCTCCAAAGG CTATGAAGGC TCAGGAGCAA CTGAATGTGG TACACACCTC TGTGCCATCG	120
	CTGAATATCA GTCCGGATGC ACGTGGCGCC GGTATGGGGG ATATAGGTGT GGCAACGACG	180
	CCGGATGCGT ATTCACAGTA TTGGAATCCG AGTAAATATG CTTCATGGA TACGAAAGCC	240
	GGTATTAGCT TCTCATATAC ACCCTGGCTG TCCAAGCTGG TCAATGATAT TGCCCTGATG	300
	CAGATGACCG GTTTCTACAA ATTGGGAACA GACGAGAATC AGGCTATTAG TGCTTCTCTG	360
20	CGTTATTCCA CATTAGGAAA GTTGGAGACT TTCGACGAAT TGGCGGAATC CATGGGAGAG	420
	GCCCATCCCA ATGAATTTGC TGTGATTTG GGCTATAGCC GCCAGTTGTC GGAGAACTTC	480
	TCCATGGCTG TTGCACTGGG TTACATCCGC TCAGACCAAA GCACTACAAA CACCGGAGAG	540
	AATCAGGCCG GAAATGCCTT TGGCGCGGAT ATAGCCGGTT ATTTCAGAA GTATGTGCTA	600
	CTGGGTAATG CGGAGAGCTT GTGGTCGTTG GGTTCACAG TAAAGAATAT CGGAACGAAG	660
25	ATCTCCTATG ACGGAGGTGT CACGAGTTTT TTCATCCCTA CTTCGTTGAA TCTCGGGACG	720
	GGGCTGTTGT ATCCGATCGA TGACTATAAC AGCATCAAT TCACCTTGA ACTTAGCAAG	780
	CTGCTGTAC CCACTCCTCC TATCATGGAT CAAAACGATC AGGCCGGGTA TGAGGCTGCA	840
	CTCAAGAAAT ATCAGGAAAC TTCTTCGATC AGCGGTATAT TCTCTCTTT CGGTGATGCG	900
	CCGGGAGGAC TCAAGGAAGA ATTCCGTGAG ATTACATGGG GACTTGGGGC TGAATATAGC	960
30	TATGACGATA AATTTTTTGT TCGTCCGCGA TATTCATACC TGCACCCAC CAAAGGCAAT	1020
	TTGCAGTACT TCACGGCCGG TGGCGGCTTC AAAATGAACA TATTCGTTAT CGATGCTTCU	1080
	TACCTGTGT CTACGATCCA GAGTAATCCG TTGGATCAGA CTCTGCGGTT TACGCTTGCT	1140
	TTGATATGG ATGGATTGCG CAATTGTTC CAC	1173

(2) INFORMATION FOR SEQ ID NO:230

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1338 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230

60	ATGAAACAA CAGTTCAACA AATTATTCTG TGCCCTGCTT TAATGATGTC AGGTGTATTG	60
	GGCGGAAACG CACAGAGCTT TTGGGAAGAA ATAGCTCCTC CTTTATCAG TAATGAGCCT	120
	AACGTCAGT ATATAATTCC CAATATGGGG ATTGATTCAA AGGGAACAAT CTATGTAACC	180
	GTGACAAAAA GGATTCAGCA GGGAGCAAAAT TATACTTCTG AGCAATTGGG TATGTACTAT	240
	CGACCATTAG GTGATAATGA ACAGTGGTGG AAACATGATC CGTATTTTGA TGACAAGATA	300
	GTTCGGGATA TTCAGACAGA TGCATATGGC AGAGTTTATG TATGTACGAC TTCCTCTCGA	360
65	GATCAAGAGT ATCAACTTTA TATAAAGGAG CAGAACGAAT GGAGGTGTAT ATTCAAAACT	420
	TCTGTGCTA CATATGAGCA TGGTATGGCT GTTTTCGCT CTTCGACAGG GGTGACTTAT	480
	ATAGGTACCA GGCATCACAT CTTGCGATCA GGTGTAAATG ATTTCGAGTT CAACACTATC	540
	TATGAGACT CTACACCTAT GAGCTGTGCG TTTGACAGG CTACGAATAG TGGCACCATC	600
	TATCTGSCAT TGATGCATGA AACCACAATG TCTACGACTA TCCTTACTTA TCAAAACGGT	660
70	GAGTTCGTCG ATATCTCGGA AAGTGAATTG AGTAACTCGA TTATTGCATC CATGTGCTCT	720
	AATAAAGAAG GTGATATAAT AGCTCTTGT ACTTCATAIA CAGGATTTAT GAGTGAACCC	780
	CTTGGGATCA GAAAGCAGA TGAAGGCAAA TGGCAACTTG TTGGCGGAGA TATACAGAA	840
	GCGATCGTTC AAAATATATG CATGATGGAC GACAACAAGA TTGCTTGTGA AGTCTTCGGG	900
	ACTCCTAACG CAGTAGATGG TCGGACAAGG GTTTGTGTTT CTGACGCATC TGTCTTGAT	960
75	TTTGAAGTGT ATGAAGATGA AATATACGGA GGCCTGATAT TTGACACTTT CTCTATAGC	1020
	CCTTGGGACA AACTTCTTTA TGCGAAATTT GGTGGGATTA TGCTCAGGAG TAAAGAGTCT	1080

158/ 490

TTTATAACCT CTTTCATTTC TCCGACAGTT GTACAAGGAG TGGATGTCCTA TACTTTGGCC 1140
GGGAAGATAA GGATCGAAGG TGAACTCCG GTGTCTGAGG TGTGCTTTT CGACCTGGCT 1200
GGCAGGATGG TACTTCGGCA AACCATTGAT AATAAATCT ATTCGGACAT AGATACTAAC 1260
GGACTAAAGC GAAGCGGTAT TTACGTAGTC TCGGTGCGGC TCTCTTCCGG ACAGGTATTC 1320
5 AGTCATAAGG TGCAGGTA 1338

(2) INFORMATION FOR SEQ ID NO:231

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 924 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 15 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 20 (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 25 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231

30 ATGATAATCC GGTGTCTTAT CCGTCGTCCG AGAACCGTCC TGTTCGGGTT GATATTCGTG 60
GTAGGTCTTT TCTCTGGGAT GGCACAGAG AAAAAGGATA GTCTCTCTAC GGTTCAGCCA 120
GTGCCGAATA GCAGCATGGT GGAGCAGACC CCTCTCTCTT CCATTGATCA CCCCGTCTG 180
CCCGCTTCTT TTCAGAATAC CCGTACACTG AAAAGGTTTA GAGACAAACA TCTTCCGAT 240
35 GCTTTGCTCA ATGGATTGAA GCCTCATCGC TCATCTTTGC AATTGAATGA GGAACCAAC 300
TTCGCGGCAG AGCGTCGGGA TTTCGTTTCT CCGCTCTTGC AAACTCGCCA CGCTGCCGGT 360
GTCTTTTCAT GSCGACCGAC CGATAGGATG CATTTTATA CATCGGGCAA TATCGGTCTT 420
GGCCATGATT TATTGACCGG TGTGCGCAAG GACTTCGGAT GGAATGCTGG TGCCGACTTC 480
TTGCTGAGTC AAAATCTTAC GGCACATGTC CAAGGCGGTT GGCAGCAGAA TTTCCGGCTT 540
40 ATACCTATGA CGGCTGTCAA TGGCCAACCTG CGTTGGCAAG CCACCGAGAG ATTGAGTTT 600
ACCACCGGTA TCGATTATCG ACAGGTACAG TGGAAATGCT TCGATAATAG AACGTTCTCG 660
CTTAAAGGAA GTGCTCGATA CGAAGTGATG GACAATGTCT TTGCAATGG ATTTGGCAGC 720
TATCCTCTCT ACAGCAGTAC GCGCTCAGGA CTCAATATGG CTGTTCCGAT GCATGGATT 780
GGCCCTCAGT ACGGTGGATC GCTTGAGCTG AAAGTCTCCG AGCGATTCCG CTTTGCCGTC 840
45 GGTATGGAGC GCGAATACAA TATCTGGACT CGTCGGTGGG AAACGCATTA CTTTGCTTAT 900
CCTGTATTCT ATGGCGATAA GAAG 924

(2) INFORMATION FOR SEQ ID NO:232

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 945 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 55 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 60 (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 65 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232

70 ATGAAAACGA ATAGACGATA CGCATTGTGT TTGCGGCTTC TGCTACTCAC CGGATTGTTG 60
GCATGGGGGC AGGATTCCTC CCAAGGTAGC AATACAGCGT TTGCAACTGA TCTTCGAGT 120
AGAGAGTTGC CCACGAGCA GTCCGCTTAC CGCATTGATT CTGCCTATAT GGTGCGTGGT 180
75 GCGGGAAGCA TAACCGCGCA CACCTATTTG TCACCCGCTC GTTATGGAGG ATGGACACTG 240

159/ 490

5 AATTGTGTGG GAGAGAAGAC GTTCCCTCTC AAAGCCTCCG ATTCCCGTTG GATGATCCGT 300
ACCGGGCATG AGCTGGATTT TGCCCTGATG GACAATCCGG CCAATAATGC TCATTTCTAT 360
TCCCTGCTGT ATAACGGTTC CGCTGCGGCT CTTACCGCC TTGGCGCTAA GCATCTGCCA 420
GCCGCGTGGA TGGACAATCT GCGCTTGGA TTGCGGCGCG GCTTGGAAAT CGGGCTTGGA 480
GSAATTTATA GTACACGCA CGGCAATAAT CCTGCGACAT TGAAGCTCTA CACCAATGCC 540
ATCGCCCAAG CCTCGATAGG ATACTACGTC CCTCCGAAA CTTTCCCT GTATTTCCGG 600
TTGCTCTCCC AGATCAATCT CTTGCGTATA GCCTATGGAA ATGGTTTGG TGAGAGCTAT 660
TAGGAGAATT TTTTGCTCAA TAACGGCATT GCAGGCTCCC TGCAATTCAC TTATCCGGGC 720
AAGTTTACTC GGTTCACGAC ACTCATACG GCGGATATTC CCATTCCGAA CTTCTGTAGG 780
10 CTTGCTGTCG GTTATCGCTA TTCCCAATTT GGCTCTTCGC TTAACGCATT GGATACTCGA 840
ATCCACAGTC ATACGGCTTT TATCGGTTTC GTCACGGAGT TTTACCGATT CCGTGGGCGC 900
AAAGCCATGA ATACCGGTG GAGAACCAGT CTTTACTATC ATGAT 945

15 (2) INFORMATION FOR SEQ ID NO:233

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 855 base pairs
20 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

25 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

30 (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

35 (B) LOCATION: 1...855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233

40 ATGGTAGTGA CGCTGCTCGT AATTGTGCGT ATTGTGGTAG TAGTGGGTA CTCCTTGCGC 60
GTCCACGTAC ATAAGACCGG CACTGTTGTA TCGGCGGCCA TATTGGCTT CATCCTCCTT 120
GGAAAGACCG TTCCATGCGA TACCCGTAAC TTCTTTTCCT CCGAAAGTGA TGACCTGAG 180
AGCCGTGTIG CTACCGAAT AGCCACCTG TGCGAAATAG GATTTCAGAT CCACGCTTCC 240
TCTATCCACG TAGCCGTCCG AACCGATTTT GGACAGGCGG GCATCCACTG CCCAATGGCG 300
ACCGATGCGT CCGCTACCGA GTTTGACCGA TCGGCGGAAT GTGCCGAACG AACCTCCGCT 360
45 CAAATCGACA CGGCCATAAG GAGCCAGTCC CAAATTATCC GTACGCATAT TGACACTTGC 420
CCCAAAAGCT CGGGACCAT TGGTGGAAGT ACCCACACCT CGCTGCACCT GAAGGTCCTC 480
GATGGAAGAG CGGAAGTCGG GCATATTAC CCAAAGACG GACTGAGATT CGGAGTCGTT 540
GAGGGTACT CCATTGGTAG TTATGTTGAT GCGATTGGCA TCGGTGCCAC GCACGCGAAA 600
GCCGGAATAT CCGATACCGG TACCGGCATC GCTGGTGGCT ACCACGGAGG GATCAGCAT 660
CAGCAGATAG GGGATGTCAC GACCATAATT GGACTTGGAA AGTTCGGCCT TGCGAAGCTT 720
50 GGTGTAGCG ACAGGGGTTT TCGCCGTGGC GCGAGTAGCT ACGACCTGTA CGGTCTGGAG 780
CTGCACATTG CTAAGACTAT CTATCTCGCT GTTGGAGACG GGTGCTTGTG CCGTCAGGCA 840
GAAGGCAGG ACGGC 855

55 (2) INFORMATION FOR SEQ ID NO:234

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1797 base pairs
60 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

65 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

70 (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

75 (B) LOCATION: 1...1797

160/490

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:234

5 ATGAAAACT TAAAGACAT TCAGCCAGA GAGGATTCA ACTGGGAAGA GTTTGAGGCC 60
GGTGGCGTCC ATGCTGCCGT GAGTCGTAG GAGCAGGAAG CTGCTTATGA CAAAACGCTC 120
AATACCATCA AGGAAAAGGA AGTGGTAATG GGTAGGGTAA CTGCTATCAA CAAGCGTGAA 180
GTGGTTATCA ATGTAGGGTA CAAATCGGAA GGTGTGGTAC CTGCAACAGA ATTCGGCTAC 240
AATCCCGAAC TCAAAGTGGG AGACGAAGTG GAAGTTTATA TCGAGAATCA GGAAGATAAG 300
AAGGGCCAGC TCGTCTTGTC TCACCGCAAG GGTCTGCGG CTGCTCTTG GAGCGCGTG 360
10 AAGGGGCTCG TCGAAAAGA CGAAATCGTA AAGGGCTATG TGAAGTGTG TACCAAGGGT 420
GGTATGATCG TCGATGTATT CGGTATCGAG GCTTTCTCTC CGGGATCACA GATCGACGTG 480
CGCCCCATTC CGGACTACGA TGCATTCTG GAGAAGACGA TGGAGTTCAA GATTGTGAAA 540
ATCAATCAAG AATATAAGAA TGTAGTTGTT TCCCAAGAG TGTCTATCGA AGCAGAGCTC 600
GAACAACAGA AGAAAGAAAT CATCGGCAAG CTCGAAAAG GGCAGGTACT CGAAGSTATC 660
GTCAAGAATA TTAATTCTTA CGGAGTATTT ATCGACCTCG GTGAGTGGG TGGTCTTATC 720
15 CATATCACTG ACCTTTCTAT GGGTCGTGTG GCTCATCCGG AAGAAATCGT ACAGCTGGAT 780
CAGAAGATCA ATGTCTTAT CCTCGACTTT GATGAAGATC GCAAGCGTAT CGCTCTCGGA 840
CTCAACACAG TGATGCTCA TCCTTGGGAT GCTCTCGACA GCGAGCTTAA GGTAGGCGAT 900
AAGGTGAAGG GTAAAGTTGT GGTGATGGCA GATTACGGTG CTITCGTTGA GATTGCACAG 960
20 GGGCTTGAAG GTCTTATCCA CGTAAGCGAA ATGTCTATGA CACAGCACTT GCGTTCTGCT 1020
CAGGACTTCC TGCATGTAGG CGACGAAGTG GAAGCCGTGA TCCTGACGCT CGACCGCGAA 1080
GAACGCAAAA TGTCTGCTCG TCTGAAGCAA CTCAAGCCGG ATCCTTGGGC TGATATCGAA 1140
ACTCGTTTCC CTGTAGGCTC TCGTCAACAT GCTCGTGTTC GCAACTTCAC CAATTTCTGG 1200
GTATTCTGTG AGATCGAAGA GGGCGTAGAT GGCCTTATCC ATATTTCCGA CCTTCTTGG 1260
25 ACGAAGAAGA TCAACACCCC CAGCGAGTTT ACGGAAGTAG GTGCTGATAT CGAAGTTCAG 1320
GTAATCGAGA TCGACAAGGA AAACCGTCGT CTCAGCTTGG GTCACAAACA GTTGAAGAG 1380
AATCCTTGGG ATGTATTCTA GACGGTATTC ACTGTAGGAT CTATCCACGA AGGAACGGTA 1440
ATCGAAGTGA TGGACAAGGG TGCTGTCTTT TCTCTGCTT ACGGTGTGGA AGGTTTGGCC 1500
ACTCCGAAGC ACATGGTGAA GGAAGATGGC TCACAGGCTG TACTCGAAGA GAAGTTACCT 1560
30 TTCAAGGTTA TTGAGTTCAA TAAGGATGCC AAGCGAATCA TTGTATCTCA TAGCCGTGTA 1620
TTCCGAAGATG AGCAGAAATG GGCTCAGCGT GAAGCCAAAT CAGAGCGTAA GGCTGAAGCC 1680
AAGCGGCTC AGAAGAAGC TGCTGCCGAA GCTGCCAATC CTGCACAGGC TGTAGAGAAA 1740
GCCACTCTCG GAGACCTCGG CGAGCTGGCC GCTTTGAAAG AAAAGCTTTC AGAAAAAC 1797

35 (2) INFORMATION FOR SEQ ID NO:235

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1650 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1650

55 (x1) SEQUENCE DESCRIPTION: SEQ ID NO:235

60 ATGGGTAGGG TAACTGCTAT CAACAAGCGT GAAGTGGTTA TCAATGTAGG GTACAAATCG 60
GAAGGTGTGG TACCTGCAAC AGAATTCGCG TACAATCCCG AACTCAAAGT GGGAGACGAA 120
GTGGAAGTTT ATATCGAGAA TCAGGAAGAT AAGAAGGGCC AGCTCGTCTT GTCTCACCGC 180
AAGGCTCGTG CCGCTCGCTC TTGGGAGCGC GTGAACGAGG CTCTCGAAA AGACGAAATC 240
GTAAAGCGCT ATGTGAAGTG TCGTACCAAG GGTGGTATGA TCGTCAATGT ATTCGGTATC 300
GAGGCTTTC TCCCGGATC ACAGATCGAC GTGCGGCCCA TTCGCGACTA CGATGCATTC 360
65 GTTGAGAAGA CGATGGAGTT CAAGATTGTG AAAATCAATC AAGAATATAA GAATGTAGTT 420
GTTTCCCAAG AGGTGCTCAT CGAAGCAGAG CTCGAACAAC AGAAGAAAAG AATCATCGGC 480
AAGCTCGAAG AAGGGCAGGT ACTCGAAGGT ATCGTCAAGA ATATTACTTC TTACGGAGTA 540
TTTATCGACC TCGGTGAGT GGATGGTCTT ATCCATATCA CTGACCTTTC ATGGGGTCTG 600
GTGGCTCATC CGGAAGAAAT CGTACAGCTG GATCAGAAGA TCAATGTCTG TATCCTCGAC 660
70 TTTGATGAAG ATCGCAAGCG TATCGCTCTC GGACTCAAAC AGCTGATGCC TCATCCTTGG 720
GATGCTCTCG ACAGCGAGCT TAAGGTAGGC GATAAGGTGA AGGGTAAAGT TGTGGTATG 780
GCAGATTACG GTGCTTCTGT TGAGATTGCA CAGGGCGTTG AGGGTCTTAT CCACGTAAAG 840
GAATGTCTAT GGACACAGCA CTTGCGTTCT GCTCAGGACT TCCTGCATGT AGGCGACGAA 900
GTGGAAGCCG TGATCCTGAC GCTCGACCGC GAAGAAGCCA AATGTCTGCT CGGTCTGAAG 960
CAACTCAAGC CGGATCCTTG GGCTGATATC GAAACTCGTT TCCCTGTAGG CTCTGCTCAC 1020
75 CATGCTCGTG TTCGCACTT CACCAATTTT GGTGTATTCT TTGAGATCGA AGAGGGCGTA 1080

161/ 490

5 GATGGCCTTA TCCATATTTC CGACCTTTCT TGGACGAAGA AGATCAAACA CCCCAGCGAG 1140
TTTACGGAAG TAGGTGCTGA TATCGAAGTT CAGGTAATCG AGATCGACAA GGAAAAACCGT 1200
CGTCTCAGCT TGGGTCACAA ACAGTTGGAA GAGAATCCTT GGGATGTATT CGAGACGGTA 1260
TTCACGTAG GATCTATCCA CGAAGGAACG GTAATCGAAG TGATGGACAA GGGTGCTGTC 1320
5 GTTTCTCTGC CTTACGGTGT GGAAGGTTTT GCCACTCCGA AGCACATGGT GAAGGAAGAT 1380
GGCTCACAGG CTGTACTCGA AGAGAAGTTA CCTTTCAGG TTATTGAGTT CAATAAGGAT 1440
GCCAAGCGAA TCATTGTATC TCATAGCCGT GTATTGGAAG ATGAGCAGAA AATGGCTCAG 1500
CGTAAGCCA ATGCAGAGCG TAAGGCTGAA GCCAAAGCGG CTCAGAAAGA AGCTGCTGCC 1560
10 GAAGCTGCCA ATCCTGCACA GGCTGTAGAG AAAGCCACTC TCGAGACCT CGGCGAGCTG 1620
GCCGCTTTGA AAGAAAAGCT TTCAGAAAAC 1650

(2) INFORMATION FOR SEQ ID NO:236

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1374 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
20 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
25 (iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
30 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236

35 ATGATCGTCG ATGTATTGGG TATCGAGGCT TTCCTCCGGG GATCACAGAT CGACGTGGCG 60
CCCATTCCGG ACTACGATGC ATTCGTTGAG AAGACGATGG AGTTCAAGAT TGTGAAAATC 120
AATCAAGAAAT ATAAGAATGT AGTIGTTTCC CACAAGGTGC TCATCGAAGC AGAGCTCGAA 180
CAACAGAAGA AAGAAATCAT CGGCAAGCTC GAAAAAGGGC AGGTACTCGA AGGTATCGTC 240
40 AAGAATATTA CTTCTTACGG AGTATTATC GACCTCGGTG GAGTGGATGG TCTTATCCAT 300
ATCACTGACC TTTTCATGGGG TCGTGTGGCT CATCCGGAAG AAATCGTACA GCTGGATCAG 360
AAGATCAATG TCGTTATCCT CGACTTTGAT GAAGATCGCA AGCGTATCGC TCTCGGACTC 420
AAACAGCTGA TGCCTCATCC TTGGGATGCT CTCGACAGCG AGCTTAAGGT AGGCGATAAG 480
GTGAAGGGTA AAGTTGTGGT GATGGCAGAT TACGCTGCTT TCGTTGAGAT TGCACAGGGC 540
45 GTTGAGGGTC TTATCCAGT AAGCGAAATG TCATGGACAC AGCACTTGGC TTCTGCTCAG 600
GACTTCCTGC ATGTAGGCGA CGAAGTGGAA GCCGTGATCC TGACGCTCGA CCGCGAAGAA 660
CGCAAAATGT CGCTCGGTCT GAAGCAACTC AAGCCGGATC CTTGGGCTGA TATCGAAAAC 720
CGTTTCCCTG TAGGCTCTCG TCACCAATGCT CGTGTTCGCA ACTTCACCAA TTTCGGTGTA 780
TTCGTTGAGA TCGAAGAGGG CGTAGATGGC CTTATCCATA TTTCCGACCT TTCTTGGAGC 840
50 AAGAAGATCA AACACCCAG CGAGTTTACG GAAGTAGGTG CTGATATCGA AGTTCAGGTA 900
ATCGAGATCG ACAAGGAAAA CCGTCGCTC AGCTTGGGTC ACAACAGTT GGAAGAGAAT 960
CCTTGGGATG TATTCGAGAC GGTATTCAC TTAGGATCTA TCCACGAAG AACGTAATC 1020
GAAGTGATGG ACAAGGGTGC TGTCTTTCT CTGCCTTACG GTGTGGAAGG TTTTGGCACT 1080
CCGAAGCACA TGGTGAAGGA AGATGGCTCA CAGGCTGTAC TCGAAGAGAA GTTACCTTTC 1140
55 AAGGTTATTG AGTTCAATAA GGATGCCAAG CGAATCATG TATCTCATAG CCGTGTATTG 1200
GAAGATGAGC AGAAATGGC TCAGCGTGAA GCCAATGCAG AGGTAAGGC TGAAGCCAAA 1260
GCGGCTCAGA AAGAAGCTGC TGCCGAAGCT GCCAATCTG CACAGGCTGT AGAGAAGGCC 1320
ACTCTCGGAG ACCTCGGCGA GCTGGCCGCT TTGAAAGAAA AGCTTTCAGA AAAC 1374

(2) INFORMATION FOR SEQ ID NO:237

65 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1278 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
70 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
75 (vi) ORIGINAL SOURCE:

162/ 490

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

5 (A) NAME/KEY: misc_feature
(B) LOCATION 1...1278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237

10	ATGGAGTTCA AGATTGTGAA AATCAATCAA GAATATAAGA ATGTAGTTGT TTCCACACAG	60
	GTGTCATCG AAGCAGACCT CGAACACAG AAGAAAGAAA TCATCGGCAA GCTCGAAAAA	120
	GGGCAGGTAC TCGAAGGTAT CGTCAAGAA ATTACTTCTT ACGGAGTATT TATCGACCTC	180
	GGTGGAGTGG ATGGTCTTAT CCATATCACT GACCTTTCAT GGGGTCTGTG GGCTCATCCG	240
	GAAGAAATCG TACAGCTGGA TCAGAAGATC AATGTCTGTA TCCTCGACTT TGTGAAGAT	300
15	CGCAAGCGTA TCGCTCTCGG ACTCAAACAG CTGATGCCTC ATCCTTGGGA TGCTCTCGAC	360
	AGCGAGCTTA AGGTAGGCGA TAAGGTGAAG GGTAAAGTTG TGGTGATGGC AGATTACGGT	420
	GCTTTGCTTG AGATTGCACA GGGCGTTGAG GGTCTTATCC ACGTAAGCGA AATGTCATGG	480
	ACACAGCACT TGGCTTCTGC TCAGGACTTC CTGCATGTAG GCGACGAAGT GGAAGCCGTG	540
	ATCCTGACGC TCGACCGCGA AGAACGCAAA ATSTCGCTCG GTCTGAAGCA ACTCAAGCCG	600
20	GATCCTTGGG CTGATATCGA AACTCGTTTC CCTGTAGGCT CTCGTACCA TGCTCGTGT	660
	CGCAACTTCA CCAATTTCGG TGTATTCTGT GAGATCGAAG AGGGCGTAGA TGGCCTTATC	720
	CATATTTCGG ACCTTCTTG GACGAAGAAG ATCAAACACC CCAGCGAGTT TACGGAAGTA	780
	GGTGCTGATA TCGAAGTTCA GGTAACTCGA ATCGACAAGG AAAACCGTCG TCTCAGCTTG	840
	GGTCAACAAC AGTTGGAAGA GAATCCTTGG GATGTATTTC AGACGGTATT CACTGTAGGA	900
25	TCTATCCACG AAGGAACGGT AATCGAAGTG ATGGACAAGG GTGCTGTCTG TTCTCTGCT	960
	TACGGTGTGG AAGGTTTTGC CACTCCGAAG CACATGTTGA AGGAAGATGG CTCACAGGCT	1020
	GTACTCGAAG AGAAGTTACC TTTCAGGTT ATTGAGTTCA ATAAGGATGC CAAGCGAATC	1080
	ATTGTATCTC ATAGCCGTGT ATTCGAAGAT GAGCAGAAA TGGCTCAGCG TGAAGCCAAT	1140
	GCAGAGCGTA AGGCTGAAGC CAAAGCGGCT CAGAAAGAAG CTGCTGCCGA AGCTGCCAAT	1200
30	CCTGCACAGG CTGTAGAGAA AGCCACTCTC GGAGACCTCG GCGAGCTGGC CGCTTTGAAA	1260
	GAAGAGCTTT CAGAAAAC	1278

(2) INFORMATION FOR SEQ ID NO:238

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 720 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
40	(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

45 (iv) ANTI-SENSE: NO

(v) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

50 (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238

55	ATGAAAAAG CTATTCTTTC CGGAGCGGCC TTGCTCCTCG GCCTATGTGC CAACGCACAA	60
	AACGTGCAGT TGCACTACGA TTTGGGTCTT TCCATCTACG ACGAACTAGA TGGACGTCCC	120
	AACTGACTA CCACAGTGGG AAACCTTACA CCGACAAAT GGGGAAGCAC GTTCTTCTC	180
60	ATCGACATGG ATTACACGGG CAAGGGTATC CAGTCGGCCT ATTGGGAGAT TTGCGCGGAA	240
	CTGAAGTTTT GGCAGCTCC CGTTTCCATT CATTGGAGT ACAACGGAGG CCTCTCCACA	300
	AGCTTTACTT TCGGACAGGA TGCTCTAATC GGTGCCACCT ACACCTACAA CAACCCCTCC	360
	TTTACACGTG GATTACGAT CACGCCCATG TACAAGCATC TGGGTGCGCA CGACTTCCAC	420
	ACCTATCAGA TCACCGGCAC TTGGTACATG CACTTCTGCG ACGGCTGCTT TACCTTCAAC	480
65	GGCTTCTCTG ATCTTTGGGG TTTCCTCCAA GAGAACCCAA TCGGGGGGCC TGTGCTCAAA	540
	GAAGGGGATA AGTTCTGATT CTGTCTCGAA CGCAGTTCT GGATCAACCT CAATCGCATC	600
	AAAGGCATCG ACAAGGATTT CAATCTCAGC ATAGGGACAG AGATGGAAT CAGCAGGAAC	660
	TTGCTCGCA TGGACAAATT CTCTGCTATC CTTACTCTTG GGTCAAAAT GACTTCAAC	720

70 (2) INFORMATION FOR SEQ ID NO:239

(i) SEQUENCE CHARACTERISTICS:

75	(A) LENGTH: 1302 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

163/490

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

5 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

10 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...1302

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:239

20 ATGTATAAAG ACTATAAGGG TTGTATGCG TCGCTTCGGT GGTATGCCCT GATCATTGGG 60

TTGCTATTTG CAGCAGACGG TATACAGGCT CAGAACAACA ACTTTACCGA GTCGCCCTAC 120

ACTCGCTTCG GCCTTGGCCG TCTCGGAGAA CGGACGACTA TTAGTGGGCA TTCCATGGGA 180

GGACTCGGCG TCGTCTGCG TCGAGGCACA TACGTCAATG CCGTCAATCC TGCTTCATAC 240

TCGGCTGTGG ATTCSATGAC GTTTATCTTC GATTTCGGTG CATCTACCGG AATTACGTGG 300

TATGCCGAGA ACGGGAAAAA GGACAATAGG AAAATGGGAA ACATTGAGTA TTTCGCCATG 360

CTTTTTCCTA TTTCCAAATC CATTGCTATG AGTGCGGGAG TGCTTCCTTA CTCGCGATCC 420

GGGTACCACT TCGGATCCGT TGATCAAGTG GAAGGAGGCA GCGTCCAGTA CACCGGTAAA 480

TACTTGGGGA CAGGCAATCT GAACGATCTC TATGTCGSTA TAGGTGCAAC CCCGTTCAAA 540

AACTTCTCAA TAGGAGCUAA TGCTTCATCC CTTTTCGGGC GATTACACA CAGCAGGCAG 600

GTAACTTCT CACCGGAGGC TCCCTACAAT CCGGTACATC TCTCGACGCT GTACTTGAAG 660

GCTGCCAAGT TCGACTTCGG TATGCAGTAT CACCTTCTTC TCAAATCAGA TCGTTCGCTC 720

30 GTTATCGGTG CCGTCTATTC TCGCGGGGTG AAGATGCATA GCGAGCTGAC TCAGATAAAG 780

AATCAGGTTT AGAACGGTGT AGTAGTGGAG AGCGAAACCC AAGAATATAT CAAGGGAATG 840

GACTATTATA CCCTGCCTCA TACATFGGGG ATAGGTTTTT CTTATGAAAA GAAAGATAAA 900

CTTCTCTTAG GAGCAGACGT CCAATATAGT AAATGGAAG GCGAGAAATT TTATAAATCC 960

35 GATTGCAAAAT TCCAGGACAG AATACGGSTA TCTCTCGGCG GAGAGATCAT ACCGGATATA 1020

AATGCCGTTG GATGTGGGCC TAAAGTTCCG TATCGCTTCG GTTTACATGG TGAAAAATCT 1080

TACCTGAAAG TGCGGACTAA AGGCGGTGTA TATCAAGGAT ACCATATCGT AGGTGCTGTA 1140

TTCCGTATAG GAATCCCGCT CAATGACAGA CGTTCGTTCC TAAATGTCTC TCTTGAATAT 1200

GACCGATTGA TCCCGAAGGA GGGTATGATC AAAGAAAAATG CTCFGAAATT GACCTTCGGC 1260

40 CTCACGTTCA ACAGTCAATG GTTTAAAAAG CTGAAACTGA AC 1302

(2) INFORMATION FOR SEQ ID NO:240

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2778 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

50 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

55 (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

60 (A) NAME/KEY: misc feature

(B) LOCATION 1...2778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240

65 ATGCGATCGA TTTATCAATT ACTGTTGTCA ATACTCCTTG CTTCTCTTGG TTTCGTGGGG 60

CTGGAAGCCC AACAGCCGG AGTAGCAGGT AGAGTATTGG ACGAAGAAGG CAACCCCATG 120

ATTCAAGCCA ACGTACAGCT TGTACAGAGT ACCGGCCAAG TAGCCGTTGC CGCAGGTGCC 180

ACTAATGAAA AAGGGTTGTT CAGCCTGAAA ACCTCACAGG AGGGTGACTA CATCTCTGCG 240

70 GTTTCATATG TAGGTTACAC TACCCACGAC GAAAAAATAT CTCCTAGAAA CGGGCAAAAC 300

ATTACGCTCA AAGATATATC CATGAACGAA GATGCCCGTC TTCTACAGAG TGTGACGGTG 360

CAGGCTAAAG CGGCAGAGGT CGTGGTACGC AACGATACGC TCGAATTCAA TGCCGGATCC 420

TATACCGTAG CACAGGGAGC TTCTATCGAG GAAGTGAATC AGAAGCTACC CGGAGCAGAG 480

ATCGGATCCG ATGGGAAGAT CACCATCAAC GGCAGGACA TTAGCAAGAT CCTTGTCTAT 540

75 GCCAAGAGT TTTTCTCCAA AGATCCACAG GTGGCAATTA AGAATCTTCC GCGCGATATG 600

GTCATAAAG TACAGGTACT GAACAAACTG AGCGAGCTGT CGCGGATGAG CGGTTTCGAT 660

165 / 490

5 GATAGAATTC AAAATTCGTC TTCGCAAAAA AATAAGTTG GATTGCAGTC GAACAAACCC 900
AATAAATATC TGCAAAATGT CAAGTCGGGA CGTACCGGCC GAGCCAATAG AGACCGAAAT 960
ATAGAAACGG TAACTCCAAA CAACGGGCA AAGCAGAATC GTCCCGTATT CCAGCAGAAT 1020
CAGTCCGGCA ATGACCGACT GACCGGACGG AATATCCGCA GCGAGAGACA GGGCGAAAT 1080
AACGATAGSA CATTTCGAC TCCTTCTCGT AGCAATAGTA ACGGTGGCTT CTCCACGCCCT 1140
TCTCGCTCTT CTCCGGCTC TATGAGCGGA GGTGGCGGAC GTAGTGGCCS GGGACGCAAT 1200

(2) INFORMATION FOR SEQ ID NO:242

10

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1194 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

15

(ii) MOLECULE TYPE: DNA (genomic)

20

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

25

(v) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION: 1...1194

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242

ATGAAGCTGA TTAAGAAGT TTTGCTCCTG CTTGGAGCGG TACTGCTGAT TACGCTTCCT 60
GCGTACTCGC AGAATGATGA CATCTTCGAA GATGACATCT ATACATCGCG AAAAGAAATA 120
CGTAACACAA ACCAAGTTAA AGACTGGCAA AACCAAGAGG ACGGATACGG CGACGATACG 180
GAATATACAG TGGCTTCCGA TCGGGACATT GACGCCTACA ATCGTAGAGA TGGCCAGTCC 240
TACGATAGGA AAAAGTTGTC CAAAGACAAG AAAAGAGACT CCACCTCGTC TTCTGTTCCT 300
GGTCGCTATA GTCGCCGCTT GGCTCGATTG TATAAGCCGA ATACGATCGT CATTTCAGGT 360
GCCGACAATG TATATGTAAAC TGATGATGGT GAGTATTTTC TCTATGGAGA CGAATACTAT 420
GATGACCGGT CGCTGTGAAA CATTTACATC AACAGTCCTT GGTGCGATCC GTTCCCTTAT 480
ACGTCATGCT ATCCATCTTT CTCCGGCTGG TACAACATA CGTGGAACTA TCCATGGTTC 540
TACTACGGTA GCCATATCGG ATGGGGCGGT TATTACCCCG GATATAATTG GTATTGGAGC 600
TACTACTATG ATCCTTTCTA CAATCCCTAT GGAATCGGTA TGGGTTGGGG ATATCCTTAT 660
GGCTGGGGCA GCTATTACGG TTGGGGTGGC TATCCGGGAG TGATACATCA CTACCACCAC 720
TACCCCAAGA AGACCTATTC CAATGGTCAG CATTCCGGAG CTTACTATTC TTATGGCCGA 780
CGAATCGTA TCAAGGTGG AACGTCGGT GCCAAACTTG GGACAGGAG CTACGATAGA 840
ATTCAAATTT CGTCTTCGCA AAAAAATAAG TTCGGATTGC ATTCGAAACA ACCCAATAAT 900
AATCTGCAAA ATGTCAAGTC GGCACGTACC GCGCGAGCCA ATAGAGACCG AATATAGAA 960
ACGGTAACCT CAAACAACGG GCAAAAGCAG AATCGTCCCG TATTCCAGCA GAATCAGTCC 1020
GGCAATGACC GACCGACCGG ACGGAATATC CGCAGCGAGA GACAGGGGGA AATAACGAT 1080
50 AGGACATTTT CGACTCCTTC TCGTAGCAAT AGTAACGGTG GCTTCTCCAC GCCTTCTCGC 1140
TCTTCTCCG GCTCTATGAG CGGAGGTGGC GGACGTAGTG GCCGGGGACG CAAT 1194

(2) INFORMATION FOR SEQ ID NO:243

55

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1743 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

60

(ii) MOLECULE TYPE: DNA (genomic)

65

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

70

(v) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION: 1...1743

75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243

166/490

5
10
15
20
25
30

ATGATCCGCA AGTTGATCTT ACTGCTTGCT CTGATGCCGG TAGCCTCTGT GGCTTTTGGG 60
GTACCAACCG ACAGCACGGA ATCGAAAGAC AATCGTATCC TTACAAGCAT GCAATCCTCC 120
TCTTTGAATA GGGATGATGC TCCGGATAAA TGGCAACCTA TGCATGCCAA TTTGAGTATT 180
CAGAGCGATA TGCTGCTTTC TACTGCCCAA AAGTCCAAGA ACACCTGGTT CGGCAACTCC 240
TATATCATGG GTATAATCAA GAACAATTAT CTGGAGTTTG GTGCCCGTTT CGAGGATCTC 300
TATAAGCCCC TGCCCGGACA TGAACCOGAG ATGGGGCGTG GCGTTCTCTCA CATGTAITGT 360
AAGGGAAGCT ATCATTGGGC GGAGCTGACT ATGGGAGACT TCTACGATCA GTTCGGTAGC 420
GGTATGSTAT TCCGCACCTA TGAAGAGCGC AACCTCGGTA TAGACAACGC GGTTCGCGGC 480
GGAGTATAG TACTCACTCC TTTTGATGGA GTGCGTGTCA AGGGTATTGC AGCACAGCAG 540
CGTAACACT TCGACCGCAC GGGCAAGGTA TTCAATTCGG GCCGAGGCTA CCTACTGGGT 600
TCTGATCTGG AGCTGAATGT AGAGCGTTGG AGCAGTGCCA TGGCGGACAA TGAATATCAT 660
TTGGGTATCG GGGGATCGTT CGTTTCCAAA CACGAAGCAG ACGAAGATAT ATTTGTGGST 720
GTAGGCGAAG ATCGCAAGCG ACTCAACCTG CCGCTCAATG TCCOGATTAT GGGCCTGCGC 780
15 ACCAACTTTC AAAAAGGAGG TCTCGCCCTC TACGCAGAGT ATGGATACAA ATACAAOGAT 840
CCCTCGGCAG ACAATGACTA TATCTACCAC GACGGACAGG CTGCACTCCT CTCTGCTCA 900
TACTCCAAAA AAGGGATGAG TATCCTGTTG CAGGCCAAAC GTTGTGAGAA CTTTGCTTTC 960
CGCAGCAAGC GAAGTGCCCA GCTCACACCG CTTATGATCA ACTATATGCC GGCTTTTACC 1020
CAAGCTCACA CTTATACGCT GCGCGCCATC TACCCCTATG CTACTCAGCC TCAGGGAGAA 1080
20 TGGGCTTTCC AAGGTGAAGT GCGTTACAACT TTTGCTCGCC GSACAGCTCT CGGTGGACGC 1140
TACGGTACCG GCTTGCGTAT CAACGTTTCC CATGTGCGTG GTCTGGACAA AAAGATGCTC 1200
AAAGAGAATC CCGACGAAGT GATCGGAACG GATGGCTACA CCGTTTCTTT CTTGCGCATG 1260
GGCGACCTCT ATTATTCGGA TATAGATGTG GAGATTACTA AAAAGGTAAG CCCAGGATTC 1320
25 AACCTTACGC TCACCTACTT GAATCAGATC TACAATAACA AGGTACTGCA CGGTGCAGCC 1380
GGAGAGAACC CTGAGAAGAT CTATGCCAAT ATCTTCGTCT ATGATGGTAA GTATAAGCTG 1440
AGTAATAAGG TAGCCCTCCG TACCGAAGTG CAATATTGCG ACACGAAGCA GGATCAGGCT 1500
GACTGGATCT ACGGCTGGC CGAGCTCTCT ATCCTGCCIT CTCTGATGCT TTCCCTCTCG 1560
GAGCAGTATA ATATCGGAGA GACCAAGAAA CATTATGTCA TGGGGTCTGT CACCTATACT 1620
30 CAGCGAGCAC ATCGASTAGC TTTCTCTGCA GGCAAAACCC GTGCAGGAT GAACCTGCTG 1680
GGAGGTGTAT GTCGTGGGT CCCTGAGACT CAGGGATTCT ACCTTTCTTA TAGCACCAAT 1740
CTG 1743

- 35 (2) INFORMATION FOR SEQ ID NO:244
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 717 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 40 (ii) MOLECULE TYPE: DNA (genomic)
- 45 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 50 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...717
- 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:244

ATGCGTTCTT TATTTTGTAG CGCGTTGCGC AGCTCCTCTC TCCATGGTTC AGAGCGACGC 60
AGTCGGATTA GTTCTTCTGT AGTCATGTCA ATAAGGCAGA AAATAAGGTT ATTCCATCTC 120
TCGGTATGCG CCCAAACGCA TGATCATCTC ATCGAAATCC ACTTGGTGTC CATCGAATTC 180
60 GGGGCCATCG ACACAGACGA ATTTGCTCTG TCCTCCACG CTTATACGAC AAGCCCCACA 240
CATACCGGTG CCATCCACCA TAATTGTATT GACAGAAGCT ATGGTCGGTA TCTCGTAACG 300
TTTGGTCAGG AGAGAAACGA ACTTCATCAT CACAGCCGCG CCGATCGTAA CGCAGAGGTC 360
TACCGTTTCC CGTTTGATAA CGCTTTCAC TCCATCCGTT ACGAGGCCCT TCGTCCCAT 420
AGACCATCG TCTGTATGA TGATCACTTC ATCGCTATTG GCTCGCATTT GTTCTTCAAG 480
65 GATAAACGGA TCTTTAGTTC TGGCAGCCAA TACGACAATT ACACGGTTGC CTGCTTTGTG 540
GAAAGCCTCC ACGATCGGGA GCAAAGGAGC CACACCCACA CCGCCTCCGG CACAAACCAC 600
TGTGCCGACC TTTTCGATAT GCGTAGCTCT TCCAGCGGA CCTACCACAT CCGTGATATA 660
70 GTGCCGACT TCGAGTTCGG CCAATTCTCTT GGAAGATTG CCCACGGCT GAACCAAC 717

- 75 (2) INFORMATION FOR SEQ ID NO:245
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 633 base pairs
(B) TYPE: nucleic acid

167/490

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245

20	ATGTCAATAA GGCAGAAAAT AAGGTTATTC CATCTCTCGG TATGCGCCCA AACGCATGAT	60
	CATCTCATCG AAATCCACTT GGTGTGCATC GAATTCGGGG CCATCGACAC AGACGAATTT	120
	CGTCTGTCTT CCCACGCTTA TACGACAAGC CCCACACATA CCGGTGCCAT CCACCATAAT	180
	TGTATTGAGA GAAGCTATGG TCGGTATCTC GTAACGTTTG GTCAGGAGAG AAACGAACTT	240
	CATCATCACA GCCGGCCCGA TCGTAACGCA GAGGTCTACC GTTTCCTGTT TGATAACGCT	300
25	TTCCACTCCA TCCGTTACGA GGCCTTTCTG CCCATAAGAC CCATCGTCTG TCATGATGAT	360
	CACCTTCATCG CTATTGGCTC GCATTGTTC TTCAAGGATA ACCAGATCTT TAGTTCTGSC	420
	AGCCAATACG ACAATACAC GGTTCCTGTC TTTGTGGAAA GCCTCCACGA TCGGGAGCAA	480
	AGGAGCCACA CCCACACCGC CTCGGGCACA AACCAGTGTG CCGACCTTTT CGATATGCGT	540
30	ACTCTGTCCC AGCGGACCTA CCACATCOGT GATATAGTCG CCGACTTCGA GTTCGGCCAA	600
	TTTCTTGGA GATTGCCCCA CGGCCTGAAC CAC	633

(2) INFORMATION FOR SEQ ID NO:246

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2343 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...2343

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246

55	ATGATCGTC CTAAGCCTTC ATATATTGTT CGAATAGCAG CCATTCTCTG CTGTTTGTG	60
	GGCAGGCCTT TGTGTCGCA GAGCTATGTG GACTACGTG ATCCGCTGAT CGGGACGCTA	120
	AGTTCTTTTG AGCTGAGTGC GGGCAATACC TATCCGGTGA TCGGTTTACC GTGGGGAAATG	180
	AATAGCTGGA CACCGATGAC CGGTGTACCC GGTGACGGCT GGCAATATAC CTAAGCTGCA	240
60	CACAAGATTG GCGGATCAA ACAGACCCAC CAACCCAGTC CTGGATCAA CGACTACGGC	300
	CAATTCTCCC TTCTTCCCCT TACGGCACCG CAGAAGCCAT CATCGAACGA CTCATAGCT	360
	CTGACTAAAT GGTGCAAGCA ACTCTTTTCG GACGAACAGA CCTCGTGGTT CTCGCACAAA	420
	GCGGAGACGG CGACGCCATA CTATTATAGT GTCTATTTCG CCGATTACGA CACACGGGTG	480
	GAGATGGCTC CGACCGAGCG TGCAGCTATC TTTCGCATAC GTTATTCGGG CAATACCGAA	540
65	AGTGGCTCCG GTCGATGGCT TCGTCTTGAT GCCTTTACCG GTGGTTGGGA GATTAGCATC	600
	GTGGATCCTC ACACCGTAGT GGGCATATCT CGCAAGAATA GCGGAGGTGT GCCGGCTAAC	660
	TTCCGCTGTT ATTTCATCCT CGAGTCCGAT ACTCCTATGG CCGATGTCCT GCTTGAGACA	720
	GATACCGGCA AGTCAGACGA AGGCACAAGG GCATGGGCAG CCTGTGCTTT CGATTGCGAA	780
	GAAGTTACCG TCGGGTGGGC ATCTTCTTTT ATCAGTGTGG AGCAGGCCGA AAGAAATCTT	840
70	GCGGAAGTCA AAGGGCAGAG TTTCGACCGG ATCAGACTTG CCGGTGCGGA AGCTTGGAAAT	900
	AAGGTGCTCG GACGCATACA TGTGGAAGGA GGAACGAAGG ATGAGCGCAC TACATTCTAT	960
	TCGCGACTCT ATCGCTGTCT GCTTTTCCCG CGTCGCTTCT ATGAGGAGGA TGCTTCCGGC	1020
	AATTTTGTGC ATTACAGCCC CTACAATGGA GAGGTACTTC CCGGTTATCT CTATACCGAT	1080
	ACCGGATTTT GGGACACTTT TCGAGCCCTT TTCCCTCTGC TCAATCTGCT GTATCCCGAT	1140
75	GAAGGATTTA AAATTCAGGA AGGTCTGCTG AATGTATATC GCGAGAGTGG CTTTTCCTCC	1200
	GAATGGGCCA GTCCGGGCCA TCGGATGTGT ATCATAGGCA ACAACTCTGC TTCTGTTCTG	1260

168/490

5 GCGGATGCGT ACCTCAACGG TGTTCGGGTA GAAGATACCC GTACACTGAT GAACGGACTC 1320
TTGCATGCTA CGAAAGCCGT CCATCCGAAA ATCTCCTCCA CGGGTCGCAA AGGTTGGGAG 1380
TGGTACAACCT CCTTAGGTTA TGTTCGGGCT GATGCAGGCA TCGACGAAAG TGTGCCCCGT 1440
ACGCTCGAAT ATGCTTATAA CGATTGGTGC ATCCTCCGAC TGGGGCGCAC ATTGGGTTGG 1500
GATAGAGCTG CATTGGACAC GTTGGCTCAT CGTTCGATGA ACTATCGTCA TCTGTTCCGAT 1560
CCGSAACCA AACTCATGCG CGGTAGAAAT CAGGATGGTA GTTTCGGGAC ACCTTTTTC 1620
CCTTTCAAAT GGGGAGATGT ATTACCGGAG GGCAATGCCT GGCACTACAC TTGGTCGGTC 1680
TTTCATGATG TGCAGGGGCT TATCGACCTG ATGGGAGGAG ATCGCCCGTT CGTGTCTATG 1740
10 CTGGATTCCG TATTCAATAC TCCTCCTATG TTCGATGAGA GCTATTACGG ATTGTGTCATC 1800
ATACAGCATA TGATATATCT GTATAATCAT GCCGGTCATC CATGGAAAGC TCAGGAGAGA 1860
CTACGCGAAG TGATGGGGCG GCTCTATCGT CCTACTCCGG ATGGGTATTG CGGCGATGAA 1920
GACAACGGAC AGACTTCGGC TTGGTACGTT TTCTCTGCTT TAGGCTTCTA TCCTGTTACA 2040
15 CCGGCTACGG ATCAGTATGT GCTCGGTTCC CCGATTTTTT CCAAGGTAAT ACTCTCTTTT 2100
CCGACGGAC ACAAACGGT GTTGCATGCT CCGGCCAACA GTGCCGATAC GCCTTACATC 2160
CGCTCGATCA CGGTAGAAAG AAAAGAATGG AGCTGCAATT ACCTGACTCA CGAACAGCTT 2220
CGCTCTTCTG CATCCATTCA ATGGATGATG GACACGAAAC CCAATTATAA TCGTGGTATG 2280
AAGGAAAGTG ACAGACCTTA TTCTTCTCC ACGGAGCAAC AGCGTCGCGC TAATCACACT 2340
20 AAT 2343

(2) INFORMATION FOR SEQ ID NO:247

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 813 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 30 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 35 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 40 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247

45 ATGATGAAT CCATGCGCAG CGTGCTGTTG CTACTCTTTC CATTGTCTTT GATCACTGCT 60
TTGGGCTGTA GCAATAACAA AGCTGCCGAA TCGAAGTCTG TCTCTTTTGA TTCGGCCTAT 120
CTCGAACGCT ACATCCCTCT GCGGGCAGAC ATAGATACGC CATCGCTGCA TGTGATGATC 180
AGCTACGTCT ATCCTTCGGG AGATGATATG CTCACAGAGA TTTTCAACGG TTTGCTCTTC 240
50 GCGCAGAGCC TGATGGATTG CTCTTCGCGG GAGAATGCCA TGGAAAGGCTA TGCACAGATG 300
CTGGGAGAAG ACTATCGCTC TAACAATGCC GAAGCCAATC TGCAAGGGCT TCCTTCTGAC 360
CTTTTGGACT ATATCTACAA GCAGGAAAAT ACCATCGCTT ATTGCGATAC GGGATTGATC 420
TCCACGCGCA TCAATACATA TACTTACGAA GCGGGTGCAAC ATACGGAGAA TACAGTCCGG 480
TTTGCCCAACA TCCTTCGCAC CACCGGCAAG GTGCTCGAAG AGCGAGATAT ATTCAAGATC 540
GACTATGCGG AAAGGCTGTC CGCACTCATC ATAGGACAAT TGGTGACGGA TTTGCGCAAG 600
55 ACCACACCTG CCGAATTGGA TGCAATAGGT TTCTTCAACG CAGAAGAAAT ACAGCCCAAT 660
GGCAATTTTA TGATCGATGA CAAAGGTCTC ACATACGTGT TCAATGAGTA TCAGATAGCT 720
GCTTATGCCA GAGGTGCTGT CTATGTCCGT CTCGGATATG ACGTATTGGC TCCTTTGCTA 780
60 AGGGATGATT CCCCACTAAA GCGTTACTTG CCG 813

(2) INFORMATION FOR SEQ ID NO:248

- 65 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 810 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 70 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 75 (vi) ORIGINAL SOURCE:

169/ 490

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- 5 (A) NAME/KEY: misc_feature
(B) LOCATION 1...810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248

10 ATGAAATCCA TGCGCAGCGT GCTGTTGCTA CTCTTTCCAT TGTCTTTGAT CACTGCTTTG 60
GGCTGTAGCA ATAACAAAGC TGCCGAATCG AAGTCTGTCT CTTTCGATTC GGCCTATCTC 120
GAACGCTACA TCCCTCTGCG GGCAGACATA GATACGCCAT CGCTGCATGT GATGATCAGC 180
TACGTCTATC CTTGCGGAGA TGATATGCTC ACAGAGATTT TCAACGGTTT GCTCTTCGGC 240
GACAGCCTGA TGGATTCTCT TTCGCCGCGAG AATGCCATGG AAGGCTATGC ACAGATGCTG 300
GGAGAAGACT ATCGCTCTAA CAATGCCGAA GCCAATCTGC AAGGCGTTCC TTCTGACCTT 360
15 TTGGACTATA TCTACAAGCA GGAATAATACC ATCGCTTATT GCGATACGGG ATTGATCTCC 420
ACGGCATCA ATACATATAC TTACGAAGGC GGTGCACATA CGGAGAATAC AGTCCGGTTT 480
GCCAACATCC TTGCGACAC CCGCAAGGTG CTCGAAGAGC GAGATATATT CAAGATCGAC 540
TATCGGAAA GGTGTCCGC ACTCATCATA GGACAATTGG TGCACGATTT CGGCAAGACC 600
ACACCTGCCG AATTGGATGC AATAGGTTTC TTCAACGCAG AAGAAATACA GCCCAATGGC 660
20 AATTTTATGA TCGATGACAA AGGTCTCACA TACTGTTTCA ATGAGTATCA GATAGCTGCT 720
TATGCCAGAG GTGCTGTCTA TGTCCGTCTC GGATATGACG TATTGGCTCC TTGCTAAGG 780
GATGATTCCC CACTAAAGCG TTACTTGCCG 810

(2) INFORMATION FOR SEQ ID NO:249

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 801 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- 45 (A) NAME/KEY: misc_feature
(B) LOCATION 1...801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249

50 ATGCGCAGCG TGCTGTTGCT ACTCTTTCCA TTGTCTTTGA TCACTGCTTT GGGCTGTAGC 60
AATAACAAG CTGCCGAATC GAAGTCTGTC TCTTTCGATT CGGCCTATCT CGAACGCTAC 120
ATCCCTCTGC GGGCAGACAT AGATACGCCA TCGCTGCATG TGATGATCAG CTACGTCTAT 180
CCTTCGGGAG ATGATATGCT CACAGAGATT TTCAACGGTT TGCTCTCGG CGACAGCCTG 240
ATGGATTCTT CTTGCGCGGA GAATGCCATG GAAGGCTATG CACAGATGCT GGGAGAAGAC 300
TATCGCTCTA ACAATGCCGA AGCCAATCTG CAAGGGCTTC CTTCTGACCT TTTGGACTAT 360
55 ATCTACAAGC AGGAAAATAC CATCGCTTAT TGGGATACGG GATTGATCTC CACGCGCATC 420
AATACATATA CTTACGAAGG CGGTGCACAT ACGGAGAATA CAGTCCGGTT TGCCAACATC 480
CTTCGCACCA CCGGCAAGGT GCTCGAAGAG CGAGATATAT TCAAGATCGA CTATGCCGAA 540
AGGCTGTCCG CACTCATCAT AGGACAATTG GTGCACGATT TCGGCAAGAC CACACCTGCC 600
GAATTGGATG CAATAGGTTT CTTCAACGCA GAAGAATAC AGCCCAATGG CAATTTTATG 660
ATCGATGACA AAGGTCTCAC ATACTGTTTC AATGAGTATC AGATAGCTGC TTATGCCAGA 720
60 GGTGCTGTCT ATGTCGTCTC CGGATATGAC GTATTGGCTC CTTTGCTAAG GGATGATTCC 780
CCACTAAAGC GTTACTTGCC G 801

(2) INFORMATION FOR SEQ ID NO:250

(i) SEQUENCE CHARACTERISTICS:

- 70 (A) LENGTH: 777 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

170/ 490

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250

ATGAAAAA	CTACTTTGAC	AGGATCGATA	TGTGCTTTAC	TCCTGTTTTT	GGGTCTCTCG	60
GCCCAATGCCC	AATCGAAGTT	AAAGATCAAG	AGCATTGAGG	CAGCTACCCAC	TTTCAGTTTCG	120
GCCACGGCOG	GAATATGGTTT	TGGTGGCAAT	ATCTTCGGCA	TGGACATGAG	CATACGGATG	180
AGGATACACC	ACAGCATTCT	GCCCGAAGGG	TTGGATTTTT	CGGTAGGAAT	ACATGAAAGA	240
AGAGCACACT	GGGAAGAGGC	CGGAAGTCCG	AAGCTCATGT	ATACGAATGT	CCCAAGTATC	300
ATTGGTATTG	TTGAAAAGGT	AATAGTCTTC	GAAGACGCG	AAGACTTTTT	TGACAAAAAA	360
GCTCTCGGCC	GCTCTCTCAT	CAGTTTGGGG	ATATCCTATA	CCAAGCATCT	GGGAGCGTAT	420
TGGGGATGGA	CCAATGACGC	CCATATCTTT	TTCTCACCAG	TACCCAAGAG	CAAGGTCCAC	480
TATGACACCT	ACACAAGAGC	TGGCAGTGAC	CTTGACTTTC	AGTCCGAAGA	TGTTGCCACA	540
GTGAGCAATG	GCTTTTCACC	GGGGATCGGA	CTCAAAAGTT	CTATTGGGTG	GAAATGCCCC	600
ATCAAGAGCA	AATATGATTT	TGCCTCGGT	TTCAAGCCTG	GCTATGAGTA	TCTGAACCTG	660
CTATATCCGT	ATCGTAATTT	CAAGCTGGAT	GGAAATAAGC	CGCTTTCAGC	ACTATCTCCT	720
CGCATGAACC	ACATCGGCCA	TGTGGGCTTC	AACCTTACCG	TGGGTCTTTG	GACTAAT	777

(2) INFORMATION FOR SEQ ID NO:251

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3798 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...3798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251

ATGGGCAAGT	ATAAAGAGC	TAAGTACCGC	TATGGCTTTT	TTCTTTCTG	TTGGGATTAT	60
TATACCTTTG	AGGGAGTTAC	TTTTTTATGC	GCATCTGAAG	ATATGACAAC	CAAGAAACCC	120
CAAGCCATTT	TAGACTTAGA	GAAGGCCTAT	AACATTGAAA	TTCTGATCT	CTCCTCACAA	180
GAAGGGATAA	GCTGGTCGGT	AAATAGATAT	TTCAAGCAAG	ATTCTTCGG	TGCAGTCGTT	240
GAGCTTTGCT	TGGCAGAAATG	TCAGATAGAA	AGCATGACTT	GGCTTATTGA	TTTTCTGCT	300
CTAAAAAGC	TTGATCTATC	GTATAACCAA	ATCAGTAAGC	TAGAGGGTCT	AGAACGCTCT	360
ACTTCGTAA	CAAAACTTCG	TCTAAGAGT	AAACCAATCC	GTAACGTAGA	GGGCTGGAT	420
AGTCTCACCT	CGCTAACAAA	ACTTCTCTC	TCCGATAACC	AAATCAGTAA	GCTAGAGGGT	480
CTGGAACGTC	TCACCTCGTT	AGCGGAGCTT	TATCTTTTGG	ATAACCAAT	CAGTAACTA	540
GAGGCTCTGG	AACGCTCAC	GTCTTACCA	ACGCTTGAAC	TATCGGGTAA	CCAAATCCGT	600
AAGCTGGAGG	GTCTGGAACG	TCTCACGTCC	TTAGCAACGC	TTGAACATC	GGGTAACCAA	660
ATCCGTAAGC	TAGAGGGTCT	GGAAACGTCT	ACTTCGTAA	CAAAGCTTCG	TCTAAGAGT	720
AACCAATCA	GTAAGCTAGA	GGGTCTGAA	CGTCTCAGT	CCTTAGCAAC	GCTTGAACCTA	780
TCGGGTAAAC	AAATCCGTAA	GCTGGAGGGT	CTGGAACGTC	TACGCTCCTT	AGCAACGCTT	840
GAAGCTGTCG	GTAACCAAT	CAGTAAGCTA	GAGGGTCTGG	AACGCTCTCT	TTCTGTAACA	900
AAAGCTTCGTC	TAAGAAGTAA	CCAGATCAGT	AAACTAGAGG	GCCTGGAACG	TCTCACCTCG	960
CTAACAAAAC	TTTCTCTCTC	CGATAACCAA	ATCAGTAAGC	TAGAGGGTCT	GGAACTCTCT	1020
ACCTCGTTAG	CGGAGCTTTA	TCTTTTGGAT	AAACCAATCC	GTAAGCTGGA	GGGCTGGAA	1080
CGTCTCACT	CGTTAACAAA	GCTTCGTCTA	AGAAGTAACC	AAATCAGTAA	ACTAGAGGGC	1140
CTGATAGTC	TCACCTCGCT	AACAAAATTT	TCTCTCTCCG	ATAACCAAT	CAGTAACTA	1200
GAGGGCTCTG	AACGCTCTAC	GTCTTAGCG	GAGCTTTATC	TTTTGGATAA	CCAAATCCGT	1260
AAGCTGGAGG	GTCTTGATGG	TCTTGCTTCC	TTAACAAAGC	TTAGTCTAAG	GCGCAACCAA	1320
ATCAGTAAGC	TGGAAGGACT	AGACAGACTA	AAGGTTTTGA	GAAAACCTGA	TGTTTCGGGC	1380
AATGATATTC	AATCTATTGA	TGATATTAAG	CTATTGGCTC	CGATTCTGGA	GCAAACTTTA	1440
GAAAACTGA	GAATCCATGA	CAATCCATTT	GTTCATCAT	CAGGCTTGAT	ACTCTCTCCT	1500
TATGATAATC	ATTTCGGGA	GATTAAAGCT	CTTCTTGAAA	AAGAAAAAGA	AAAAACAGAA	1560

171/490

	AAGACTTCAG	TTGAATATCA	CCCATTTCG	AAAGTAATGC	TATTGGGAAA	TCATTCTTCG	1620
	GGTAAACAA	CATTTCTTAG	TCAATACGAT	ACAAATTATA	CGTATCAGAA	AAATACACAT	1680
	GTGTTGTCGA	TACATCGAAG	CAATAACCCT	AATGCGATCT	TTTACGACTT	TGGGGGACAG	1740
5	GACTATTATC	ATGGGATTTA	CCAAGCCTTT	TTTACCACCC	AATCGTTATA	CCTTCTCTTT	1800
	TGGGATGCTA	AGAAGGATCG	AAACTTTGTG	AGCGTAGATG	ATAAAGAATA	TCAGACTCTT	1860
	AATTTCAATC	GCCCCATTG	GTAGGACAG	ATAGCCTATG	CCTGCAATCG	TTGTATGTCC	1920
	GTGGAGGAA	ATCCTGATGG	CAAGGACACA	CCACAGACCA	CASACGATAC	AATTATCATT	1980
	CAGACTCATG	CCGATGAAAC	GGGCGCTAAG	CAGCAAACCT	TAGGCTGTGC	AGCCGAGAAT	2040
	GGAGTATTGG	AAGAAATCTA	TGTATCCTTA	GAGCCCAAGG	CGAATAGTGC	CGTACATGGG	2100
10	CTCAACTATC	TGAATGAGCG	GGTCCGAGAA	GTGTGCGCAA	GCAGGAGTAA	ATCAATTGAG	2160
	ATCACAGAAA	AAGATAAGGG	ATTGTACGAA	GCTCTTCCCA	CAATCGCCGG	TGATAATAAA	2220
	CACATGCCCTA	TCTCTCTCGA	AGCTCTTGCG	GCTCAATTGA	ATAAGGGAAG	AGCTGAAAAT	2280
	GATCTTTACA	CCATAGAGTA	TCTACAGACC	GAATTGAACC	AGCTTAGTCT	GCGAGGGGAG	2340
	GTGCTTTACT	ATCGTGAGAA	TGAGAAGCTG	AACAATTATG	TCTGGTTAGA	TCCGGCAGCT	2400
15	TTTGCCAAA	TGATTATG	AGAAATCCTC	CAAAAGACA	ACATCAATAG	AGGAACAGTT	2460
	CCTAAAGACA	TTTTGAATG	CAAACCTGCAT	AATCTAAGTT	CCGGAAGTAT	ATTTGAAGAA	2520
	GATGCCAAA	ATGGTAATAT	GATCTTGCG	CTATTATTGG	AAGAGCTGAT	CGTATATGAA	2580
	GATAAGGACT	GCTATGTGAT	ACCGGGCTAT	CTCCCTTTGC	ATTCCGATGA	CGAAGCCTAT	2640
20	AAATGGCTTA	CTTTGGGATT	CGAGAGSCCC	AATTTTGTCC	TCAAATTCGA	ACGTTTATC	2700
	CCCTTTGGCC	TGATCAACCA	GATTATAGCC	TACTATGGCC	GGGAAGAAGG	TGCTCTAAG	2760
	CGGTATTGCG	GAGATCAGGT	CATCTTCACA	GCAGGCCGTG	AGATGGATAG	GCAACCGCTT	2820
	GAGCAAGAA	AAGAGAAAG	GGGTTTGCCC	AAGACGAATG	CCGAGGATTA	TCAGATCTGG	2880
	ATCAAGCTCG	ACTTTACCGA	CTTGCCCAT	TCCGTATTCA	TCAAAGAGCA	GAGAAAGACA	2940
25	TCAGCTAAG	ATATGACGG	GAAAGAGGCT	ACTATCCTCA	GTGATATGTT	GGATATGTAT	3000
	TGGAACAATA	TCCCTCCGAG	GGAGCAAATA	GGAGATAAGG	ATACGGAGCA	AACGAGAAGC	3060
	ACTATTCTGT	AAACAAACAG	AAAGAAGAGA	CCCATCCAGG	ATCTCTACCT	CTCCTGTGCC	3120
	CAAGCGGATA	AAGATTGAC	GGAGTCTCAT	TATATCCATT	TGGGCACGCT	GGACGATGAA	3180
	AGCAAGACTA	CGGCGAGGAT	TGCAGCCTAT	CCGTTGAAGA	ACGCGCTTAT	CGATAAAGAG	3240
30	CGGGTGCGAG	AAGTATCGAC	TGCTCCCTAC	AAACATCTTT	CCGTCAATAA	AAATCTGGCT	3300
	ACTGCAAAAC	AGATCTTTAT	TTCTTATTC	AAAGAGGATC	AGACTGAAC	GGAGACCTGT	3360
	CTGCAATTTT	TCAACCCCTT	GGAGAAGAAT	GGTCAGATCG	AGATCTACTA	TGATAAGTTG	3420
	ACTAAGTTTG	AAACACCTAT	TCACCCCTGAA	ATAGAAAGCC	GTATTGTGCA	AGCCGACTGT	3480
	ATAATCGCTT	TGATCAGCCA	ACGCTATCTG	GCCACGGATT	ACATCCTGGA	TCATGAGTTG	3540
35	CCTGTATTTC	GGGAGTATA	CAAGACCATA	GTGCCSATAT	TGATCAAGCC	TTGTACATT	3600
	GAAGACGATG	AGTTCCTTCG	GGAGAAATAT	TTTGCTCAGA	AAGCTCAAT	AATCAATCTT	3660
	GGAAAGAGG	GAAAAACCAT	TAAAGCTTAT	GATAGTATTA	CGGCATCAG	CCATCGTGAT	3720
	GAAATTTGGG	TGGCAGTAGT	CAGAGAGTTC	AAAGAGAAGA	TATTAAGAT	AACAAAACAG	3780
	GAGGTAAATA	CAGATGAA					3798

(2) INFORMATION FOR SEQ ID NO:252

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3696 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
(B) LOCATION: 1...3696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252

65	ATGACAACCA	AGAAACCCCA	AGCCATTTTA	GACTTAGAGA	AGGCCTATAA	CATTGAAATT	60
	CCTGATCTCT	CCTCACAAGA	AGGGATAAGC	TGGTCGGTAA	ATAGATATTT	CAAGCAAGAT	120
	TCCTCCGGTG	CAGTCGTTGA	GCTTTGCTTG	CGAGAATGTC	AGATAGAAAG	CATGACTTGG	180
	CTTATTGATT	TTCTGCTCT	AAAAAGCTT	GATCTATCGT	ATAACCAAT	CAGTAAGCTA	240
	GAGGCTCTAG	AACGTCTTAC	TTCGTTAACA	AACTTCGTC	TAAGAAGTAA	CCAAATCCGT	300
70	AACTAGAGG	GCCTGGATAG	TCTCACCTCG	CTAACAAAAC	TTTCTCTCTC	CGATAACCAA	360
	ATCAGTAAGC	TAGAGGGTCT	GGAACTGCTC	ACCTCGTTAG	CGGAGCTTTA	TCTTTTGGAT	420
	AACCAATCA	GTAAACTAGA	GGGTCTGGAA	CGTCTCACGT	CCTTAGCAAC	GCTTGAACTA	480
	TCGGGTAAAC	AAATCCGTAA	GCTGGAGGGT	CTGGACGTC	TCACGTCCTT	AGCAACGCTT	540
	AACTATCGG	GTAAACCAAT	CCGTAAGCTA	GAGGGTCTGG	AACGCTCTAC	TTCGTTAACA	600
75	AAGCTTCGTC	TAAGAAGTAA	CCAAATCAGT	AAGCTAGAGG	GTCTGGAAAG	TCTCAGCTCC	660
	TTAGCAACAC	TTGAACATAT	GGGTAACCAA	ATCCGTAAGC	TGGAGGGTCT	GGAACGTCTC	720

	ACGTCCTTAG	CAACGCTTGA	ACTGTGCGGT	AACCAAAATCA	GTAAGCTAGA	GGGTCTGGAA	780
	CGTCTCTCTT	CGTTAAACAA	GCTTCGTCTA	AGAAGTAACC	AGATCAGTAA	ACTAGAGGGC	840
	CTGGAAACGTC	TCACCTCGCT	AACAAAACCT	TCTCTCTCCG	ATAACCAAAT	CAGTAAGCTA	900
5	GAGGGTCTGG	AACGCTCTAC	CTCGTTAGCG	GAGCTTTATC	TTTTGGATAA	CCAAATCCGT	960
	AAGCTGGAGG	GCCTGGAACG	TCTCAGCTCG	TTAACAAAGC	TTGCTCTAAG	AAGTAACCAA	1020
	ATCAGTAAAC	TAGAGGGGCT	GGATAGTCTC	ACCTCGCTAA	CAAAACTTTC	TCTCTCCGAT	1080
	AACCAATCA	GTAACCTAGA	GGGCTCTGAA	CGTCTCAGT	CCTTAGCGGA	GCTTTATCTT	1140
	TTGGATAACC	AAATCCGTAA	GCTGGAGGGT	CTTGATGGTC	TTGCTTCCTT	AACAAGGCTT	1200
10	AGTCTAAGGC	GCAACCAAAT	CAGTAAGCTG	GAAGGACTAG	ACAGACTAAA	GGTTTTGAGA	1260
	AAACTTGATG	TTTCGGGCAA	TGATATTCAA	TCTATTGATG	ATATTAAGCT	ATTGGCTCCG	1320
	ATTCTGGAGC	AAACTTTAGA	AAAACCTGAG	ATCCATGACA	ATCCATTGTG	TGCATCATCA	1380
	GGCTTGATAC	TCTCTCCTTA	TGATAATCAT	TTGCCGGAGA	TTAAAGCTCT	TCTTGAAAAA	1440
	GAAAAAGAAA	AACAGAAAAA	GACTTCAGTT	GAATATCACC	CATTTTGCAA	AGTAATGCTA	1500
15	TTGGGAAATC	ATTCTTCGGG	TAAAAACAAC	TTTCTTAGTC	AATACGATAC	AAATTATACG	1560
	TATCAGAAAA	ATACACATGT	GTGTGCGATA	CATCGAAGCA	ATAACCCCTA	TGCGATCTTT	1620
	TACGACTTTG	GGGGACAGGA	CTATTATCAT	GGGATTTACC	AAGCCTTTTT	TACCACCCAA	1680
	TCGTTATACC	TTCTCTTTTG	GGATGCTAAG	AAGGATCGAA	ACTTTGTGAG	CGTAGATGAT	1740
	AAAGAAATATC	AGACTCTTAA	TTTCAATCGC	CCCTATTGGT	TAGGACAGAT	AGCCTATGCC	1800
20	TGCAATCGTT	GTATGTCGTT	TGGAGGAAAT	CCTGATGGCA	AGGACACACC	ACAGACCACA	1860
	GACGATACAA	TTATCATTTCA	GACTCATGCC	GATGAAACGG	GGCCTAAGCA	GCAAACTTTA	1920
	GGCTGTGACG	CCGAGAATGG	AGTATTGGAA	GAAATCTATG	TATCCTTAGA	GCCCAAGGCG	1980
	AATAGTGCCG	TACATGCCGT	CAACTATCTG	AATGAGCGGG	TGCGAGAAGT	TGTCGCAAGC	2040
	AGGAGTAAT	CAATTGAGAT	CACAGAAAAA	GATAAGGGAT	TGTACGAAGC	TCTTCCACAC	2100
25	ATCGCCGGTG	ATAATAAACCA	CATCCCTATC	TCTCTCGAAG	CTCTTGGCGC	TCAATTGAAT	2160
	AAGGGAAGAG	CTGAAATGTA	TCTTTACACC	ATAGAGTATC	TACAGACCGA	ATTGAACCAG	2220
	CTTAGTCTGC	GAGGGGAGGT	GCTTTACTAT	CGTGAGATG	AGAAGCTGAA	CAATTATGTC	2280
	TGGTTAGATC	CGGCAGCTTT	TGTCCAAATG	ATTATGAGAG	AAATCCTCCA	AAAAGACAAC	2340
	ATCAATAGAG	GAACAGTTCC	TAAAGACATT	TTTGAATGCA	AATGCAATAA	TCTAAGTTCC	2400
30	GGAAATATAT	TTGAAAGAGA	TGCGCCAAAT	GGTAATATGA	TCTTGCAAGT	ATTATTTGAA	2460
	GAGCTGATCG	TATATGAAGA	TAAGGACTGC	TATGTGATAC	CGGCTATCT	CCCTTTGCAT	2520
	TCCGATGACG	AAGCCTATAA	ATGGCTTACT	TTGGGATTG	AGAGGCCCAA	TTTTGTCTCT	2580
	AAATTCGAAC	GTTTTATCCC	CTTTGGCCTG	ATCAACCAGA	TTATAGCCTA	CTATGGCCCG	2640
35	GAAGAAGGTG	CTCTAAAGCG	GTATTGGCGA	GATCAGGTCA	TCTTCACAGC	AGGCCGTGAG	2700
	ATGGATAGGC	AAACGCTTGA	GCAAGAGGAA	GAGAAAGAGG	GTITGCCCAA	GACCAATGCC	2760
	GAGGATTATC	AGATCTGAT	CAAGCTCGAC	TTTACCGACT	TGGCCATATC	CGTATTATC	2820
	AAAGAGCAGA	GAAAGACATC	AGCTAAGGAT	ATGCAGCGGA	AAGAGGCTAC	TATCCTCAGT	2880
	GATATGTTGG	ATATSTATTG	GAACAATATC	CCTCCGAGGG	AGCAAAATAGG	AGATAAGGAT	2940
40	ACGAGAGCAA	CGAGAAGCAC	TATTCTGTGA	ACAAACAGAA	AGAAGAGACC	CATCCAGGAT	3000
	CTCTACCTCT	CCTGTGCCCA	AGCGGATAAA	GATTGACGG	AGTCTCATT	TATCCATTG	3060
	GGCAGCTGG	ACGATGAAAG	CAAGACTACG	GCGAGGATTG	CAGCCTATCC	GTGGAAGAAC	3120
	GGCGTTATCG	ATAAAGAGCG	GGTGCGAGAA	GTATCGACTC	GTCCCTACAA	ACATCTTTCC	3180
	GTCAATAAAA	ATCTGGCTAC	TGCAAAACAG	ATCTTTATTT	CCTATTCCAA	AGAGGATCAG	3240
45	ACTGAACCTG	AGACCTGTCT	GCAATTTTTC	AAACCCCTGG	AGAAGAATGG	TCAGATCGAG	3300
	ATCTACTATG	ATAAGTTGAC	TAAGTTTGAA	ACACCTTATC	ACCCTGAAAT	AAGAAAGCGT	3360
	ATTGTGGAAG	CCGACTGTAT	AATCGCTTTG	ATCAGCCAAC	GCTATCTGGC	CACGGATTAC	3420
	ATCTTGGATC	ATAGTTGCC	TGTATTTCGG	GAGTATAACA	AGACCATAGT	GCCGATATTG	3480
	ATCAAGCCTT	GTACATTGCA	AGACGATGAG	TTCTTGGGG	AGAAATATTT	TGCTCAGAAA	3540
50	GCTCAATAAA	TCAATCTTGG	AAAAGAGGGA	AAAACCATTA	AAGCTTATGA	TAGTATTACG	3600
	GCTACAGCCC	ATCGTGATGA	AAATTGGGTG	GCAGTAGTCA	GAGAGTTCAA	AGAGAAGATA	3660
	TTAAGAATAA	CAAAACAGGA	GGTAATATCA	GATCAA			3696

(2) INFORMATION FOR SEQ ID NO:253

55	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 3525 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
60	(D) TOPOLOGY: circular
	(ii) MOLECULE TYPE: DNA (genomic)
	(iii) HYPOTHETICAL: NO
65	(iv) ANTI-SENSE: NO
	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
70	(ix) FEATURE:
	(A) NAME/KEY: misc_feature
	(B) LOCATION 1...3525
75	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253

	ATGACTTGGC	TTATTGATT	TCCTGCTCTA	AAAAAGCTTG	ATCTATCGTA	TAACCAATC	60
	AGTAAGCTAG	AGGGTCTAGA	ACGTCTTACT	TCGTTAACAA	AACCTCGTCT	AAGAAGTAAC	120
	CAAAATCCGTA	AACTAGAGGG	CCTGGATAGT	CTCACCTCGC	TAACAAAAC	TTCTCTCTCC	180
	GATAACCAAA	TCAGTAAGCT	AGAGGGCTCG	GAACGTCTCA	CCTCGTTAGC	GGAGCTTTAT	240
5	CTTTTGGATA	ACCAATCAG	TAAACTAGAG	GGTCTGGAAC	GTCTCAGTCT	CTTAGCAACG	300
	CTTGAACAT	CGGGTAACCA	AATCCGTAA	CTGGAGGGTC	TGGAACGTCT	CACGTCTCTA	360
	GCAACGCTTG	AACTATCGGG	TAACCAAAATC	CGTAAGCTAG	AGGGTCTGGA	ACCTCTCACT	420
	TCGTTAACAA	AGCTTCGTCT	AAGAAGTAAC	CAAATCAGTA	AGCTAGAGGG	TCTGGAACGT	480
	CTCACGTCTCT	TAGCAACGCT	TGAACTATCG	GGTAACCAAA	TCCGTAAGCT	GGAGGGTCTG	540
10	GAACGTCTCA	CGTCTTAGC	AACGCTTGAA	CTGCGGGTA	ACCAATCAG	TAAGCTAGAG	600
	GGTCTGGAAC	GTCTCTCTC	GTTAACAAAG	CTTCGTCTAA	GAAGTAACCA	GATCAGTAAA	660
	CTAGAGGGCC	TGGAACGTCT	CACCTCGCTA	ACAAAACCTT	CTCTCTCGA	TAACCAAAATC	720
	AGTAAGCTAG	AGGGTCTGGA	ACGTCTCACC	TCGTTAGCGG	AGCTTTATCT	TTTGGATAAC	780
	CAAAATCCGTA	AGCTGGAGGG	CCTGGAACGT	CTCACCTCGT	TAACAAAGCT	TCGTCTAAGA	840
15	AGTAACCAAA	TCAGTAAACT	AGAGGGCCTG	GATAGTCTCA	CCTCGCTAAC	AAAACCTTCT	900
	CTCTCCGATA	ACCAATCAG	TAAACTAGAG	GGCCTGGAAC	GTCTCAGTCT	CTTAGCGGAG	960
	CTTTATCTTT	TGGATAACCA	AATCCGTAA	CTGGAGGGTC	TTGATGGTCT	TGCTTCTCTA	1020
	ACAAGGCTTA	GTCTAAGGCG	CAACCAATC	AGTAAGCTGG	AAGGACTAGA	CAGACTAAAG	1080
20	GTTTGGAGAA	AACTTGATGT	TTGCGGCAAT	GATATTCAAT	CTATTGATGA	TATTAAGCTA	1140
	TTGCTCCGTA	TTCTGGAGCA	AACTTTAGAA	AACTGAGAA	TCCATGACAA	TCCATTGTGT	1200
	GCATCATCAG	CTCTGATACT	CTCTCTTAT	GATAATCATT	TGCCGGAGAT	TAAAGCTCTT	1260
	CTTGAAAAAG	AAAAAGAAAA	ACAGAAAAAG	ACTTCAGTTG	AATATCACCC	ATTTTGCAAA	1320
	GTAATGCTAT	TGGGAAATCA	TTCTTGGGT	AAAACAACAT	TTCTTAGTCA	ATACGATACA	1380
25	AAITATACGT	ATCAGAAAAA	TACACATGTG	TTGTGATAC	ATCGAAGCAA	TAACCTAAT	1440
	GGCATCTTTT	ACGACTTTGG	GGGACAGGAC	TATTATCATG	GGATTTACCA	AGCCTTTTTT	1500
	ACCACCCAAT	CGTTATACCT	TCTCTTTTGG	GATGCTAAGA	AGGATCGAAA	CTTTGTGAGC	1560
	GTAGATGATA	AAGAATATCA	GACTCTTAAT	TTCAATCGCT	CCTATTGGTT	AGGACAGATA	1620
	GCCTATGCCT	GCAATCGTTG	TATGTCCGTT	GGAGGAAATC	CTGATGGCAA	GGACACACCA	1680
	CAGACCCAG	ACGATACAAT	TATCATTCAG	ACTCATGCCG	ATGAACCGGG	CGCTAAGCAG	1740
30	CAAACTTAG	GCTGTGCAGC	CGAGAATGGA	GTATTGGAAG	AAATCTATGT	ATCCTTAGAG	1800
	CCCAGGCSA	ATAGTCCCGT	ACATGCCGTC	AACTATCTGA	ATGAGCGGGT	GCGAGAAGTT	1860
	GTCCGAAGCA	GGAGTAAATC	AATTCAGATC	ACAGAAAAAG	ATAAGGGATT	GTACGAAGCT	1920
	CTTCCCAAA	TCGCCGGTGA	TAATAAACAC	ATCCCTATCT	CTCTCGAAGC	TCTTGCGGCT	1980
	CAATTGAATA	AGGGAAGAGC	TGAAAAATGAT	CTTACACCA	TAGAGTATCT	ACAGACCGAA	2040
35	TTGAACGATA	TTAGTCTGCG	AGGGGAGGTG	CTTACTATC	GTGAGATGA	GAAGCTGAAC	2100
	AAITATGTCT	GGTTAGATCC	GGCAGCTTTT	GTCCAAATGA	TTGATGGAGA	AATCTTCCAA	2160
	AAGACAACA	TCAATAGAGG	AACAGTTTCT	AAAGACATTT	TTGAATGCAA	ACTGCATAT	2220
	CTAAGTCCG	CAAGTATATT	TGAAGAAGAT	GGCCAAAATG	GTAATATGAT	CTTGAGCTA	2280
40	TTATTGGAAG	AGCTGATCGT	ATATGAAGAT	AAGGACTGCT	ATGTGATACC	GGGCTATCTC	2340
	CCTTTGCAAT	CCGATGACGA	AGCCTATAAA	TGGCTTACTT	TGGGATTGGA	GAGGCCCAAT	2400
	TTTGTCTCTA	AATTGGAACG	TTTTATCCCC	TTTGGCTGTA	TCAACAGAT	TATAGCCTAC	2460
	TATGGCCGGG	AAGAAGGTGC	TCTAAAGCGG	TATTGGCGAG	ATCAGGTCAAT	CTTCACAGCA	2520
	GGCCGTGAGA	TGGATAGGCA	AACGCTTGAG	CAAGAAGAAG	AGAAAGAGGG	TTTGCCCAAG	2580
	ACGAATGCCG	AGGATTATCA	GATCTGGATC	AGCTCGACT	TTACCGACTT	GGCCATATCC	2640
45	GTATTCTATCA	AAGAGCAGAG	AAAGACATCA	GCTAAGGATA	TGCAGCGGAA	AGAGGCTACT	2700
	ATCCTCAGTG	ATATGTTGGA	TATGTATTTG	AACAATATCC	CTCCGAGGGA	GCAATAGGA	2760
	GATAAGGATA	CGGAGCAAA	GAGAAGCACT	ATTCTGTAAA	CAACAGAAA	GAAGAGACCC	2820
	ATCCAGGATC	TCTACCTCTC	CTGTGCCCAA	GCGGATAAAG	ATTTGACGGA	GTCTCATTTAT	2880
	ATCCATTGG	GCAACGCTGGA	CGATGAAAGC	AAGACTACGG	CGAGGATTGC	AGCCTATCCG	2940
50	TTGAGAAACG	GGGTTATCGA	TAAAGAGCGG	GTGCGAGAAG	TATCGACTCG	TCCCTACAAA	3000
	CATCTTTCCG	TCAATAAAAA	TCTGGCTACT	GCAAAACAGA	TCTTTATTTT	CTATTCCAAA	3060
	GAGGATCAGA	CTGAACCTGGA	GACCTGTCTG	CAATTTTTC	AACCTTTGGA	GAAGAATGGT	3120
	CAGATCGAGA	TCTACTATGA	TAGTTGACT	AAGTTTGAAA	CACCTATTCA	CCCTGAAATA	3180
	AGAAAGCGTA	TTGTGGAAGC	CGACTGTATA	ATCGCTTTGA	TCAGCCAAAG	CTATCTGGCC	3240
55	ACGGATTACA	TCTTGGATCA	TGAGTTGCCT	GTATTTCGGG	AGTATAACAA	GACCATAGTG	3300
	CGGATATTGA	TCAAGCCTTG	TACATTGAAA	GACGATGAGT	TCCTTCGGGA	GAAATATTTT	3360
	GCTCAGAAAG	CTCAAATAAT	CAATCTTGGA	AAAGAGGGAA	AAACCATTAA	AGCTTATGAT	3420
	AGTATTACGG	CATCAGCCCA	TCGTGATGAA	AATTGGGTGG	CAGTAGTCAG	AGAGTTCAAA	3480
60	GAGAAGATAT	TAAGAAATAC	AAAACAGGAG	GTAATAACAG	ATGAA		3525

(2) INFORMATION FOR SEQ ID NO:254

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 687 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

174/ 490

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

5 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254

10 ATGATGAAAA AAGCATTGTG TTTCTACTA CTGGTTTGCC TATTCTCCTC GTTCAGCAGT 60
TCCGCCCAAA CAAGACGAA CAGTAGCCGG AGTTATTTTA CAGGACGAAT CGAGAAGGTG 120
AGTTTGAACT TAGGGGTCCC CCCGTAAGC ACAGAGGTTT GGGGAATGAC CCATGATGCG 180
AACGGTCTCC CTTTCGAAAT ACCTATCTCT TTCAGTCGTT TCAACAGCCA GGGAGATATA 240
GCTACCACTT ATTACATAGC GAATAGCGAG GCAACTTTGA ATGAATGGTG CGACTATGCA 300
15 CACCCGGGCG GCATCGTGAG GGTAGAAGGT CGTTTTTGGG AAATGACTTA CAACATACCA 360
ACCTACAATG CAGTCTGCAC CCGGATTACA TTCGAAAATC AAGAAATAGA AGGAACGATC 420
GTCTTGATAC CCAAGCCCAA AGTCTCGCTG CCTCATGTGT CGGAATCGGT GCCTTGCATC 480
CSAACCGAAG CCGGGAGGGA ATTTATCCTT TCGGAAGAAG ACGACACCTT TGTGTCTCAC 540
20 GATGGTAACG AAGTAACGAT AGGCGGTAAA CCTTCTTTCG TCAATACCAA CGTAAAGATT 600
GTGGGGGACG TATCTCAAAA GTATCCGTG GGGGTAGGAG AAATTCGATT CCTGCAGATT 660
TGTGCCCAAA CAGTATCACA AAAAAA 687

(2) INFORMATION FOR SEQ ID NO:255

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 684 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

35 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
40 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...684

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:255

ATGAAAAAAG CATTGTGTTT CGTACTACTG GTTTCCTTAT TCTCCTCGTT CAGCAGTTCC 60
GCCCCAAACAA CGACGAACAG TAGCCGGAGT TATTTTACAG GACGAATCGA GAAGGTGAGT 120
50 TTGAACTTAG GGGTCCCCCC CGTAAGCACA GAGGTTTGGG GAATGACCCA TGATGCGAAC 180
GGTCTCCCTT TCGAAATACC TATCTCTTTC AGTCGTTTCA ACAGCCAGGG AGATATAGCT 240
ACCACTTATT ACATAGCGAA TAGCGAGGCA ACTTTGAATG AATGGTGCGA CTATGCACAC 300
CCGGGCGGCA TCGTGAGGGT AGAAGGTGCT TTTTGAAAAA TGAATTACAA CATACCAACC 360
TACAATGCAG TCTGCACCCG GATTACATTC GAAAATCAAG AATAGAAGG AACGATCGTC 420
55 TTGATACCCA AGCCCAAAGT CTGCTGCCCT CATGTGTCGG AATCGGTGCC TTGCATCCGA 480
ACCGAAGCCG GGAGGGAATT TATCCTTTGC GAAGAAGACG ACACCTTTGT GTCTCAGGAT 540
GGTAACGAAG TAACGATAGG CGGTAAACCT TTCTTGCTCA ATACCAACGT AAAGATTGTG 600
GGGGACGTAT CTCAAAAGTA TGCCGTGGGG GTAGGAGAAA TTCGATTCCT GCAGATTGTG 660
60 GCCCCAACAG TATCACAACA AAAA 684

(2) INFORMATION FOR SEQ ID NO:256

65 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1620 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

70 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

75 (vi) ORIGINAL SOURCE:

175/ 490

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256

10	ATGAAGACAA AAGTTTACG CAAATTCGTG GTGGCGGCTT TCGCCGTCGC AACCCCTCTGT	60
	CCTCTCGCCC AAGCGCAGAC GATGGGAGGA GATGATGTCA AGGTGGTCCA GTACAATCAG	120
	GAAAACTGG TACAAACGAG GATGAGTGTG GCGGACACCG GATGGATCTA TGTAAATGACC	180
	CACAGTGGAT ACGACACCGG CAATAGCAAT GTGAAGATCT TCGCTCCAA AGACCAAGGT	240
	GCCACATACC AAAAGTTGAG GGATTGGGAT CCATCGGATG ATTATCAGTT TCAAGACTTC	300
15	GATATCGTGG TAACGGGTAA GAATGAATCC GACATCAAGA TTTGGTCCGT AGAGCTCATG	360
	AATAAGCCCG GAGGATATAA CAGTAGAGTT GCGGTCTTCA GTCGCGATGC CAACGCGCAG	420
	AATGCGAAAC TCGTGTATAA GGAAGACTTC TCCAATGTGC AGTTGTACGA TGTGGATATA	480
	GCCTCCAACT ATCGTTCCGC TTCTTCTCTT AACATGGTG GCAACCCCTT TGCTTTGGCT	540
	TTCCGTTACA CCGGCTTCAA CAATACGCAC AAATAAGTT TTTGGACTA TGTGTTCTCT	600
20	CTGAATGGAG GGCAAAATTT CAATAAAAAC TTACTCTTCA GTCAAGATGG AGAGAAGAAA	660
	ATTGACAAGG TGGATCTCTC ATTGGGTAGC ACCTCTGAAT CCATGGGTCA CAATGCCTGG	720
	CCGCTAATGG GTGTGGTATT CGAAATGAAT AAACAAGGGG GAAAAAGCGA TATCGGTTTC	780
	TTGTGCAACT TTGTGACAAA TGATCCCGAA TTTCAGTGGT CAGGCCCTAT AAAAGTGAGT	840
	GAAAGCGACA TCTCGTTCAG CCCCAAAATC CAAATGTGTC TGGACGAGGA TAACAAATACG	900
25	ATCAATGGGG AGAGTTGCCA CAACTTCATG ATTACGTACA GCGATTATGA TTCTGAATAT	960
	TCCGATTGGG ACATTCCGTA TGTATATCCC AAGAAATCST TCAAGTATGA AAAAGGAAAA	1020
	ACTCCGACTA TGGATGATCT GGTGGAAAGCT TTCCTTACAG CTTCGTACCA GAGTGAGACC	1080
	AATCGGCGGC TGGGGTATGA CAAGAACGCC AATCACTACC TGATTACATA TGCCAAAAAA	1140
	GAAGAGAACG GTACGAACAC GCTGAAATAC CGCTGGGCCA ATTATGACAA GATTCAATAAC	1200
30	AAAGATTGGT GGAACGACAC ATTTACGTAT ACATCATCTG CCAATGCTCT CTACACACCT	1260
	CAAGTAGACA TCAATCCGAC CAAGGGTCTC GTGTGCTGGT CATGGGTGGA ATATCTGCCG	1320
	GGCAAAACGGA TCGTTTGGTC TGATACGCAG TGGACCCATG CCAACGGTGT AGAAGACATC	1380
	GTATGCAAG AAGGCAGCAT GAAGCTCTAC CCGAATCCGG CTCAGAATA TGCTGTGATT	1440
	AGCTGCGGA CGGCAGCAAA CTCGAAGGCT GTTGTTTACG ATATGCAAGG CAGAGTAGTC	1500
35	GCTGAGGCTT TTTTCTCCGG CAACGAATAC AGGCTGAACG TGCAGCACTT GGCTAAGGGT	1560
	ACGTACATAC TCAAGGTCGT ATCCGATACG GAGCGTTTCG TAGAGAAGCT CATCGTGGAA	1620

(2) INFORMATION FOR SEQ ID NO:257

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 2313 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
45	(D) TOPOLOGY: circular
	(ii) MOLECULE TYPE: DNA (genomic)
	(iii) HYPOTHETICAL: NO
50	(iv) ANTI-SENSE: NO
	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
55	(ix) FEATURE:
	(A) NAME/KEY: misc_feature
	(B) LOCATION 1...2313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257

60	ATGCTGACGA TCCGAAACTT CCTCCTCTTT TGTGTCTGT CGCTGATAGC GTTTGCTGCC	60
	GATGCACAAA GCTCTGTCTC TTCGGGTAGA CCACTGACAG AATATGTCAA TCCCTTTATC	120
	GGAAACGGCA ATTACGGTAC CACGAATCCG GAGGAGTAT TGCCCAATGG GTTGATGAGC	180
65	GTTACCCCTT TCAATGTCTG CCGATCGACA GAGAATCGCT TCGACAAAGA TTCCGCTTGG	240
	TGGAGTGGCG CTATTCCGGC CGACAATAGT TACTGCATCG GTTTCAGCCA TGTGAATCTG	300
	AGTGGAGTAG GCTGTCCCGA ACTGAGTGGG ATACTGTGTA TGGCCACTTC CGGCACATTC	360
	GATCCTGATT ACTGCTGCTA TGGCTCTTCG CTCAGTCTGAG AATATGCGCG CCCGGAGAGG	420
	TACAGGCGTG TATTGGACAA ATACGGTATA GATGACGCG TGACCGTAAAC CGAGCGGACT	480
	GCTTTGACCG AATTGTCTTT TCCCGAAGGA GAAGGCCATA TCCTGCTGAA CCTGGGACAG	540
70	GCCCTAAGCA ATGAATCGGG AGCCTCTGTT CGATTCTTAA ACGACTCCAC AGTCGTGGGC	600
	AGCAGGCTGA TGGGGACGTT CTGCTACAA CCGCAAGCAG TTTTTCGTCA GTATTTCTGA	660
	CTTCAGGTGA GTCCGCGACC GATCTCTGCC GGCTATTGGA AGAAGCAGCC TCCTATGACA	720
	GTGGAAGCCG AATGGGATTC GACTGCAGGG AATATAGAAG AGTACGACGG CTACAAGCGT	780
75	GAGATGAGCG GTGATGACAT CCGGTGTCGA TTCTCGTTCA ACTGCGATCA GGGGGAAGAG	840
	ATCTATGTAC GATCGGCGGT TTCATTCGTC AGCGAAGCCA ATGGGCTCTA TAACTGGA	900

176/ 490

5 GCGGAGCAAG AAGAGGTGTT CAAAGTGTG GGAGGGAATC CGGCCAAGGC TTTCTCCGCT 960
ATACGCTCTC GCGCTATAGA GCGTTGGGAG GAAGCCCTCG GTACGGTGGG AGTGGGAAGGA 1020
GGCACACCGG ATGAAAAGAC GATATTCTAT ACUGCACTCT ATCACCCTGCT GATACATCCG 1080
AATATCCTAC AAGATGCCAA TGGAGAATAT CCTATGATGG GCAGTGGCAA AACGGGTAAT 1140
ACGGCTCACC ACCGCTACAC CGTGTCTCT CTTTGGGACA CGTACCGCAA TGTACACCGG 1200
CTGCTCTGCC TCCTCTATCC GGAGAAGCAG TTGGATATGG TACGGACACT GATCGACATG 1260
TACCGAGAGA GCGGGTGGCT GCCGAGATGG GAGCTGTACG GACAGGAGAC CCTGACGATG 1320
GAGGCGCACC CCTCGCTTAT CSTCATCMY GACACTTGGC AAAGGGGCTT TCGTGTCTTC 1380
GATACGGCAA CGGCCTATGA AGCCATGAAA AAAAATGCTT CTTCGGCAGG AGCGACCCAT 1440
10 CCGATCCGTC CTGACAACGA CGACTATCTC ACCCTCGGCT TCGTACCGCT TCGGAAACAG 1500
TACGACAATT CCGTATCGCA TCGCTGGAA TACTATCTG CCGACTGGAA TCTGTCCCGC 1560
TTTGCCACG CACTTGGGCA TAAAGAAGAC GCAGCTCTAT TCGGAAACG CTGTTGGGC 1620
TACGACACT ATTATAATAA GGAGTATGGT ATGCTGTGTC CATTGCTGCC GGATGGATCA 1680
TTCTCTACTC CTTTCGATCC CAAACAGGGT GAAAACCTCG AGCCTAATCC CGGTTTCCAC 1740
15 GAGGGCAGTG CTTATAACTA TGCCTTTTTC GTTCCCGACG ATATACAAGG GCTTGGCCGG 1800
CTGATGGGAG GAGCAAGGT TTTTTCGAAA AGGTTGACGA AAGTCTTGA TGAAGGATAT 1860
TATGATCGGA CCAACGAGCC GGACATCGCC TATCCTTACC TCTTCTCTA TTTCCCAAG 1920
GAAGCATGGC GAACGCAGAA ATTGACCCGG GAGTTGATAG ACAACATTT TTGCAATGCT 1980
20 CCTAACGGCT TGCCCGGTAA TGACGATGCC GGTACGATGA GTGCTTGGCT TGTCTATTCC 2040
ATGCTGGGAT TCTACCGTGA CTGTCGGGCG AGCCCCACCT ATACACTGAC CTGCGCGGTA 2100
TTCCCGCGAG TTAGGATTCG GCTCAATCCG CAGTATTATC CTCAGGGGGA GTTGATCATT 2160
ACGACCMNTA CAGAGAATCA ACCGACAGAT TCCATTTACA TCCATACGGT TTCTCTTGGC 2220
AATAAACAC TTCCGCATGG AACAAAGCAT ATCAGCCATG CCGATTGGT GCGCTCGGCT 2280
25 CACCTCCGTT ACGAACTAAG CAATCGTCT CGA 2313

(2) INFORMATION FOR SEQ ID NO:258

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2328 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 35 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 40 (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 45 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...2328
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:258

50 ATGTGCAAAA TAAGATTGAG CCTCTTGCG GCTCTGTGCT TCTGCTTATT GTTCACCTCT 60
TTTTCTCTCC AAGCTCAAGA GGAAGGTATT TGGAAATACC TCTTGGCTAT CCACAAGAGG 120
GAAAAAGCCG TAGAAGCCGC CAAGAAAGTC TTTGCCGTAG CCNACGGAGT ACTTTACTCG 180
GTGGGCAAGG AAGCTCCCCA TGAGGCAAGG ATCTTCGAGC GTATCAGCGG ATCAGCGGAT 240
ACATCGGTAA GCAGCATAGC CTACTCCGAG CAACTAAAAT CTTGGTCAAT ATACTATGCA 300
55 TCAGGCAATA TCGACATCTT GGACGAAGCA GGCCGTGTGA CCAACGTACC TGCATTGAAA 360
GACAATATCG ATCTGATAGA CAAAACGCTC AATCGGCTTT TGATCGTAGG CAACAGGGCT 420
TATTTGSCAG GAGGATTCGG CCTCTCCGTT CTGGATGTG CCGAAGCTCG CATACCGGCT 480
ACCTAGGCCA AGGGAAGTAA GGTGACCGAT GTGGCTAAGT TGGACAATGA TCGCTTGTCT 540
ATGCTGAAAG AAGGSCAGCT CTTTATCGGA AAAGAGACCG ATAACCTGCA AGATCCGGGC 600
60 GCATGGACAG CCTTGTCTTT GAATTTGCCG ATGGGCTCGG TCACCGGTCT GGGCATTGTC 660
GGGGAAGACA TCTGTTTCCT GCTGGCCGAT GGCCGTGTAT ATGTGCTGTC AAACCAATCG 720
TTTGAGCCGG AGCTATTGCT CTCTCTCTCC GCGATTAC GACTGTATGT GACGGATCGT 780
GGTCTGTTCA TCTGTGCCGA GAATCGAATT TATTTCAATG AAAAAGGTCT CAAAACGACA 840
CAATTTCTTA TAGCCGACGT CTTTGGGTGC GGTGCCATGA ACGAAAGCAA TACGGCATA 900
65 ATAGCATTGG GAGAAGAAGG TTTGGCTTCA CTCTTCTCG CAGAGGGAAG TACGGCCGAA 960
GCCATGCCGT TAGCATTGGA CGGACCGGGG GACAATGAT TCTACGAGAT GCGGTTTGT 1020
CACGGACGTC TGTATGCAGC CAGCGGACTC TGGGAACAA ACCTGATGG ACATGCCGCT 1080
ATGGTGAAGC TATACGACGG CAACCGATGG ACTAATCTG ACAAGAAGAC CGTACAGGAA 1140
CAGTTGGGCG GCGGATTCAG TTCAATGAT GCTATCGATA TAGCTGTTTC CAACGGAGAC 1200
70 CCGATCACT TTTTGTGCG TACATGGGGA AACGGTCTGT TCGAATTCAA GGATGGCAA 1260
GCGATAGCTC GCTATTCGGG AAACGAAACT GCTATCGCAG AATGTAATCC CGGAGATGCC 1320
CGTGTGAAGG CGATTGCTT TGACAATAAG GGCACCTCT GGGGACGCT CGGTGCCGTA 1380
GGCAAGACA TCTTCATGTA CGATCCGCG AGTAGCACAT GGCATTCTTT CAGCTATCCG 1440
GATSTAGCCA ATCTGGCCCT CTTCGGCAAT ATGATTATCT TACCCAACGG AGACAAATCG 1500
75 GTAATATACC TTACCCGTAG TGGCGGATCC ACSCGCAAG GTGTCTTGAT CTTCAAGAT 1560

177/490

CGGGGTACAC CGGAAACGAC TTCGGACGAC AGCCATCTTT ACCTCGAGCA GTTTGTCAAT 1620
CGCCTCGGG CAGCCATAGG ACATAAGACT ATCTATGCAA TGGCCGTCGA TCATAACGGC 1680
TCTGTCTGGA TGGGATCGGA TATAGGCATT TTCGGCGTCT ACAATGCAGC CGGAGTATTG 1740
TCCTCGACTT CTACCCCTAT CGCTGTTCCG CCGGTCCGAG GAGAAGAACC CAATTTGTAC 1800
5 TATGTGCTGG ACAAGGTGAC GGTGACAGAC ATCGTCTGGG ACAAACCTCA TCACAAATGG 1860
GTTGCCACCC AAGGGACAGG ACTCTATCTC CTTTCGGGAG ATTGCAGTAA GATCCTCGCG 1920
CAATTTACCG TAGAAACAG CCCTTTGCTT TCTAACAACA TACTATCCCT GGCCTTAAAT 1980
GACGATAACG GACTGCTGTA CATCGGTACG GCGGACGGAC TGATGACGTT CCAACCGGCT 2040
10 ACGGGGAGTG GATCAGCTTC CGAACTGGAC GGCCTCTATG TATACCCCAA TCCGCTAAGG 2100
CCGGAATATC CCGATGGCGT CACCATTTGCC GGAATGCAAG CCGGCTGTAG TGTCAAAATC 2160
ACCGATACCA CCGGCAGACT GCTATACCAG ACTGAGAGCG TAACCAACCGA AGTCAAAATG 2220
AATGCTCAGG GTGCCGATGG CAATAGGGTA GCTTCGGGCG TATATGCCGT TGCAGTGTAC 2280
GATCCGSTAT CGAAAAAGTC CAACTAATT CGCTTCGCAG TGATTTCG 2328

15

(2) INFORMATION FOR SEQ ID NO:259

- (i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 3474 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
25 (iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:
30 (A) ORGANISM: PORPHYROMONAS GINGIVALIS
- (vi) FEATURE:
35 (A) NAME/KEY: misc_feature
(B) LOCATION: 1...3474
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:259

ATGAACGAA TACTTCCAAT AGTCGCATTC CTTTCTCTCT TCCTTGCCCT TGCTTTGCCT 60
40 GCGAAAGCGC AACGAGCTAT GGGGAAGACG GCGGACCGTT CGCTAATGGC TTCGGGACAT 120
TGGGTCAAGA TACGTGTGGA TGCAAGTGGG GTGTATCGCC TTACGGACGA ACAGCTCCGT 180
GCCAATGGCT TCTCCGATCC GTCCAAGGTA GGTGTGTTCG GTTATGGTGG AGGGGTGCTT 240
CCCGAAGATC TGAGCCGGAT CACGACAGAC GATTTGCCCT CGGTACCGGT ACTCCGTCAG 300
GGCAATGCGC TGTATTTCTA TGCCGTGGGG CCGGTGACAT GGTCTTACAA TCCGGCCAAA 360
45 ACCACCATGG AGCATACGGT GAATACATAC AGTACGCGATG GCTACTACTT CCGTCCGAT 420
GCTGCCGGAG CACCTTTGCA GATGTCCCAA TATACGGGTG GAGGTGCGTC GGCCGAGGCT 480
TTGATCGACT ACTACGATGA GCTGATGCTC CATGAACAGG AATTGTATTG GCCCAAAGAA 540
TCGGGACGAG ATCTGTATGG CGAGTCTTTC AGTGCAGTCA ATACGGGTAC GGTCAAGTTC 600
50 CCTTTGAGGG GCAACACCCG CTCGTCTGGC GAACTCGGTA CCGTATTCTC ATACATAGCC 660
AAGGCCAGAT CCGCCCGTGG CCGCCGTGAG ATGTCGCTCT CCGCGAATGG CATTCTGATC 720
TTCAGCGATC CTTTTCCAT GACATCGAAT GAAGTCTCCA ATTCCATT TTGCCCCGTT 780
AAGCGTCGTC TCTATCACAG TACGCCGATG AACAGCTTGG TCAATGAGTT GCGCTTGGAC 840
GCCAATATA GCATGACAGG AGATGCGGTC AATCTGGATT TCATAGAGGT GGCTACACAG 900
55 AACGACCTCC GGTACGATGG CGCACCCATG CATATCAGGC GGTTTTCCAA TTGCCCCGTT 960
TTGGGGGGCG AGTCCCTGCC GTTCGTATTC AGTGAGGTGC CCGAGTCTCT GGTGGTTTTG 1020
CAGGCCAATT CTTCCCTGAC AGCATCGCTT GTTCCCGTTA AGACTGTGG GGATAAGACC 1080
ATTGAGTTTG TGGCTCCGCC GAAGGGTCAG GATCGTAGGA CTATCAATAC GTTTTATGCC 1140
GTGGACTTGT CACAGGCTTC TGCTCCGGAG ATCCTCGGAG CGGTACCCAA TCAAAACCTG 1200
60 CATGGAGAGG AATCCCTGA TCTGATCATT GTCTCTACTC AGGCGCTCCT CTTGAGGCT 1260
GATCGACTGG CCACCTATCG TAGAGAGAAA AACGGGCTGA AGGTTTGGT CGTGTTCAG 1320
GAACAGGTGT TCAACGAGTT TTCGGGTGGA ACTCCCGATG CTACAGCATA CCGCCTCTTT 1380
GCCAAATGT TCTACGACAG ATGGAAGGCA AATGCACCTG TGGGAGAGAC CTTCCCGATG 1440
CAAATGCTTC TCTTCGGTGA TCGGGCTCAT GACAACAGGA AGGTCTCCGT AGCTTGGCAG 1500
65 AAACCGTATC TCCAACAAAC GGAGTTCTTG CTGACATTCC AAGCGTCAA TTCGACGAAC 1560
GTAAACAGTT ATGTGACGGA TGATTACTTC GGCTTGCTCG ATGATCAGCC GGCCTCGGTC 1620
AATATCGSTT GCGCAATTA TAATATGGCT GTAGGGCGAT TCCCGTAGC TACTCCGGCC 1680
GAAGCTCGCA TCGCAGTGGG CAAGACCATC CGATATGAGG AGGATCGAGA GAGTGGTGCC 1740
TGCGGTATTG GTGCTGTTT TGCGGCAGAC AACGGGGAACA AGCAGCGAAC CGAGACTTCC 1800
CGTTTGATCG ATACCGTCAA GCGTTATGCT CCGTCCATCA TGCCGGTACG CGCCTTCAG 1860
70 GAGTATATC CCGATGTCT CGAGAACGGG TTGCACAGCA TTCGGGTGCG AAAGAAAAG 1920
ATGCTGGAAG CCCTTCAGTC GGTATATATC CTGCTTAATT ATGCTGGTCA TGGCGGTCT 1980
CCGGATGCT CCGACGAGCA TTTGCTGAGC CTCAACGATA TACAAATTT CAATATATAG 2040
CATATGCTCA TTTGATTAC TGCCACGTGC GACTTTCCCA ACTATGACAG TCAGACGACC 2100
TCGGCAGGGG AGGAGGTTT CCTCCATGAG AAGAGTGGCA CTCGATCAT GTTCTCGACT 2160
75 ACCCGTGTG TTTACAATAC GCAGATGAG AAGATCAATG GTTTTATGCT TCGCGGTATG 2220

5 TTCGAGAAAG CTAAGGATGG GCGTTATCGT ACGATGGGCG AGATTATCCG ATCGGGCCAAA 2280
CAGGGGATGC TCAGTACTGT TTTCCCCGAT TCGATCAACC AGTTGAGTTT CTTTCTGATG 2340
GGTGATCCGT CCGTGGGTAT GAATCTTCTT ACCCACAAGG TGCAATTGAC CGCAATCAAC 2400
GGGCAGGATC CCGAAGGGCA GTATGGAAGT ATTATGCTCA AGTCTTTGGA ACGGGTAGCT 2460
C'GAAGGGTA AGGTAAACCGA TGAAAAGGGG ACATTTCAGG AGACATTGAG TGGCAAGGTT 2520
TTCTGACCG TCTTCGATGG CAGAAAAGAA ATGACAGCTT TGGAGAGGA GGGAAACGAT 2580
CTCTCTCTTG TATATTATGA CTATCCTAAC GTGATGTATG CCGGTATTGC CGAGGTGAAA 2640
GACGGACTCT TCGAACTTC GTTATCGTA CCCAAGGATG TGAATATTG CGAGCAGGAA 2700
GGCCGGATCA ATCTTTATCC TTATAACGAG AGCACAAGG CGGAAGCCAT GGGGGTAGAC 2760
10 TTCTCCATCA GAGTCCAACC GGGTATTCTT GATGAGGTAA CGGAAGATAA TACACCGCCT 2820
GAAATCATAA GCTGCTTCTT CAATGACAGT ACATTCCGAT CGGAGATGA GGTAAATCCT 2880
ACTCCTCTGT TTATGGCCGA AGTATTGAC TTGAATGGAA TCAATATCAC GGGTAGCGGA 2940
GTAGGGCATG ATATTACGCT TTGTATCGAT GGGCGTGCCG ACCTGACCTA CAACCTCAAT 3000
15 GCATATTICA CAAGTTCGGC TACGGATGCA GGTGTGGGCA CTATTCTCTT CATGATACCG 3060
GCTTTGGCCG AAGGAGATCA TACTGCCCGA CTGACGGTTT GGGACATTTT CAATAATGCC 3120
GTCCATCATG ACTTTTCATT CAGAGTGGTA GATGGCATTG CTCGGATGT GGTGATGTG 3180
ATTCTATTCC CGAATCCGGT ACGCGAGAGT GCTACGTTCC GAATCTTCCA CAATCGCCCC 3240
GGAAGCGATT TGAACGTGGC CGTGGAGATC TATGACTTCA CCGGTCTGCT TGTGAACAGT 3300
20 TTGCCAGTCA AGACCTATTG GTCTTCCTAC GGAGAACCFA TAGAGATCAA GTGGGATCTG 3360
ACCTCCAAAT ACGGAGTGAA GATCGGAAAC GGATTCTACC TCTATCGTIG TGTGGTGAAC 3420
TCTCCCGGAG GACAGACGGC CTCCATGGCC AAGAAAATGA TCGTGGTAGG ACAA 3474

(2) INFORMATION FOR SEQ ID NO:260

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2883 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

35 (iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
40 (A) ORGANISM: PORPHYROMONAS GINGIVALIS
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2883
45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:260

ATGAAGAAAC TTTTCCCAT ATTATTACT ATAT'IGTCGA TTTTGGTCGG ATGTGGAAAA 60
AAAGAAAAC ACTCTGTAAC TGAATCCGCC CGAGAGAAAA AGCTATTAC TGCATTGCTG 120
TACGAAAAAG AACTCCCCAC TGATTCTGTT AACAGCTTTT ACGAGAACAG CGTACAGAAC 180
AAGAACCTTG TGGGACAAAT GTTATTCCGG ATCGAGGTCC GCAACCGGAT GCGTAATATG 240
TCCCAATACA CAGATGCCAT GCTATATCAC CAAAAGGGT TGAACGCTGC ATTGAATCTA 300
AGGGACACCA TCGTAGCCGC ACAAGCATGG AATCATCTCG GAACGGATAG CCGTCGTATC 360
GGTGTCTTGG CAGAAGCTTC GGATTATCAT TACAAGGCTC TTTCTTGTAT AGAATCTTTT 420
AGCCGAAACC AGAATAGGCC TGCGATCAAA GCCAGATCGG CGGCCCTGAA CGGCATCGGC 480
55 AACATCAATC TTGAGTTAGG ATACCATGAT GAGGCCGAAA AGAATTTCTT GAAGCACTG 540
CAAGGTGAGA AAGAACTCGA CAGTCCCTCC GGGCAAGCTA TCAACTATGC GAACCTCGGA 600
CGTATCTATC GACAACGCAA AGAATACGAC AAGGCTCGTA CCTACTTCCT CTGTCTCTG 660
GAGCAGAAAC ATATGGCAGA GAATCTGATG GGTATCGGAC TCTGTAGCAT CAATCTCGGA 720
GAAGTAGACG AAGAAAAGG GGATTATCAA AAGGCTTTCG AAGAGTATGC CACGGCATAAC 780
60 AAATCTGATG AACAGTTGTC CGATCGATGG CACTGGCTGA ATTCTGTAT CCGATGGCA 840
CGTATCAATC TCAACCAAGG TAACGAAAGG CTCTACCAAC ATTTCATTTC TTTGGCCGAA 900
GGGACTCGCA AAGAAATTA TCGACTTCA CATCTGATAG AATATACAA TCTTCAATAC 960
GAGAATCTCG AGCGTAAAA AGAATACAAA CAAGCCCTCG AAGCATTTCT TCTGAGCAAG 1020
ACGTTGAGCG ACAGCATGTC CATTCGCGAC AAGGTGAGCA GCATACAAGA AACCGGATTG 1080
65 AACTACGAAC GAAACAAGTC CCAAAAAGAG CTTGAAGAAA TACAGCAAGT AAGCAAGGCA 1140
AAACAAGAGA AATCGAAGTT TATCTCTCTG AGCACTCTTT TTGCCCTTTT CATCTCGATT 1200
CTTTTGATTT CTGTTCTGAC ATATGCATAC CGTCAGGGCA AGAAGCATAA CAAGCTGATC 1260
AAAGAGACGG ATAAACTTCG CTCGGGCTTT TTAACCGGTA TTACACAGCA ATTTCTGATG 1320
70 CCTATCACCG TCAATACAAG TTTGAATGAG AAAATGAGT CAAGTCTGTA TCTCCAAGCA 1380
TCGGACAGAA CCGAGCTGCA CAAGATAATA GACAGACAGA GTAGCCATAT GCTGAATTTG 1440
GTGAACCAGC TGTGTGATAT TTGCAAGATC AGAAGCGGAG TATCCACGCC CGAATGGGCG 1500
AATGGCGACA TCGTCTCCTT CGTACAGATT CTCTCGATT CGTTTGACCC ATACGCACAG 1560
GCTCAAGACA TAACCTTGGG GCTACAACCC GAGAGCAAAC CTATTGTCGT GCACCTCGTC 1620
75 CCCTCCTACT TGCAAAAAAT CATATCCAAT CTTTGTGCCA ATGCCATCAA GTATTCTTTA 1680
GCCGGAGGGA GAGTGGTCAT ATCTCTGGCA AAAACCAAGA ATGAAAAAAA TCTGATCATA 1740

179/ 490

CGGCTTGCAG ACAATGGCAT AGGAATAGAT AAAACTGATC AGGCTCATAT CTTCGACATC 1800
 TTCTATCGAG GACAGTCCGC TACCGAAAAG CATGGATCAG GCGTCGGACT CTCGTTTACC 1860
 AATATACTGG TCGAAAACCT TCGAGGTACG ATCAAAGTGG AAAGCCAGCC GGGGAAAGGA 1920
 AGTCCCTTCA CCATCAGTAT TCCTACACAA AACCAGTCTT CTTCGGCAGA GATTCTTCCT 1980
 TGGCTACCCCT COTCCGATGA CATTGTCTAT COTGTCCACA TCGCGCCCGA TGACTCACCG 2040
 ACATCTCCGA TGGTAGCAGC TCTGAATCAT CCGTTCGAGG ACGAAGCTCC GACCATACTG 2100
 CTCGTGAGG ACAATAAGGA TATCAACCTG CTCGTCAAAC TACTCCTTTG CGATCGCTAC 2160
 AATGTGCTAT CCGCCGCAAA CGGAAAAGAG GGTATAGCCC TCGCTACCGA GCATATTCOC 2220
 GACATTATCA TTACGGATAT TATGATGCCG ATAATGGATG GGATAGAAAT GACATCCGG 2280
 ATGAAGCAAT CGCCTCTGCT CTGTCACTT CCCATTGTCT CTTTGACGGC CAAGAGTACC 2340
 GAACAGGACA GATTGGAAGG AATCAAAGC GGTGTAGTCT CTTATCTATG CAAGCCATTG 2400
 TCTCCGGAGG AGCTTTTGAT GCGGATCGAG CAGCTTCTGA AAGACCGTGA GTTGCTCAAG 2460
 AAGTTCTATA TGCAAAACT CATGCTGGAT CGGAAGCCGG AGGAGGAGCC TCAACCGATA 2520
 GATGACAGCA GTATGCAGTT TCTCCTTGCT GCCAAAGATG CAGTGTCCGG TGGAAATCAA 2580
 CAAAATCCGG ATTTTTCGCG TCAAGACTTG GCCGAAAAA TGTGCATGAG TCCATCCCAA 2640
 CTCAACAGAA AGCTCACGAG TGTCTAGGT TGCTCCACCA TCGGCTACAT ACAGCAGATC 2700
 AAGATAAAAT TGGCCTGCAA GCTCCTTGCC GATGAGAGCA AAAACATCTC CGACATTAGC 2760
 ATTGAGGCAG GCTTTTCGGA TCCGGCTTAC TTCTCTCGCA CCTTCAAACG CTACATGAAC 2820
 TGCTCTCCCT CCCAATATCG GCAAAAACCT CTTGCCATGC CGGGGAGCGA CAAGGAGACA 2880
 GTT 2903

(2) INFORMATION FOR SEQ ID NO:261

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1668 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
 30 (ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
 35 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS
 40 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261

ATGAAAAAGC TTTTACAGGC TAAAGCCTTG ATTCTGGCAT TGGGACTCTT CCAACTGCCC 60
 GCAATCGCCC AAACGCAAAAT GCAAGCAGAC CGAACAACCG GTCAATTGTC AACAGAAGAG 120
 ATGCAACGAG CATTCAGGGA AACGAATCCC CCTGCAGGTC CTGTGCGTGC TATCGCTGAG 180
 TACGAACGCT CTGCAGCCGT TTTGGTACGC TACCCGTTGG GTATCCGAT GGAATTGATC 240
 AAAGAGCTGG CCAAGAACGA CAAGGTGATT ACCATTGTGG CGAGTGAAAG CCAAAAAAAC 300
 ACCGTTATAA CCCAGTACAC CCAAGCGGT GTGAATCTCT CTAATTGCGA TTTCATCATT 360
 GCGAAAAGTG ACTCTTACTG GACACCGGAC TATACCGGTT GGTTCCGAAT GTACGATACG 420
 AACAAAGTAG GTCTCGTGGG CTTTATTAT AACCGCCCTC GTCCCTAACGA TGATGAATTC 480
 CCCAAATACG AAGCACAATA TCTGGGCATC GAGATGTTCG GGATGAAGCT CAAGCAGACC 540
 GGTGGCAACT ACATGACGGA CGGATATGGA TCCGCTGTGC AGTCACATAT CGCATATACG 600
 GAGAACTCCT CTCTGTCTCA AGTCCAAGTA AATCAAAGA TGAAAGACTA TCTCGGCATC 660
 ACACATCATG ATGTGGTACA AGATCCGAAC GCGAATATA TCAACCATGT GGACTGTTGG 720
 GGCAAGTATT TGGCACCGBA CAAAATCCTC ATCAGGAAAG TGCCCTGACAA TCACCTCAG 780
 CACCAAGCCC TGAAGATAT GGCAGCCTAC TTGCGAGCAC AGACCTGCGC ATGGGGAACG 840
 AAGTACGAGG TATATCGCGC TTTGGCCACC AATGAACAAC CGTACACGAA CTCTCTGATT 900
 CTGAACAACA GGGTATTGTT TCCTGTCAAT GGCCCGGCTT CCGTGGACAA CGATGCTCTG 960
 AACGTCTATA AGACGGCAAT GCCCGGTTAC GAAATTATAG GTGTCAAAGG GGCTTCAGGA 1020
 ACACCTTGGT TAGGAACAGA TGCCCTGCAT TGTCTACTC ACGAGGTAGC GGATAAGGGC 1080
 TATCTCTATA TCAAGCACTA CCCGATACTG GCGGAACAGG CAGGCCCTGA TTATAAGATC 1140
 GAAGCAGATG TCGTCTCATG CGCCAATGCT ACTATCTGCG CGGTACAATG TTAATATCGT 1200
 ATCAATGGTT CCGGTAGCTT TAAGGCTGCT GATATGACGA TGGAAATCAAC AGGTCACTAT 1260
 ACTTATAGCT TTACAGGTCT TAACAAGAAT GATAAGGTAG AATACTATAT CTCTGCCGCT 1320
 GACAATAGTG TTCGCAAGA GACTTATCCC TTTATCGGCG AACCTGATCC TTTCAAGTTT 1380
 ACGTGTATGA ACGAAACCAA TACATGTACT GTGACCGGAG CTGCCAAAGC TCTTCGTGCA 1440
 TGGTTCAAGC CCGGTCGTTT AGAACTGGCT GTTTCGGTAA GTTTGAATAT TGCCGGCACA 1500
 TATCGGATAA AGCTTTATAA CACCGCAGGA GAAGAAGTCG CTGCAATGAC CAAGGAATTA 1560
 GTAGCAGGGA CGAGTGTCTT CAGTATGGAT GTGTATTCTC AGGCTCCGGG CACATATGTT 1620
 CTGGTTGTTG AAGGAAATGG AATCCGTGAG ACAATGAAAA TTCTCAAA 1668

(2) INFORMATION FOR SEQ ID NO:262

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1284 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1284

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262

25 ATGAACTTT CATCTAAGAA AATCTTAGCA ATCATTGCAT TSCGTGACGAT GGGACATGCT 60
GTGCAGGCAC AGTTTGTTC GGCCTCCACC ACAGGGATTC GCATGTCTCT CACTACAAACC 120
AAGGCCGTAG GCGAAAAAT CGAATTGTGT GTTCATTCCA TAGAGAGAA AGGCATCTGG 180
ATCGATCTCA ATGGGATGC CACTTACCA CAAGGAGAGG AAATAACCGT ATTCGATGAG 240
GCATACCACG AATACACGAT CGGGACGCAA ACCCTCACTA TCTATGGTAA TACGACCCGA 300
TTGGGCTGTC GATCTACCGG TGCAACGGCT GTCGATGTAA CGAAAAACCC TAATCTGACC 360
30 TATCTCGCAT GCCCGAAAAA TAACTCTGAA TCATTGGACT TGACGCAAAA CCCAAAGCTG 420
CTGCGAGTTT GGTGCGACTC TAACGAATA GAAAGTTGG ACCTGAGTGG CAATCCGGCT 480
TTGATCATCC TCGGCTGTA CAGGAATAAG CTGACTGAGC TGAAGACCGA TAACAACCCC 540
AAGTTGGCCT CTCTTTGGTG TTCTGATAAT AACCTGACGG AGTTGGAAT CAGTGCCCAT 600
35 CCTGCTCTCA ATGATCTTTG GTGCTTCGGT AATCGGATCA CGAAACTCGA TCTGAGTGCC 660
AATCCTCTAT TGGTAACACT TTGGTGCACT GACAATGAGC TTTCGACCTT GGATCTTTCC 720
AAGAATTGGG ACGTTGCTTA CCTTTGGTGT TCATCGAACA AACTTACATC CTTGATCTG 780
TCGGGGGTGA AGGGAAGTGA TGTTTGGTGT TGTCTATCCA ATCAGATCGC AGGTGAAGAA 840
40 ATGACGAAAG TGGTGAATGC TTTGCCACCA CTATCTCCCG GCGCAGGCGC TCAGAGCAAG 900
TTCTGCTGTG TAGACCTCAA GGACACTGAT GAGAAGAATA TCTGTACCGT AAAGGATGTG 960
GAAAAAGCTA AAAGTAAGAA CTGGCGAGTA TTGCACTTCA ACGGTGATTC TGACAATATG 1020
CTTCCATAGC AAGGAAGTCC GACATCGAAC TTGGCAGTAG ATGCTCCCAC TGTGAGGATA 1080
TATCCCAATC CGGTAGGAAG ATATGCGCTC GTCGAGATCC CCGAGTCTCT TTTAGGGCAG 1140
GAAGCTGCTT TATACGATAT GAATGGGATA AAAGTCTATA GTTTCGGGT AGAGTCTCTT 1200
45 CGTCAGAAAC TTGACCTGAC ACATCTTCCC GACGGCACTT ATTTCTTCCG TCTCGATAAC 1260
TATACCACTA AGTCATCAA ACAG 1284

(2) INFORMATION FOR SEQ ID NO:263

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 930 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263

70 ATGAGAAAA CAATAATTTT CTGCTTGTG CTGCCCCTAT TTGGCTGTTT TTGGGCACAA 60
GAAAGAGTCG ATGAAAAAGT ATTCTCCGCA GGAACAAGTA TTTTATGGG CATCCTTGAA 120
AAGGTGAAG CACCGCTTAT GTATGGAGAT CGTGAGGTAT GGGGTATGGC TCGTGCGAGC 180
75 GAGGATTTCT TTTTATACT TCCGTTACG GATGACCTCA CTCCGTGCT TTTCTATAAC 240
CGTCTTACAA ACGAACCTG CTTTGTGTCA GACCAAGGAA TAACTGAGTA TTTCAAAATC 300

181/490

5 GCTCAAGAAG GTGATTACAT TGAAGTCGAA GGAAGCTCTG TATTCATGGC GAATCTTTTC 360
TACTATCGTT TTTTCCCGAC AAGAATTACC TCCTATAATG CTCCCATTTA AGGTGTTGTG 420
AGCAAGACGG GAAATCCTGC TTTTACAATC CCGATGCTCC CGGGGGTTTC TGATTGCATA 480
GAAATCTCAA ACAACCGCAA AGTCTTTCTG ACCAATCAAT TAGCGGTTGT AAACATCACT 540
GACGGGATGG AACCTCCGAT TATTGCCGGA GTCTCTGCTT CCTATGGATC TTCCGTCCGG 600
GTGTATGGTC ATGTCTCACA GCGGTGGGAC ATCATAGGCC ATTGCTATTT GGATATCTAC 660
CCAAACCAATT GCTATCCGCT CAGCACGAAA CCCGTTGCAG GAGACGATGA GGTTTTTGTC 720
AAACAAAGAG GCAGGCAAAAT AGAGATCGAT AGCAACAGCC CCATAGTCCA AGTGGTCGTA 780
TACGATCTTG AGGGGAAAAG TGTTTTTCGC AAAAGAATGA CCGAAACGC TTATACCCTA 840
10 TCCTTTAGAG CACCCATGCT CGGCTTTATG ACCATCATGA TCGAAACACA AAATTCGATT 900
ATCAATAAAA AACTTAATGT TACACAGCTA 930

(2) INFORMATION FOR SEQ ID NO:264

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1215 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: circular
(ii) MOLECULE TYPE: DNA (genomic)
25 (iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(v) ORIGINAL SOURCE:
30 (A) ORGANISM: PORPHYROMONAS GINGIVALIS
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1215
35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:264

ATGAAAAAAA CAACCATAT TTCTTTGATT GTCTTCGGTG CTTTCTTTGC AGCCGTGGGC 60
CAAAACCAAGG ACAATTCTTC TTACAAACCT TTTTCGAAAG AAGATATTGC CGGAGGAGTT 120
TACTCTCTCC CGACTCAAAA TCGTGCGCAG AAGGACAATG CCGAGTGGCT TCTTACAGCG 180
40 ACCGTCTCCA CAACCAAGTC TGCAGATACT CACTTTATCT TCGATGAGAA CAACCGCTAT 240
ATCGCTCGTG ACATAAAAGC CAATGGGGTA AGAAAAATCCA CGGACTCCAT TTACTACGAT 300
GCCAACGGGC GAATATCGCA TGTGGATCTT TATATCTCGT TCAGTGGCGG AGAGCCTGCA 360
CTGCACACCC GATTCAGTA CACCTATGAT GACGAGGGA AGATGACCGT GAGGGAAGTA 420
TTATGCTGG TAATGGATCC GAATACACCT ATCTCAGGCT TGAATATCA TTATGATGCA 480
45 CAGGSCAGAG TGACCCACTG GATTTCTTTT GCTTTCGGGG CAGAATCCCA AAAGAATACG 540
TATCACTATA ATGAAAAAGG TCTGTTGGTC AGCGAAGTGC TGAGCAATGC AATGGGGACA 600
ACCTATTAG ACACCGGCAA AACGGAATAC AGCTATGACG ATGCAGATAA TATGGTGAAG 660
GCCGAGTACT TCGTCGTCCA GCAAGGAAAG GCATGGCAAG TACTCAAAAG AGAGGAATAC 720
ACCTATGAGG ACAATATCTG CATACAAAT TTGGCTATTA ACGGTACCGA CACAAAGGTG 780
50 TACAAGCGAG ACATCGAGAG CGATAAGTCC ATCTCCGCAA ATCTCATTGA CATTCCGTCA 840
ATGCCGGAAC AGACCTGGCC TAATATGTAC GGATTCAAAG CAAAGCGACT GAAAGAGACT 900
TATTCCTCCT ACGAAGGAGA TGTGGCTACT CCTATATTGG ACTATATCTA TACGTACAG 960
GCTCTTACCT CAATGGCAAC ACCTTCGACA GAAGCTCAGG TAGCAGTCTA TCTCAATCCG 1020
TCACCGGACC GGTAGTGTAT TCTGGCCAAC GGCATCACAC ATCTGAGCAT GTACGACTTG 1080
55 CAGGGTAAGC TTATCCGTGA TTGTGCCTTG AGCGGCGATA AGGTGGAAAT GGGGTGCGGA 1140
TCTTTGACCA AAGGGACATA CTTGCTTAAA GTGAATACGG ATCAGGGAGC CTTTGTGAGA 1200
AAAGTCGTGA TTCGA 1215

(2) INFORMATION FOR SEQ ID NO:265

- 60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 454 amino acids
65 (B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
70 (iii) HYPOTHETICAL: YES
(v) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
75 (ix) FEATURE:
(A) NAME/KEY: misc_feature

(B) LOCATION 1...454

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:265

5 Phe Cys Val Met Ala Lys Val Ile Lys Thr Lys Lys Gly Leu Ala Leu
1 5 10 15
Acn Leu Lys Gly Lys Pro Leu Pro Glu Met Leu Ala Glu Pro Ala Gln
20 25 30
10 Ser Pro Thr Tyr Ala Val Val Pro Asp Asp Phe Glu Gly Val Ile Pro
35 40 45
Lys Val Thr Ala Arg Pro Gly Asp Lys Val Arg Ala Gly Ser Ala Leu
50 55 60
Met His His Lys Ala Tyr Pro Glu Met Lys Phe Thr Ser Pro Val Ser
65 70 75 80
15 Gly Glu Val Ile Ala Val Asn Arg Gly Ala Lys Arg Lys Val Leu Ser
85 90 95
Ile Glu Val Lys Pro Asp Gly Leu Asn Glu Tyr Glu Ser Phe Pro Val
100 105 110
20 Gly Asp Pro Ser Ala Leu Ser Ala Glu Gln Ile Lys Glu Leu Leu Leu
115 120 125
Ser Ser Gly Met Trp Gly Phe Ile Lys Gln Arg Pro Tyr Asp Ile Val
130 135 140
Ala Thr Pro Asp Ile Ala Pro Arg Asp Ile Tyr Ile Thr Ala Asn Phe
145 150 155 160
25 Thr Ala Pro Leu Ala Pro Asp Phe Asp Phe Ile Val Arg Gly Glu Glu
165 170 175
Arg Ala Leu Gln Thr Ala Ile Asp Ala Leu Ala Lys Leu Thr Thr Gly
180 185 190
30 Lys Val Tyr Val Gly Leu Lys Pro Gly Ser Ser Leu Gly Leu His Asn
195 200 205
Ala Glu Ile Val Glu Val His Gly Pro His Pro Ala Gly Asn Val Gly
210 215 220
Val Leu Ile Asn His Thr Lys Pro Ile Asn Arg Gly Glu Thr Val Trp
225 230 235 240
35 Thr Leu Lys Ala Thr Asp Leu Ile Val Ile Gly Arg Phe Leu Leu Thr
245 250 255
Gly Lys Ala Asp Phe Thr Arg Met Ile Ala Met Thr Gly Ser Asp Ala
260 265 270
40 Ala Ala His Gly Tyr Val Arg Ile Met Pro Gly Cys Asn Val Phe Ala
275 280 285
Ser Phe Pro Gly Arg Leu Thr Ile Lys Glu Ser His Glu Arg Val Ile
290 295 300
Asp Gly Asn Val Leu Thr Gly Lys Lys Leu Cys Glu Lys Glu Pro Phe
305 310 315 320
45 Leu Ser Ala Arg Cys Asp Gln Ile Thr Val Ile Pro Glu Gly Asp Asp
325 330 335
Val Asp Glu Leu Phe Gly Trp Ala Ala Pro Arg Leu Asp Gln Tyr Ser
340 345 350
50 Met Ser Arg Ala Tyr Phe Ser Trp Leu Gln Gly Lys Asn Lys Glu Tyr
355 360 365
Val Leu Asp Ala Arg Ile Lys Gly Gly Glu Arg Ala Met Ile Met Ser
370 375 380
Asn Glu Tyr Asp Arg Val Phe Pro Met Asp Ile Tyr Pro Glu Tyr Leu
385 390 395 400
55 Leu Lys Ala Ile Ile Ala Phe Asp Ile Asp Lys Met Glu Asp Leu Gly
405 410 415
Ile Tyr Glu Val Ala Pro Glu Asp Phe Ala Thr Cys Glu Phe Val Asp
420 425 430
60 Thr Ser Lys Ile Glu Leu Gln Arg Ile Val Arg Glu Gly Leu Asp Met
435 440 445
Leu Tyr Lys Glu Met Asn
450

(2) INFORMATION FOR SEQ ID NO:266

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 201 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(111) ORIGINAL SOURCE:

183/490

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

5

(A) NAME/KEY: misc_feature
(B) LOCATION 1...201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266

10 Glu Leu Ser Lys Cys Tyr Met Asp Lys Val Ser Tyr Ala Leu Gly Leu
1 5 10 15
Ser Ile Gly Asn Asn Phe Lys Ser Ser Gly Ile Asp Ser Val Val Met
20 25 30
Asp Asp Phe Met Gln Gly Leu Ser Asp Val Leu Glu Glu Lys Ala Pro
35 40 45
15 Gln Leu Ser Tyr Asp Glu Ala Lys Arg Glu Ile Glu Ala Tyr Phe Met
50 55 60
Asp Leu Gln Gln Lys Ala Val Lys Leu Asn Lys Glu Ala Gly Glu Glu
65 70 75 80
Phe Leu Lys Ile Asn Ala His Lys Glu Gly Val Thr Thr Leu Pro Ser
85 90 95
20 Gly Leu Gln Tyr Glu Val Ile Lys Met Gly Glu Gly Pro Lys Pro Thr
100 105 110
Leu Ser Asp Thr Val Thr Cys His Tyr His Gly Thr Leu Ile Asn Gly
115 120 125
25 Ile Val Phe Asp Ser Ser Met Asp Arg Gly Glu Pro Ala Ser Phe Pro
130 135 140
Leu Arg Gly Val Ile Ala Gly Trp Thr Glu Ile Leu Gln Leu Met Pro
145 150 155 160
30 Val Gly Ser Lys Trp Lys Val Thr Ile Pro Ser Asp Leu Ala Tyr Gly
165 170 175
Asp Arg Gly Ala Gly Glu His Ile Lys Pro Gly Ser Thr Leu Ile Phe
180 185 190
Ile Ile Glu Leu Leu Ser Ile Asn Lys
195 200

35

(2) INFORMATION FOR SEQ ID NO:267

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 279 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

45

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

50

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267

55

60 Gln Lys Asn Lys Arg Lys Met Lys Lys Ala Leu Leu Ile Gly Ala Ala
1 5 10 15
Leu Leu Gly Ala Val Ser Phe Ala Ser Ala Gln Ser Leu Ser Thr Ile
20 25 30
Lys Val Gln Asn Asn Ser Val Gln Gln Pro Arg Glu Glu Ala Thr Ile
35 40 45
Gln Val Cys Gly Glu Leu Ala Glu Gln Val Asp Cys Ile Gly Thr Gly
50 55 60
65 Asn Ser Ala Ile Ile Ala Ala Ala Lys Phe Glu Ser Asp Asp Leu
65 70 75 80
Glu Ser Tyr Val Gly Trp Glu Ile Met Ser Val Asp Phe Phe Pro Gly
85 90 95
Tyr Lys Ala Cys Lys Tyr Thr Ser Ala Val Trp Ala Asp Asp Met Thr
100 105 110
70 Ile Leu Gly Gln Ser Glu Asp Ser Asp Pro Glu Met Gln Thr Ile Asn
115 120 125
Asn Leu Ala Leu Lys Thr Ser Val Lys Ile Glu Ala Gly Lys Asn Tyr
130 135 140
75 Ile Val Gly Tyr Ile Ala Asn Thr Ala Gly Gly His Pro Ile Gly Cys
145 150 155 160

184/ 490

Asp Gln Gly Pro Ala Val Asp Gly Tyr Gly Asp Leu Val Ser Ile Ser
 165 170 175
 Glu Asp Gly Gly Ala Thr Phe Pro Pro Phe Glu Ser Leu His Gln Ala
 180 185 190
 5 Val Pro Thr Leu Asn Tyr Asn Ile Tyr Val Val Val His Leu Lys Lys
 195 200 205
 Gly Glu Gly Val Glu Ala Val Leu Thr Asn Asp Lys Ala Asn Ala Tyr
 210 215 220
 10 Val Gln Asn Gly Val Ile Tyr Val Ala Gly Ala Asn Gly Arg Gln Val
 225 230 235 240
 Ser Leu Phe Asp Met Asn Gly Lys Val Val Tyr Thr Gly Val Ser Glu
 245 250 255
 Thr Ile Ala Ala Pro Gln Lys Gly Met Tyr Ile Leu Arg Val Gly Ala
 260 265 270
 15 Lys Ser Ile Lys Leu Ala Ile
 275

(2) INFORMATION FOR SEQ ID NO:268

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 157 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 25 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 30 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...157
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:268

Arg Unk Phe Leu Pro Glu Lys Ala Leu Tyr Ile Gly Cys Arg Val Glu
 1 5 10 15
 40 Thr Gln Glu Gly His Ala Val Gly Phe Gly Leu Asp Asp Gly Pro Ala
 20 25 30
 Met Lys Gly Lys Gly Asp Leu Val Gly Ser Tyr Leu Pro Gly Ala Ala
 35 40 45
 45 Pro Met Pro Phe Val Pro Leu Ser Asp Ile Pro Ala Arg Ser Met Asp
 50 55 60
 Ala Asn Phe Tyr Ile Tyr Ser Arg Ile Ser Leu Gly Ser Gly Thr Gln
 65 70 75 80
 Asp Val Leu Gln His Arg Met Lys Val Tyr Pro Asn Pro Ala Thr Thr
 85 90 95
 50 Glu Leu His Val Glu Ala Leu Ser Ala Trp Val Gly Glu Gln Ala Ala
 100 105 110
 Val Tyr Asp Met Arg Gly Arg Val Ser Ala Arg Thr Val Asp Ser
 115 120 125
 55 Glu Lys Leu Cys Ile Asp Ile Ala Ser Leu Pro Val Gly Val Tyr Met
 130 135 140
 Leu Arg Ile Gly Ser Tyr Ser Ala Lys Phe Glu Lys Arg
 145 150 155

(2) INFORMATION FOR SEQ ID NO:269

- 60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 562 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 65 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 70 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...562
 75

185/490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269

5	Thr	Arg	Asn	Val	Ser	Leu	Ile	Lys	Met	Pro	Arg	Ile	Met	Lys	Leu	Lys
	1				5					10				15		
	Ile	Ala	Leu	Arg	Leu	Leu	Leu	Ala	Thr	Phe	Ala	Ile	Val	Leu	Phe	Ser
				20					25					30		
	Pro	Leu	Ala	Lys	Ala	Gln	Met	Asp	Ile	Gly	Gly	Asp	Asp	Val	Leu	Ile
				35				40					45			
10	Glu	Thr	Met	Ser	Thr	Leu	Ser	Gly	Tyr	Ser	Glu	Asp	Phe	Tyr	Tyr	Lys
				50			55					60				
	Met	Ala	Val	Ala	Asp	Asn	Gly	Trp	Ile	Tyr	Val	Met	Leu	Asp	Phe	Ser
				65			70				75				80	
	Arg	Ile	Tyr	Phe	Asp	Asp	Val	Arg	Leu	Tyr	Arg	Ser	Lys	Asp	Gly	Gly
					85					90				95		
15	Ala	Thr	Tyr	Gln	Lys	Leu	Gly	Ser	Leu	Gly	Ser	Leu	Val	Pro	Tyr	Asp
				100					105					110		
	Phe	Asp	Val	Ser	His	Cys	Asp	Phe	Ile	Val	Thr	Gly	Lys	Asp	Glu	Asp
				115				120					125			
20	Asp	Ile	Asn	Val	Trp	Thr	Val	Met	Thr	Ala	Phe	Glu	Tyr	Val	Gly	Gly
				130			135					140				
	Thr	Ile	Gly	Asn	Gly	Val	Leu	Leu	Met	His	Arg	His	Asp	Ala	Asp	Ile
				145			150				155				160	
	Asn	Asn	Thr	Glu	Cys	Val	Tyr	Lys	Lys	Asp	Phe	Pro	Asn	Asn	Arg	Leu
				165						170				175		
25	Met	Gly	Val	Ala	Ile	Ala	Ser	Asn	Tyr	Arg	Ala	Pro	Ser	Pro	Tyr	Gly
				180					185					190		
	Leu	Gly	Gly	Asp	Pro	Phe	Ala	Leu	Ala	Val	Ala	Val	Ser	Gly	Ser	Gly
				195			200					205				
30	Ser	Asp	His	Ser	Phe	Leu	Asp	Tyr	Ile	Phe	Ser	Leu	Asp	Gly	Gly	Val
				210			215					220				
	His	Phe	Glu	Gln	Lys	Arg	Ile	Tyr	Thr	Arg	Pro	Gln	Lys	Leu	Thr	Ile
				225			230				235				240	
	Asn	Arg	Val	Asp	Leu	Ser	Leu	Gly	Ser	Thr	Ser	Pro	Ser	Leu	Gly	Phe
				245						250				255		
35	Asn	Thr	Trp	Pro	Leu	Met	Gly	Val	Val	Phe	Glu	Met	Asn	Lys	Asn	Leu
				260					265					270		
	Asp	Gly	Phe	Asp	Ile	Gly	Phe	Ile	Ser	Asn	Phe	Val	Asp	Tyr	Asp	Pro
				275				280					285			
40	Arg	Tyr	Ala	Trp	Ser	Glu	Pro	Ile	Ile	Ile	Glu	Glu	Asp	Cys	Gly	Trp
				290			295					300				
	Thr	Asp	Phe	Asn	Pro	Leu	Gly	Ala	Leu	Ser	Ile	Glu	Ile	Gln	Met	Met
				305			310				315				320	
	Leu	Asp	Asp	Asn	Ser	Asp	Asn	Thr	Val	Gly	Gly	Glu	Arg	Ser	His	Asn
				325						330				335		
45	Phe	Leu	Ile	Thr	Tyr	Pro	Gly	His	Tyr	Val	Tyr	Pro	Lys	Gln	Ser	Phe
				340				345					350			
	Asn	Tyr	Ser	Pro	Gly	His	Thr	Pro	Thr	Lys	Lys	Asp	Leu	Val	Phe	Lys
				355			360						365			
50	His	Cys	Ile	Gly	Ile	Pro	Ala	Leu	Ala	Tyr	Asp	Lys	Glu	Gly	Asp	Arg
				370			375					380				
	Tyr	Leu	Thr	Thr	Phe	Gln	Asp	His	Asn	Leu	Met	Arg	Tyr	Arg	Trp	Ile
				385			390				395				400	
	Lys	Tyr	Asp	Asp	Ile	Asn	Ser	Phe	Tyr	Gly	Trp	Ser	Trp	Pro	Tyr	Val
				405						410				415		
55	Tyr	Ala	Lys	Glu	Ala	Lys	Asp	Lys	Lys	Arg	Arg	Arg	Pro	Gln	Val	Ala
				420				425					430			
	Leu	Asn	Pro	Thr	Asn	Gly	Lys	Ala	Cys	Trp	Val	Trp	His	Thr	Arg	Lys
				435			440					445				
60	Ser	Pro	Tyr	Asp	Glu	Thr	Lys	Pro	His	Pro	Thr	Pro	Val	Ile	Ile	Lys
				450			455					460				
	His	Phe	Leu	Trp	Ser	Asp	Thr	Glu	Trp	Val	His	Ala	Leu	Asp	Val	Gly
				465			470				475				480	
	Asp	Val	Leu	Gln	Lys	Glu	Gly	Ser	Met	Lys	Leu	Tyr	Pro	Asn	Pro	Ala
				485						490				495		
65	Lys	Glu	Tyr	Val	Leu	Ile	Asn	Leu	Pro	Lys	Glu	Gly	Gly	His	Glu	Ala
				500					505					510		
	Val	Val	Tyr	Asp	Met	Gln	Gly	Arg	Ile	Val	Glu	Lys	Val	Ser	Phe	Ser
				515				520					525			
70	Gly	Lys	Glu	Tyr	Lys	Leu	Asn	Val	Gln	Tyr	Leu	Ser	Lys	Gly	Thr	Tyr
				530			535					540				
	Met	Leu	Lys	Val	Val	Ala	Asp	Thr	Glu	Tyr	Phe	Val	Glu	Lys	Ile	Ile
				545			550				555				560	
75	Val	Glu														

(2) INFORMATION FOR SEQ ID NO:270

5 (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 391 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

15 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...391

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:270

Gln Met Lys Arg Leu Leu Pro Phe Leu Leu Leu Ala Gly Leu Val Ala
1 5 10 15
Val Gly Asn Val Ser Ala Gln Ser Pro Arg Ile Pro Gln Val Asp Val
20 25 30
His Thr Arg Ile Ala Arg Asn Ala Arg Tyr Arg Leu Asp Lys Ile Ser
35 40 45
Val Pro Asp Ser Arg Gln Ile Phe Asp Tyr Phe Tyr Lys Glu Glu Thr
50 55 60
Ile Pro Thr Lys Ile Gln Thr Thr Thr Gly Gly Ala Ile Thr Ser Ile
65 70 75 80
Asp Ser Leu Phe Tyr Glu Asp Asp Arg Leu Val Gln Val Arg Tyr Phe
85 90 95
Asp Asn Asn Leu Glu Leu Lys Gln Ala Glu Lys Tyr Val Tyr Asp Gly
100 105 110
Ser Lys Leu Val Leu Arg Glu Ile Arg Lys Ser Pro Thr Asp Glu Thr
115 120 125
Pro Ile Lys Lys Val Ser Tyr His Tyr Leu Cys Gly Ser Asp Met Pro
130 135 140
Phe Glu Ile Thr Thr Glu Met Ser Asp Gly Tyr Phe Glu Ser His Thr
145 150 155 160
Leu Asn Tyr Leu Asn Gly Lys Ile Ala Arg Ile Asp Ile Met Thr Gln
165 170 175
Gln Asn Pro Ser Ala Glu Leu Ile Glu Thr Gly Arg Met Val Tyr Glu
180 185 190
Phe Asp Ala Asn Asn Asp Ala Val Leu Leu Arg Asp Ser Val Phe Leu
195 200 205
Pro Leu Gln Asn Lys Trp Val Glu Met Phe Thr His Arg Tyr Thr Tyr
210 215 220
Asp Asn Lys His Asn Cys Ile Arg Trp Glu Gln Asp Glu Phe Gly Thr
225 230 235 240
Leu Thr Leu Ala Asn Asn Phe Glu Tyr Asp Thr Thr Ile Pro Leu Ser
245 250 255
Ser Val Leu Phe Pro Thr His Glu Glu Phe Phe Arg Pro Leu Leu Pro
260 265 270
Asn Phe Met Lys His Met Arg Thr Lys Gln Thr Tyr Phe Asn Asn Ser
275 280 285
Gly Glu Gly Leu Ser Glu Val Cys Asp Tyr Asn Tyr Phe Tyr Thr Asp
290 295 300
Met Gln Gly Asn Ala Leu Thr Asp Val Ala Val Asn Glu Ser Ile Lys
305 310 315 320
Ile Tyr Pro Arg Pro Ala Thr Asp Phe Leu Arg Ile Glu Gly Ser Gln
325 330 335
Leu Leu Arg Leu Ser Leu Phe Asp Met Asn Gly Lys Leu Ile Arg Ala
340 345 350
Thr Glu Leu Thr Gly Asp Leu Ala Ile Ile Gly Val Ala Ser Leu Pro
355 360 365
Arg Gly Thr Tyr Ile Ala Glu Ile Thr Ala Ala Asn Ser Lys Thr Ile
370 375 380
70 Arg Ala Lys Val Ser Leu Arg
385 390

(2) INFORMATION FOR SEQ ID NO:271

75 (1) SEQUENCE CHARACTERISTICS:

187/ 490

(A) LENGTH: 428 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...428

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:271

Lys Arg Asn Pro Leu Pro Leu Thr Ala Ser Asn Arg Lys Ile Phe Ile
 1 5 10 15
 20 Lys Met Arg Gln His Leu Ser Leu Phe Pro Phe Ile Leu Phe Leu Leu
 20 25 30
 Leu Ala Phe Ser Tyr Val Gly Cys Arg Thr Val Arg Gln Thr Pro Lys
 35 40 45
 25 Gln Ser Glu Arg Tyr Val Val Val Leu Ser Leu Asp Gly Phe Arg Pro
 50 55 60
 Asp Tyr Thr Asp Arg Ala Arg Thr Pro Ala Leu Asp Arg Met Ala Gln
 65 70 75 80
 Glu Gly Leu Ser Gly Ser Leu Gln Pro Cys Phe Pro Ser Leu Thr Phe
 85 90 95
 30 Pro Asn His Tyr Ser Met Ala Thr Gly Leu Tyr Pro Asp His His Gly
 100 105 110
 Ile Val Ala Asn Glu Phe Val Asp Ser Leu Leu Gly Ile Phe Arg Ile
 115 120 125
 35 Ser Asp Arg Lys Ala Val Glu Thr Pro Gly Phe Trp Gly Gly Glu Pro
 130 135 140
 Val Trp Asn Thr Ala Ala Arg Gln Gly Ile Arg Thr Gly Val Tyr Phe
 145 150 155 160
 Trp Val Gly Ser Glu Thr Ala Val Asn Gly Asn Arg Pro Trp Arg Trp
 165 170 175
 40 Lys Lys Phe Ser Ser Thr Val Pro Phe Arg Asp Arg Ala Asp Ser Val
 180 185 190
 Ile Ala Trp Leu Gly Leu Pro Glu Lys Glu Arg Pro Arg Leu Leu Met
 195 200 205
 45 Trp Tyr Ile Glu Glu Pro Asp Met Ile Gly His Ser Gln Thr Pro Glu
 210 215 220
 Ser Pro Leu Thr Leu Ala Met Val Glu Arg Leu Asp Ser Val Val Gly
 225 230 235 240
 Tyr Phe Arg Lys Arg Leu Asp Ser Leu Pro Ile Ala Ala Gln Thr Asp
 245 250 255
 50 Phe Ile Ile Val Ser Asp His Gly Met Ala Thr Tyr Glu Asn Glu Lys
 260 265 270
 Cys Val Asn Leu Ser His Tyr Leu Pro Ala Asp Ser Phe Leu Tyr Met
 275 280 285
 55 Ala Thr Gly Ala Phe Thr His Leu Tyr Pro Lys Pro Ser Tyr Thr Glu
 290 295 300
 Arg Ala Tyr Glu Ile Leu Arg Ala Ile Pro His Ile Ser Val Tyr Arg
 305 310 315 320
 Lys Gly Glu Val Pro Lys Arg Leu Arg Cys Gly Thr Asn Pro Arg Leu
 325 330 335
 60 Gly Glu Leu Val Val Ile Pro Asp Ile Gly Ser Thr Val Phe Phe Ala
 340 345 350
 Ile Asn Glu Asp Val Arg Pro Gly Ala Ala His Gly Tyr Asp Asn Gln
 355 360 365
 65 Ala Pro Glu Met Arg Ala Leu Arg Ala Val Gly Pro Asp Phe Arg
 370 375 380
 Pro Gly Ser Arg Val Glu Asn Leu Pro Asn Ile Thr Ile Tyr Pro Leu
 385 390 395 400
 Ile Cys Arg Leu Leu Gly Ile Glu Pro Ala Pro Asn Asp Ala Asp Glu
 405 410 415
 70 Thr Leu Leu Asn Gly Leu Ile Arg Asp Lys Arg Pro
 420 425

(2) INFORMATION FOR SEQ ID NO:272

75 (i) SEQUENCE CHARACTERISTICS:

188/ 490

(A) LENGTH: 282 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

10 (vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...282

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272

Leu Ser Arg Gly Val Phe Pro Leu Met Tyr Gly Arg Arg Gly Ser Ile
1 5 10 15
20 Arg Ala Ser Ser Gly His Arg Asp Lys Ile Phe Lys Asn Thr Ile Ile
20 25 30
Arg Phe Ile Thr Met Lys Val Gly Leu Phe Ile Pro Cys Tyr Val Asn
35 40 45
25 Ala Val Tyr Pro Glu Val Gly Ile Ala Thr Tyr Lys Leu Leu Lys Ser
50 55 60
Leu Asp Ile Asp Val Asp Tyr Pro Met Asp Gln Thr Cys Cys Gly Gln
65 70 75 80
Pro Met Ala Asn Ala Gly Phe Glu Gln Lys Ala Gln Lys Leu Ala Leu
85 90 95
30 Arg Phe Glu Glu Leu Phe Glu Ser Tyr Asp Val Val Val Gly Pro Ser
100 105 110
Ala Ser Cys Val Ala Phe Val Lys Glu Asn Tyr Asp His Ile Leu Arg
115 120 125
35 Pro Thr Gly His Val Cys Lys Ser Ala Ala Lys Val Arg Asp Ile Cys
130 135 140
Glu Phe Leu His Asp Asp Leu Lys Ile Thr Ser Leu Pro Ser Arg Phe
145 150 155 160
Ala His Lys Val Ser Leu His Asn Ser Cys His Gly Val Arg Glu Leu
165 170 175
40 His Leu Ser Thr Pro Ser Glu Val His Arg Pro Tyr His Asn Lys Val
180 185 190
Arg Arg Leu Leu Glu Met Val Gln Gly Ile Glu Val Phe Glu Pro Lys
195 200 205
45 Arg Ile Asp Glu Cys Cys Gly Phe Gly Gly Met Tyr Ser Val Glu Glu
210 215 220
Pro Glu Val Ser Thr Cys Met Gly His Asp Lys Val Leu Asp His Ile
225 230 235 240
Ser Thr Gly Ala Glu Tyr Ile Thr Gly Pro Asp Ser Ser Cys Leu Met
245 250 255
50 His Met Gln Gly Val Ile Asp Arg Glu Lys Leu Pro Ile Lys Thr Ile
260 265 270
His Ala Val Glu Ile Leu Ala Ala Asn Leu
275 280

55 (2) INFORMATION FOR SEQ ID NO:273

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 251 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

65

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...251

70

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273

75

Pro Leu Lys Lys Arg Met Asp Ile Val Ser Met Ala Asp Lys Ala Leu

189/490

1 Val Val Glu Met Arg Asp Val Thr Leu Cys Gln Glu Glu Asn Val Ile
 20 25 30
 5 Phe Gln Asn Leu Asn Leu Thr Leu Ser Ala Gly Asp Phe Val Tyr Leu
 35 40 45
 Ile Gly Ser Val Gly Ser Gly Lys Ser Thr Leu Leu Lys Ala Leu Tyr
 50 55 60
 Ala Glu Val Pro Ile Ser Ala Gly Tyr Ala Arg Val Ile Asp Tyr Asp
 65 70 75 80
 10 Leu Ala Lys Leu Lys Arg Lys Gln Leu Pro Tyr Leu Arg Arg Asn Leu
 85 90 95
 Gly Ile Val Phe Gln Asp Phe Gln Leu Leu Asn Gly Arg Thr Val Ala
 100 105 110
 15 Glu Asn Leu Asp Phe Val Leu Arg Ala Thr Asp Trp Lys Asn Arg Ala
 115 120 125
 Asp Arg Glu Gln Arg Ile Glu Glu Val Leu Thr Arg Val Gly Met Ser
 130 135 140
 Arg Lys Ala Tyr Lys Arg Pro His Glu Leu Ser Gly Gly Glu Gln Gln
 145 150 155 160
 20 Arg Val Gly Ile Ala Arg Ala Leu Leu Ala Lys Pro Ala Leu Ile Leu
 165 170 175
 Ala Asp Glu Pro Thr Gly Asn Leu Asp Ser Val Thr Gly Leu Gln Ile
 180 185 190
 25 Ala Ser Leu Leu Tyr Glu Ile Ser Lys Gln Gly Thr Ala Val Leu Met
 195 200 205
 Ser Thr His Asn Ser Ser Leu Ser His Leu Pro Ala Arg Thr Leu
 210 215 220
 Ala Val Arg Lys Asn Gly Asp Ala Ser Ser Leu Val Glu Leu Ser Ala
 225 230 235 240
 30 Asp Ala Val Ser Arg Lys Asn Thr Glu Ile Asp
 245

(2) INFORMATION FOR SEQ ID NO:274

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 238 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 40 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 45 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...238
- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:274

Thr Arg His Cys Pro Ala Cys Arg Ser Ser Phe His Leu Ile Lys Thr
 1 5 10 15
 55 Ser Lys Thr Met Ile Glu Ile Ser Asn Leu Thr Lys Val Phe Arg Thr
 20 25 30
 Glu Glu Ile Glu Thr Val Ala Leu Asp Gly Val Ser Leu Lys Val Asp
 35 40 45
 60 Lys Gly Glu Phe Ile Ala Ile Met Gly Pro Ser Gly Cys Gly Lys Ser
 50 55 60
 Thr Leu Leu Asn Ile Leu Gly Leu Leu Asp Asn Pro Thr Ser Gly Ile
 65 70 75 80
 Tyr Lys Leu Asp Gly Ala Glu Val Gly Asn Leu Arg Glu Lys Asp Arg
 85 90 95
 65 Thr Ala Val Arg Lys Gly Asn Ile Gly Phe Val Phe Gln Ser Phe Asn
 100 105 110
 Leu Ile Glu Glu Met Thr Val Ser Glu Asn Val Glu Leu Pro Leu Val
 115 120 125
 70 Tyr Leu Gly Val Lys Ala Ser Glu Arg Lys Glu Arg Val Glu Glu Ala
 130 135 140
 Leu Arg Lys Met Ser Ile Ser His Arg Ala Gly His Phe Pro Asn Gln
 145 150 155 160
 Leu Ser Gly Gly Gln Gln Arg Val Ala Ile Ala Arg Ala Val Val
 165 170 175
 75 Ala Asn Pro Lys Leu Ile Leu Ala Asp Glu Pro Thr Gly Asn Leu Asp

190/ 490

180 185 190
 Ser Lys Asn Gly Ala Asp Val Met Glu Leu Leu Arg Gly Leu Asn Arg
 195 200 205
 5 Glu Gly Ala Thr Ile Val Met Val Thr His Ser Glu His Asp Ala Arg
 210 215 220
 Ser Ala Gly Arg Ile Ile Asn Leu Phe Asp Gly Lys Ile Arg
 225 230 235

(2) INFORMATION FOR SEQ ID NO:275
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 604 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION: 1...604
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:275

30 Ser Thr Glu Thr Asn Ser Lys Ser Glu Met Lys Glu Phe Phe Lys Met
 1 5 10 15
 Phe Phe Ala Ser Ile Leu Gly Val Ile Thr Ala Gly Ile Ile Leu Phe
 20 25 30
 Cys Ile Phe Leu Phe Ile Phe Phe Gly Ile Val Ala Gly Ile Ala Ser
 35 40 45
 Lys Ala Thr Gly Gly Thr Ile Pro Lys Ile Glu Ala Asn Ser Ile Leu
 50 55 60
 His Ile Unk Asn Ser Ser Phe Pro Glu Ile Val Ser Ala Asn Pro Trp
 65 70 75 80
 40 Ser Met Leu Thr Gly Lys Asp Glu Ser Val Ser Leu Ser Gln Ala Val
 85 90 95
 Glu Ala Ile Gly Gln Ala Lys Asn Asn Pro Asn Ile Thr Gly Ile Phe
 100 105 110
 Leu Asp Leu Asp Asn Leu Ser Val Gly Met Ala Ser Ala Glu Glu Leu
 115 120 125
 45 Arg Arg Ala Leu Gln Asp Phe Lys Met Ser Gly Lys Phe Val Val Ser
 130 135 140
 Tyr Ala Asp Arg Tyr Thr Gln Lys Gly Tyr Tyr Leu Ser Ser Ile Ala
 145 150 155 160
 50 Asp Lys Leu Tyr Leu Asn Pro Lys Gly Met Leu Gly Leu Ile Gly Ile
 165 170 175
 Ala Thr Gln Thr Met Phe Tyr Lys Asp Ala Leu Asp Lys Phe Gly Val
 180 185 190
 Lys Met Glu Ile Phe Lys Val Gly Thr Tyr Lys Ala Ala Val Glu Pro
 195 200 205
 55 Phe Met Leu Asn Arg Met Ser Asp Ala Asn Arg Glu Gln Ile Thr Thr
 210 215 220
 Tyr Ile Asn Gly Leu Trp Asp Lys Ile Thr Ser Asp Ile Ala Glu Ser
 225 230 235 240
 60 Arg Lys Thr Ala Met Asp Ser Val Lys Met Phe Ala Asp Lys Gly Glu
 245 250 255
 Met Phe Gly Leu Ala Glu Lys Ala Val Glu Met Lys Leu Val Asp Glu
 260 265 270
 Leu Ala Tyr Arg Thr Asp Val Glu Lys Glu Leu Lys Lys Met Ser Gln
 275 280 285
 65 Arg Gly Glu Lys Asp Glu Leu Arg Phe Val Ser Leu Ser Gln Val Leu
 290 295 300
 Ala Asn Gly Pro Met Asn Lys Thr Lys Gly Ser Arg Ile Ala Val Leu
 305 310 315 320
 70 Phe Ala Glu Gly Glu Ile Thr Glu Glu Ile Ile Lys Lys Pro Phe Asp
 325 330 335
 Thr Asp Gly Ser Ser Ile Thr Gln Glu Leu Ala Lys Glu Ile Lys Ala
 340 345 350
 Ala Ala Asp Asp Asp Asp Ile Lys Ala Val Val Leu Arg Val Asn Ser
 355 360 365
 75 Pro Gly Gly Ser Ala Phe Thr Ser Glu Gln Ile Trp Lys Gln Val Ala

191/ 490

370 375 380
 Asp Leu Lys Ala Lys Lys Pro Ile Val Val Ser Met Gly Asp Val Ala
 385 390 395 400
 5 Ala Ser Gly Gly Tyr Tyr Ile Ala Cys Ala Ala Asn Ser Ile Val Ala
 405 410 415
 Glu His Thr Thr Leu Thr Gly Ser Ile Gly Ile Phe Gly Met Phe Pro
 420 425 430
 Asn Phe Ala Gly Val Ala Lys Lys Ile Gly Val Asn Met Asp Val Val
 435 440 445
 10 Gln Thr Ser Lys Tyr Ala Asp Leu Gly Asn Thr Phe Ala Pro Met Thr
 450 455 460
 Val Glu Asp Arg Ala Leu Ile Gln Arg Tyr Ile Glu Gln Gly Tyr Asp
 465 470 475 480
 15 Leu Phe Leu Thr Arg Val Ser Glu Gly Arg Asn Arg Thr Lys Ala Gln
 485 490 495
 Ile Asp Ser Ile Ala Gln Gly Arg Val Trp Leu Gly Asp Lys Ala Leu
 500 505 510
 Ala Leu Gly Leu Val Asp Glu Leu Gly Gly Leu Asp Thr Ala Ile Lys
 515 520 525
 20 Arg Ala Ala Lys Leu Ala Gln Leu Gly Gly Asn Tyr Ser Ile Glu Tyr
 530 535 540
 Gly Lys Thr Lys Arg Asn Phe Phe Glu Glu Leu Leu Ser Ser Ser Ala
 545 550 555 560
 25 Ala Asp Met Lys Ser Ala Ile Leu Ser Thr Ile Leu Ser Asp Pro Glu
 565 570 575
 Ile Glu Val Leu Arg Glu Leu Arg Ser Met Pro Pro Arg Pro Ser Gly
 580 585 590
 30 Ile Gln Ala Arg Leu Pro Tyr Tyr Phe Met Pro Tyr
 595 600
 (2) INFORMATION FOR SEQ ID NO:276
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 324 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...324
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:276
 Leu Thr Leu Phe Cys Cys Asn Tyr Phe Lys Gln Met Arg Ala Asn Ile
 1 5 10 15
 Trp Gln Ile Leu Ser Val Ser Val Leu Phe Phe Gly Thr Ala Ile
 20 25 30
 55 Gly Gln Ala Gln Ser Arg Asn Arg Thr Tyr Glu Ala Tyr Val Lys Gln
 35 40 45
 Tyr Ala Asp Glu Ala Ile Arg Gln Met Ser Arg Tyr Asn Ile Pro Ala
 50 55 60
 60 Ser Ile Thr Ile Ala Gln Ala Leu Val Glu Thr Gly Ala Gly Ala Ser
 65 70 75 80
 Thr Leu Ala Ser Val His Asn Asn His Phe Gly Ile Lys Cys His Lys
 85 90 95
 Ser Trp Thr Gly Lys Arg Thr Tyr Arg Thr Asp Asp Ala Pro Asn Glu
 100 105 110
 65 Cys Phe Arg Ser Tyr Ser Ala Ala Arg Glu Ser Tyr Glu Asp His Ser
 115 120 125
 Arg Phe Leu Leu Gln Pro Arg Tyr Arg Pro Leu Phe Lys Leu Asp Arg
 130 135 140
 70 Glu Asp Tyr Arg Gly Trp Ala Thr Gly Leu Gln Arg Cys Gly Tyr Ala
 145 150 155 160
 Thr Asn Arg Gly Tyr Ala Asn Leu Leu Ile Lys Met Val Glu Leu Tyr
 165 170 175
 Glu Leu Tyr Ala Leu Asp Arg Glu Lys Tyr Pro Ser Trp Phe His Lys
 180 185 190
 75 Ser Tyr Pro Gly Ser Asn Lys Lys Ser His Gln Thr Thr Lys Gln Lys

192/ 490

195 200 205
 Gln Ser Gly Leu Lys His Glu Ala Tyr Phe Ser Tyr Gly Leu Leu Tyr
 210 215 220
 5 Ile Ile Ala Lys Gln Gly Asp Thr Phe Asp Ser Leu Ala Glu Glu Phe
 225 230 235 240
 Asp Met Arg Ala Ser Lys Leu Ala Lys Tyr Asn Asp Ala Pro Val Asp
 245 250 255
 Phe Pro Ile Glu Lys Gly Asp Val Ile Tyr Leu Glu Lys Lys His Ala
 260 265 270
 10 Cys Ser Ile Ser Lys His Thr Gln His Val Val Arg Val Gly Asp Ser
 275 280 285
 Met His Ser Ile Ser Gln Arg Tyr Gly Ile Arg Met Lys Asn Leu Tyr
 290 295 300
 15 Lys Leu Asn Asp Lys Asp Gly Glu Tyr Ile Pro Gln Glu Gly Asp Ile
 305 310 315 320
 Leu Arg Leu Arg

(2) INFORMATION FOR SEQ ID NO:277

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 533 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...533

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277

40 Arg Ile Pro Asp Glu Gln Thr Gly Arg Ile Met Asp Gly Arg Arg Tyr
 1 5 10 15
 Ser Asp Gly Leu His Gln Ala Ile Glu Ala Lys Glu His Val Lys Val
 20 25 30
 Glu Ala Ala Thr Gln Thr Phe Ala Thr Ile Thr Leu Gln Asn Tyr Phe
 35 40 45
 45 Arg Met Tyr His Lys Leu Ala Gly Met Thr Gly Thr Ala Glu Thr Glu
 50 55 60
 Ala Gly Glu Leu Trp Asp Ile Tyr Lys Leu Asp Val Val Ile Pro
 65 70 75 80
 50 Thr Asn Lys Pro Ile Ala Arg Lys Asp Met Asn Asp Arg Ile Tyr Lys
 85 90 95
 Thr Ala Arg Glu Lys Tyr Ala Ala Val Ile Glu Glu Ile Val Arg Leu
 100 105 110
 Val Glu Glu Gly Arg Pro Val Leu Val Gly Thr Thr Ser Val Glu Ile
 115 120 125
 55 Ser Glu Leu Leu Ser Arg Met Leu Arg Leu Arg Gly Ile Gln His Asn
 130 135 140
 Val Leu Asn Ala Lys Leu His Gln Lys Glu Ala Glu Ile Val Ala Gln
 145 150 155 160
 60 Ala Gly Gln Lys Gly Thr Val Thr Ile Ala Thr Asn Met Ala Gly Arg
 165 170 175
 Gly Thr Asp Ile Lys Leu Ser Ala Glu Val Lys Lys Ala Gly Gly Leu
 180 185 190
 Ala Ile Ile Gly Thr Glu Arg His Glu Ser Arg Arg Val Asp Arg Gln
 195 200 205
 65 Leu Arg Gly Arg Ser Gly Arg Gln Gly Asp Pro Gly Ser Ser Ile Phe
 210 215 220
 Tyr Val Ser Leu Glu Asp His Leu Met Arg Leu Phe Ala Thr Glu Lys
 225 230 235 240
 70 Ile Ala Ser Leu Met Asp Arg Leu Gly Phe Lys Glu Gly Glu Val Leu
 245 250 255
 Glu Asn Asn Met Leu Ser Lys Ser Val Glu Arg Ala Gln Lys Lys Val
 260 265 270
 Glu Glu Asn Asn Phe Gly Ile Arg Lys His Leu Leu Glu Tyr Asp Asp
 275 280 285
 75 Val Met Asn Ser Gln Arg Glu Val Ile Tyr Thr Arg Arg Arg His Ala

193/490

290 295 300
 Leu Met Gly Glu Arg Ile Gly Met Asp Val Leu Asn Thr Ile Tyr Asp
 305 310 315 320
 Val Cys Lys Ala Leu Ile Asp Asn Tyr Ala Glu Ala Asn Asp Phe Glu
 325 330 335
 Gly Phe Lys Glu Asp Leu Met Arg Ala Leu Ala Ile Glu Ser Pro Ile
 340 345 350
 Thr Gln Glu Ile Phe Arg Gly Lys Lys Ala Glu Glu Leu Thr Asp Met
 355 360 365
 10 Leu Phe Asp Glu Ala Tyr Lys Ser Phe Gln Arg Lys Met Asp Leu Ile
 370 375 380
 Ala Glu Val Ala His Pro Val Val His Gln Val Phe Glu Thr Gln Ala
 385 390 395 400
 15 Ala Val Tyr Glu Arg Ile Leu Ile Pro Ile Thr Asp Gly Lys Arg Val
 405 410 415
 Tyr Asn Ile Gly Cys Asn Leu Arg Glu Ala Asp Glu Thr Gln Gly Lys
 420 425 430
 Ser Ile Ile Lys Glu Phe Glu Lys Ala Ile Val Leu His Thr Ile Asp
 435 440 445
 20 Glu Ser Trp Lys Glu His Leu Arg Glu Met Asp Glu Leu Arg Asn Ser
 450 455 460
 Val Gln Asn Ala Ser Tyr Glu Asn Lys Asp Pro Leu Leu Ile Tyr Lys
 465 470 475 480
 25 Leu Glu Ser Tyr Glu Leu Phe Arg Lys Met Val Glu Ala Met Asn Arg
 485 490 495
 Lys Thr Val Ala Ile Leu Met Arg Ala Arg Ile Pro Val Pro Glu Ala
 500 505 510
 Pro Ser Gln Glu Glu Leu Glu His Arg Arg Gln Ile Glu Ile Arg His
 515 520 525
 30 Ala Thr Gln Gln Arg
 530

(2) INFORMATION FOR SEQ ID NO:278

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 720 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 40 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 45 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...720
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:278

Lys Ser Cys Arg Val Ile Gly Gln Thr Arg Arg Tyr Gly Cys Cys Pro
 1 5 10 15
 55 Val Gly Leu Arg Pro Cys His Gln Ser Leu Ser Gly Val Cys Arg Cys
 20 25 30
 Leu Phe Gln Ser Arg Pro Ala Val Ala Phe Ala Arg Lys Gly Gln Arg
 35 40 45
 60 Arg His Arg Arg Ser Glu Ser Gly Arg Arg Ile Arg Ala Leu Gln Gly
 50 55 60
 Val Gln His His Gln Thr Asn Glu His Glu Val Met Ile Ser Val Asn
 65 70 75 80
 Asn Leu Thr Val Asp Phe Gly Thr Arg Leu Leu Phe Asp Gln Val Ser
 85 90 95
 65 Phe Val Ile Asn Arg Arg Asp Arg Ile Ala Leu Val Gly Lys Asn Gly
 100 105 110
 Ala Gly Lys Ser Thr Leu Leu Lys Leu Ile Ala Gly Met Glu Glu Pro
 115 120 125
 70 Thr Ser Gly His Ile Ala Arg Pro Lys Gly Ile Arg Ile Gly Tyr Leu
 130 135 140
 Pro Gln Val Met Arg Leu Gln Asp Gly His Thr Val Tyr Glu Glu Val
 145 150 155 160
 Glu Gln Ala Phe Asn Asp Ile Arg Gln Ile Glu Glu Glu Ile Arg Arg
 165 170 175
 75 Leu Ser Asp Glu Met Ala Gly Arg Thr Asp Tyr Glu Ser Asp Asp Tyr

194/ 490

180 185 190
Ile Arg Leu Ile Glu His Tyr Thr Asn Met Ser Glu Thr Leu Ser Leu
195 200 205
Met Gln Gln Gly Asn Tyr His Ala Ala Ile Glu Gln Thr Leu Ile Gly
210 215 220
Leu Gly Phe Gly Arg Glu Asp Phe His Arg Pro Thr Ala Asp Phe Ser
225 230 235 240
Gly Gly Trp Arg Met Arg Ile Glu Leu Ala Lys Leu Leu Leu Gln Arg
245 250 255
10 Pro Glu Val Leu Leu Asp Glu Pro Thr Asn His Leu Asp Ile Glu
260 265 270
Ser Ile Gly Trp Leu Glu Gln Phe Ile Ala Thr Asn Ala Gly Ala Val
275 280 285
15 Ile Leu Val Ser His Asp Arg Ala Phe Ile Asp Asn Thr Thr Thr Arg
290 295 300
Thr Ile Glu Ile Glu Leu Gly His Ile Tyr Asp Tyr Lys Thr Asn Tyr
305 310 315 320
Ser His Tyr Val Glu Leu Arg Glu Glu Arg Leu Arg Gln Gln Met Arg
325 330 335
20 Ala Tyr Glu Asn Gln Gln Lys Met Ile Arg Asp Thr Glu Asp Phe Ile
340 345 350
Glu Arg Phe Arg Tyr Lys Ala Thr Lys Ser Val Gln Val Gln Ser Arg
355 360 365
25 Ile Lys Gln Leu Glu Lys Val Glu Arg Val Glu Ile Asp Glu Arg Asp
370 375 380
Arg Ser Ala Phe His Phe Arg Phe Ile Pro Ala Gln Pro Ser Gly Ser
385 390 395 400
Tyr Pro Leu Ile Val Asp Asp Leu Ala Lys Ala Tyr Gly Asp His Gln
405 410 415
30 Val Phe Ser Gly Ala Thr Tyr Thr Ile Glu Arg Gly Glu Lys Val Ala
420 425 430
Phe Val Gly Lys Asn Gly Ala Gly Lys Ser Thr Met Val Lys Cys Ile
435 440 445
35 Met Gly Glu Leu Thr Asp Tyr Thr Gly Lys Leu Glu Leu Gly His Asn
450 455 460
Val Gln Leu Gly Tyr Phe Ala Gln Asn Glu Ala Gln Glu Leu Arg Gly
465 470 475 480
Asp Leu Thr Val Phe Asp Thr Ile Asp Arg Glu Ala Val Gly Asp Ile
485 490 495
40 Arg Leu Arg Leu Asn Asp Leu Leu Gly Ala Phe Leu Phe Gly Gly Glu
500 505 510
Ala Ser Glu Lys Lys Val Ser Val Leu Ser Gly Gly Glu Arg Ala Arg
515 520 525
45 Leu Ala Ile Ile Arg Leu Leu Gln Pro Ala Asn Phe Leu Ile Leu
530 535 540
Asp Glu Pro Thr Asn His Leu Asp Met Arg Ser Lys Asp Val Leu Lys
545 550 555 560
Glu Ala Ile Lys Asn Phe Asp Gly Thr Val Ile Val Val Ser His Asp
565 570 575
50 Arg Glu Phe Leu Asp Gly Leu Val Ser Lys Val Tyr Glu Phe Ala Asp
580 585 590
Gly Gln Val Asn Glu His Leu Gly Gly Ile Tyr Asp Tyr Leu Arg Thr
595 600 605
55 Arg Arg Met Gln Thr Leu Thr Glu Leu Glu Arg Thr Thr Thr Ile Glu
610 615 620
Thr Lys Thr Thr Arg Glu Ala Ile Pro Glu Thr Glu Ala Lys Ala Asp
625 630 635 640
Tyr Arg Arg Gln Lys Glu Val Ala Lys Gln Leu Arg Thr Leu Glu Arg
645 650 655
60 Thr Val Ala Thr Cys Glu Glu Arg Ile Gly Lys Leu Glu Ser Glu Leu
660 665 670
Gln Ala Ile Glu Met Leu Leu Gln Asp Pro Lys His Ala Thr Asp Ala
675 680 685
65 Asn Leu Phe Glu Arg Tyr Ala Gly Met Lys Gln Glu Leu Glu Lys Ala
690 695 700
Met Glu Asp Trp Glu Gln Ala Ser Glu Ala Leu Ser Glu Ala Gln Gly
705 710 715 720

(2) INFORMATION FOR SEQ ID NO:279

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 386 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

195 / 490

(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
5 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc feature
10 (B) LOCATION 1...386
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279
15 Tyr Leu Lys Leu Leu Ile Leu Gln Ile Ala Leu Met Asn Phe Leu Lys
1 5 10 15
Lys Glu Pro Phe Lys Ile Phe Ser Met Ile Tyr Leu Leu Leu Asp Thr
20 20 25 30
Ile Thr Asn Arg Ala Gly Thr Glu Arg Ala Val Ile Asn Leu Ala Asn
35 40 45
20 Asn Leu His Ala Asn Gly His Arg Val Ser Leu Val Ser Val Cys Thr
50 55 60
Lys Glu Gly Glu Pro Ser Phe Gln Val Glu Lys Gly Ile Glu Val His
65 70 75 80
25 His Leu Gly Ile Arg Leu Tyr Gly Asn Ala Leu Ala Arg Lys Thr Val
85 90 95
Tyr Phe Lys Ala Tyr Arg Arg Ile Lys Ala Leu Tyr Lys Lys Arg Glu
100 105 110
Pro Val Leu Leu Ile Gly Thr Asn Ile Phe Ile Asn Thr Ile Leu Ser
115 120 125
30 Gln Ile Ser Asn Arg Gly Arg Ile Phe Thr Ile Gly Cys Glu His Ile
130 135 140
Ser Tyr Asp Ile Ala Arg Pro Ile Thr Lys Arg Ile Arg Gly Phe Leu
145 150 155 160
35 Tyr Ser Gly Leu Asp Ala Val Val Ala Leu Thr Lys Arg Asp Gln Gln
165 170 175
Ser Phe Glu Ala Ile Leu Arg Gly Arg Ser Lys Ala Tyr Val Ile Pro
180 185 190
Asn Gln Val Ser Phe Thr Thr Val Gln Arg Asp Ala Thr Thr His Lys
195 200 205
40 Gln Met Leu Ala Ile Gly Arg Leu Thr Tyr Gln Lys Gly Phe Glu Phe
210 215 220
Met Ile Glu Asp Ala Ser Arg Val Leu Arg Glu Arg Pro Asp Trp Lys
225 230 235 240
45 Leu Ile Ile Val Gly Asp Gly Glu Asn Glu Ser Met Leu Arg Lys Glu
245 250 255
Ile Ala Ser Arg Asn Met Glu Ser Gln Ile Glu Ile His Pro Ser Thr
260 265 270
Pro Glu Ile Arg Lys Tyr Tyr Glu Ser Ser Ala Ile Tyr Leu Met Thr
275 280 285
50 Ser Arg Phe Glu Gly Leu Pro Met Val Leu Leu Glu Ala Glu Ala Tyr
290 295 300
Ala Leu Pro Ile Ile Ser Tyr Asp Cys Pro Thr Gly Pro Arg Glu Leu
305 310 315 320
55 Ile Glu Asn Gly Arg Asn Gly Phe Leu Val Pro Met Glu Ala His Glu
325 330 335
Asp Phe Ala Asp Lys Leu Arg Leu Leu Met Asp Asp Glu Thr Leu Arg
340 345 350
Lys Lys Met Gly Gln Glu Ser Glu Leu Met Val Lys Ser Tyr Ser Pro
355 360 365
60 Ala Asn Ile Tyr Glu Cys Trp Lys Lys Leu Phe Val Glu Ile Gly Tyr
370 375 380
Met Asn
385
65 (2) INFORMATION FOR SEQ ID NO:280
(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 655 amino acids
70 (B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
75 (iii) HYPOTHETICAL: YES

196/490

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

5 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...655

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280

10 Thr Thr Lys Glu Asn Glu Thr Thr Thr Lys Asn Glu Tyr Arg Ile Met
1 5 10 15
Gly Lys Ile Ile Gly Ile Asp Leu Gly Thr Thr Asn Ser Cys Val Ser
20 25 30
15 Val Leu Glu Gly Asn Glu Pro Ile Val Ile Thr Asn Ser Glu Gly Lys
35 40 45
Arg Thr Thr Pro Ser Val Val Ala Phe Val Asp Gly Glu Arg Lys
50 55 60
Val Gly Asp Pro Ala Lys Arg Gln Ala Ile Thr Asn Pro Thr Lys Thr
65 70 75 80
20 Ile Tyr Ser Ile Lys Arg Phe Met Gly Glu Thr Tyr Asp Gln Val Ser
85 90 95
Arg Glu Val Glu Arg Val Pro Phe Lys Val Val Arg Gly Asp Asn Asn
100 105 110
25 Thr Pro Arg Val Asp Ile Asp Gly Arg Leu Tyr Thr Pro Gln Glu Ile
115 120 125
Ser Ala Met Ile Leu Gln Lys Met Lys Lys Thr Ala Glu Asp Tyr Leu
130 135 140
Gly Gln Glu Val Thr Glu Ala Val Ile Thr Val Pro Ala Tyr Phe Asn
145 150 155 160
30 Asp Ala Gln Arg Gln Ala Thr Lys Glu Ala Gly Glu Ile Ala Gly Leu
165 170 175
Lys Val Arg Arg Ile Val Asn Glu Pro Thr Ala Ala Ser Leu Ala Tyr
180 185 190
35 Gly Leu Asp Lys Ser Asn Lys Asp Met Lys Ile Ala Val Phe Asp Leu
195 200 205
Gly Gly Gly Thr Phe Asp Ile Ser Ile Leu Glu Leu Gly Asp Gly Val
210 215 220
Phe Glu Val Lys Ser Thr Asn Gly Asp Thr His Leu Gly Gly Asp Asp
225 230 235 240
40 Phe Asp His Val Ile Ile Asp Trp Leu Ala Glu Glu Phe Lys Ser Gln
245 250 255
Glu Gly Val Asp Leu Arg Gln Asp Pro Met Ala Met Gln Arg Leu Lys
260 265 270
45 Glu Ala Ala Glu Lys Ala Lys Ile Glu Leu Ser Ser Thr Ser Ser Thr
275 280 285
Glu Ile Asn Leu Pro Tyr Ile Met Pro Val Asn Gly Ile Pro Lys His
290 295 300
Leu Val Met Thr Leu Thr Arg Ala Lys Phe Glu Gln Leu Ala Asp Arg
305 310 315 320
50 Leu Ile Gln Ala Cys Val Ala Pro Cys Glu Thr Ala Leu Lys Asp Ala
325 330 335
Gly Met Ser Arg Gly Asp Ile Asp Glu Val Ile Leu Val Gly Gly Ser
340 345 350
55 Thr Arg Ile Pro Ala Ile Gln Glu Ile Val Glu Lys Ile Phe Gly Lys
355 360 365
Ala Pro Ser Lys Gly Val Asn Pro Asp Glu Val Val Ala Val Gly Ala
370 375 380
Ala Ile Gln Gly Gly Val Leu Thr Gly Glu Val Lys Asp Val Leu Leu
385 390 395 400
60 Leu Asp Val Thr Pro Leu Ser Leu Gly Ile Glu Thr Met Gly Gly Val
405 410 415
Met Thr Arg Leu Ile Asp Ala Asn Thr Thr Ile Pro Thr Lys Lys Ser
420 425 430
65 Glu Ile Phe Thr Thr Ala Val Asp Asn Gln Pro Ser Val Glu Ile His
435 440 445
Val Leu Gln Gly Glu Arg Ser Leu Ala Lys Asp Asn Lys Ser Ile Gly
450 455 460
Arg Phe Asn Leu Asp Gly Ile Ala Pro Ala Pro Arg Gln Thr Pro Gln
465 470 475 480
70 Ile Glu Val Thr Phe Asp Ile Asp Ala Asn Gly Ile Leu Asn Val Thr
485 490 495
Ala His Asp Lys Ala Thr Gly Lys Lys Gln Asn Ile Arg Ile Glu Ala
500 505 510
75 Ser Ser Gly Leu Ser Asp Asp Glu Ile Lys Arg Met Lys Glu Glu Ala
515 520 525

197/490

Gln Ala Asn Ala Glu Ala Asp Lys Lys Glu Lys Glu Arg Ile Asp Lys
 530 535 540
 Ile Asn Gln Ala Asp Ser Met Ile Phe Gln Thr Glu Lys Gln Leu Lys
 545 550 555 560
 5 Glu Leu Gly Asp Lys Phe Pro Ala Asp Lys Lys Ala Pro Ile Asp Thr
 565 570 575
 Ala Leu Asp Lys Leu Lys Glu Ala His Lys Ala Gln Asp Val Ala Ala
 580 585 590
 10 Ile Asp Thr Ala Met Ala Glu Leu Gln Thr Ala Leu Ser Ala Ala Gly
 595 600 605
 Glu Glu Leu Tyr Lys Asn Ala Gly Ala Ala Gln Gly Gly Ala Gln Pro
 610 615 620
 Gly Pro Asp Phe Gly Gly Ala Gln Gly Pro Ser Ala Gly Asp Gln Pro
 625 630 635 640
 15 Ser Asp Asp Lys Asn Val Thr Asp Val Asp Phe Glu Glu Val Lys
 645 650 655

(2) INFORMATION FOR SEQ ID NO:281

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 467 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 25 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 30 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...467
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:281

Lys Trp Ala Arg Thr Thr Thr Leu Arg Ile Ser Asn Ala Thr Ile Tyr
 1 5 10 15
 40 Lys Thr Met Arg Tyr Asp Leu Ala Ile Ile Gly Gly Gly Pro Ala Gly
 20 25 30
 Tyr Thr Ala Ala Glu Arg Ala Ala Lys Gly Gly Leu Lys Thr Leu Leu
 35 40 45
 45 Ile Glu Lys Asn Ala Leu Gly Gly Val Cys Leu Asn Glu Gly Cys Ile
 50 55 60
 Pro Thr Lys Thr Leu Leu Tyr Ser Ala Lys Val Leu His Gln Ile Ala
 65 70 75 80
 Thr Ala Ser Lys Tyr Ala Val Ser Gly Thr Ala Asp Gly Leu Asp Leu
 85 90 95
 50 Gly Lys Val Ile Ala Arg Lys Gly Lys Ile Ile Arg Lys Leu Thr Ala
 100 105 110
 Gly Ile Arg Ser Arg Leu Thr Glu Ala Gly Val Glu Met Val Thr Ala
 115 120 125
 55 Glu Ala Thr Val Thr Gly Cys Asp Ala Asp Gly Ile Ile Gly Ile Thr
 130 135 140
 Ala Gly Glu Ala Gln Tyr Lys Ala Ala Asn Leu Leu Cys Thr Gly
 145 150 155 160
 Ser Glu Thr Phe Ile Pro Pro Ile Pro Gly Val Glu Gln Thr Glu Tyr
 165 170 175
 60 Tip Thr Asn Arg Glu Ala Leu Gln Asn Lys Glu Ile Pro Thr Ser Leu
 180 185 190
 Val Ile Ile Gly Gly Gly Val Ile Gly Met Glu Phe Ala Ser Phe Phe
 195 200 205
 65 Asn Gly Ile Gly Thr Gln Val His Val Val Glu Met Leu Pro Glu Ile
 210 215 220
 Leu Asn Gly Ile Asp Pro Glu His Ala Ala Met Leu Arg Ala His Tyr
 225 230 235 240
 Glu Lys Glu Gly Ile Lys Phe Tyr Leu Gly His Lys Val Thr Ser Val
 245 250 255
 70 Arg Asn Gly Ala Val Thr Val Glu Tyr Glu Gly Glu Ser Lys Glu Ile
 260 265 270
 Glu Gly Glu Arg Ile Leu Met Ser Val Gly Arg Arg Pro Val Leu Gln
 275 280 285
 75 Gly Phe Glu Ser Leu Gly Leu Val Leu Ala Gly Lys Gly Val Lys Thr
 290 295 300

198/490

Asn Glu Arg Met Gln Thr Ser Leu Pro Asn Val Tyr Ala Ala Gly Asp
 305 310 315 320
 Ile Thr Gly Phe Ser Leu Leu Ala His Thr Ala Val Arg Glu Ala Glu
 325 330 335
 5 Val Ala Val Asp Gln Ile Leu Gly Lys Thr Asp Glu Thr Met Ser Tyr
 340 345 350
 Arg Ala Val Pro Gly Val Val Tyr Thr Asn Pro Glu Val Ala Gly Val
 355 360 365
 10 Gly Glu Thr Glu Glu Ser Leu Arg Lys Ala Gly Arg Ala Tyr Thr Val
 370 375 380
 Arg Arg Leu Pro Met Ala Phe Ser Gly Arg Phe Val Ala Glu Asn Glu
 385 390 395 400
 Gln Gly Asn Gly Glu Cys Lys Leu Leu Asn Asp Glu Glu Asn Arg Leu
 405 410 415
 15 Ile Gly Ala His Leu Ile Gly Asn Pro Ala Gly Glu Leu Ile Val Thr
 420 425 430
 Ala Ala Met Ala Ile Glu Thr Gly Met Thr Asp Arg Gln Ile Glu Arg
 435 440 445
 20 Ile Ile Phe Pro His Pro Thr Val Gly Glu Ile Leu Lys Glu Thr Leu
 450 455 460
 Ala Gly Gly
 465
 (2) INFORMATION FOR SEQ ID NO:282
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 945 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...945
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:282
 Pro Lys Ile Leu Met Glu Leu Lys Arg Phe Leu Ser Leu Gly Leu Leu
 1 5 10 15
 Leu Val Gly Phe Ile Pro Met Lys Leu Ser Ala Gln Gln Ala Gln Pro
 20 25 30
 Leu Pro Thr Asp Pro Ala Val Arg Val Gly Lys Leu Asp Asn Gly Leu
 35 40 45
 50 Thr Tyr Phe Ile Arg His Asn Glu Asn Pro Lys Asp Arg Ala Asp Phe
 50 55 60
 Phe Ile Ala Gln Lys Val Gly Ser Ile Leu Glu Glu Asp Ser Gln Ser
 65 70 75 80
 Gly Leu Ala His Phe Leu Glu His Met Ala Phe Asn Gly Thr Lys Asn
 85 90 95
 55 Phe Pro Gly Lys Asn Leu Ile Asn Tyr Leu Glu Thr Ile Gly Val Arg
 100 105 110
 Phe Gly Gln Asn Leu Asn Ala Ser Thr Gly Phe Asp Lys Thr Glu Tyr
 115 120 125
 60 Thr Ile Met Asp Val Pro Thr Thr Arg Gln Gly Ile Ile Asp Ser Cys
 130 135 140
 Leu Leu Ile Leu His Asp Trp Ser Asn Asn Ile Thr Leu Asp Gly His
 145 150 155 160
 Glu Ile Asp Glu Glu Arg Gly Val Ile Gln Glu Glu Trp Arg Ala Arg
 165 170 175
 65 Arg Asp Ala Asn Leu Arg Met Phe Glu Ala Ile Leu Ala Lys Ala Met
 180 185 190
 Pro Gly Asn Lys Tyr Ala Glu Arg Met Pro Ile Gly Leu Met Asp Val
 195 200 205
 70 Val Leu Asn Phe Lys His Asp Glu Leu Arg Asn Tyr Tyr Lys Lys Trp
 210 215 220
 Tyr Arg Pro Asp Leu Gln Gly Leu Val Ile Val Gly Asp Ile Asp Val
 225 230 235 240
 75 Asp Tyr Val Glu Asn Lys Ile Lys Glu Leu Phe Lys Asp Val Pro Ala
 245 250 255

199/ 490

Pro Val Asn Pro Ala Glu Arg Ile Tyr Thr Pro Val Glu Asp Asn Asp
260 265 270
Glu Pro Ile Val Ala Ile Ala Thr Asp Ala Glu Ala Thr Thr Thr Gln
275 280 285
5 Leu Ser Ile Ser Phe Lys Ser Asp Pro Thr Pro Gln Glu Val Arg Gly
290 295 300
Ser Ile Phe Gly Leu Val Glu Asp Tyr Met Lys Gln Val Ile Thr Thr
305 310 315 320
10 Ala Val Asn Glu Arg Leu Ser Glu Ile Thr His Lys Pro Asn Ala Pro
325 330 335
Phe Leu Ser Ala Gly Ala Phe Phe Ser Asn Phe Met Tyr Ile Thr Gln
340 345 350
Thr Lys Asp Ala Phe Asn Phe Val Ala Thr Val Arg Glu Gly Glu Ala
355 360 365
15 Glu Lys Ala Met Asn Ala Leu Val Ala Glu Ile Glu Ser Leu Arg Gln
370 375 380
Phe Gly Ile Thr Lys Gly Glu Tyr Asp Arg Ala Arg Thr Asn Val Leu
385 390 395 400
20 Lys Arg Tyr Glu Asn Gln Tyr Asn Glu Arg Asp Lys Arg Lys Asn Asn
405 410 415
Ala Tyr Ala Asn Glu Tyr Ser Thr Tyr Phe Thr Asp Gly Gly Tyr Ile
420 425 430
Pro Gly Ile Glu Val Glu Tyr Gln Thr Val Asn Ala Phe Ala Pro Gln
435 440 445
25 Val Pro Leu Glu Ala Phe Asn Gln Ala Ile Ala Gln Met Ile Asp Pro
450 455 460
Val Lys Asn Ala Val Val Thr Leu Thr Gly Pro Ser Lys Ala Glu Ala
465 470 475 480
30 Lys Ile Pro Ser Glu Ala Asp Phe Leu Ala Ala Phe Lys Ala Ala Arg
485 490 495
Gln Gln Lys Val Glu Ala Lys Lys Asp Glu Val Ser Asp Gln Lys Leu
500 505 510
Met Glu Lys Ala Pro Lys Ala Gly Lys Ile Val Ser Glu Lys Lys Asp
515 520 525
35 Gln Lys Phe Gly Thr Thr Glu Leu Thr Leu Ser Asn Gly Ile Lys Val
530 535 540
Tyr Leu Lys Lys Thr Asp Phe Lys Ser Asn Glu Ile Leu Met Ser Ala
545 550 555 560
40 Leu Ser Pro Gly Gly Ile Leu Ser Gly Lys His Ala Pro Asn Gln Ser
565 570 575
Val Met Asn Ser Phe Met Asn Val Gly Gly Leu Gly Asn Phe Asp Ala
580 585 590
Ile Gln Leu Asp Lys Val Leu Thr Gly Arg Ser Ala Ser Val Ser Pro
595 600 605
45 Ser Leu Ser Leu Leu Ser Glu Gly Leu Ser Gly Lys Thr Thr Val Glu
610 615 620
Asp Met Glu Thr Phe Phe Gln Leu Ile Tyr Leu Gln Met Thr Ala Asn
625 630 635 640
50 Arg Lys Asp Pro Glu Ala Phe Lys Ala Thr Gln Glu Lys Leu Tyr Asn
645 650 655
Asn Leu Lys Asn Gln Glu Ala Asn Pro Met Ala Ala Leu Met Asp Ser
660 665 670
Ile Arg His Thr Met Tyr Gly Asp Asn Pro Met Met Lys Pro Met Lys
675 680 685
55 Ala Ala Asp Val Glu Lys Val Asn Tyr Asp Gln Val Met Ala Phe Tyr
690 695 700
Asn Glu Arg Phe Ala Asp Ala Gly Asp Phe Met Phe Phe Ile Gly
705 710 715 720
60 Asn Leu Asp Glu Ala Lys Met Lys Pro Leu Ile Glu Thr Tyr Leu Ala
725 730 735
Ser Leu Pro Asn Leu Lys Arg Gly Asp Lys Met Asn Lys Ala Gln Val
740 745 750
Pro Ala Ala Arg Ser Gly Lys Ile Asp Cys Lys Phe Glu Lys Glu Met
755 760 765
65 Asp Thr Pro Ser Thr Thr Ile Phe Asp Val Val Ser Gly Asn Val Glu
770 775 780
Tyr Thr Leu Lys Asn Ser Leu Leu Leu Glu Val Phe Ser Ala Val Met
785 790 795 800
70 Asp Gln Val Tyr Thr Ala Thr Val Arg Glu Lys Glu Gly Gly Ala Tyr
805 810 815
Ser Val Ala Ala Phe Gly Gly Leu Glu Gln Tyr Pro Gln Pro Lys Ala
820 825 830
Leu Met Gln Ile Tyr Phe Pro Thr Asp Pro Ala Arg Ala Glu Glu Met
835 840 845
75 Asn Ala Ile Val Phe Ala Glu Leu Glu Lys Leu Ala Lys Glu Gly Pro

200/ 490

850 855 860
 Asn Val Glu Tyr Phe Lys Lys Thr Ile Glu Asn Leu Asn Lys Gln His
 865 870 875 880
 Lys Glu Ser Leu Arg Glu Asn Arg Phe Trp Leu Glu Ala Met Lys Ala
 5 885 890 895
 Ser Phe Phe Glu Gly Asn Asp Phe Ile Thr Asp Tyr Glu Ser Val Leu
 900 905 910
 Asn Gly Leu Thr Pro Ala Glu Leu Gln Lys Phe Ala Ala Asp Leu Leu
 915 920 925
 10 Lys Gln Gln Asn Arg Val Val Val Met Met Ala Pro Val Ala Lys Ala
 930 935 940
 Gln
 945
 15 (2) INFORMATION FOR SEQ ID NO:283
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 686 amino acids
 (B) TYPE: amino acid
 20 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 25 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 30 (B) LOCATION 1...686
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:283
 35 Tyr Thr Met Ser Lys Lys Gly Thr Ile Gly Val Thr Ser Asp Asn Ile
 1 5 10 15
 Phe Pro Val Ile Lys Lys Phe Leu Tyr Ser Asp His Glu Ile Phe Leu
 20 25 30
 40 Arg Glu Ile Val Ser Asn Ala Val Asp Ala Thr Gln Lys Leu Lys Thr
 35 40 45
 Leu Thr Ser Val Gly Glu Phe Lys Gly Glu Thr Gly Asp Leu Arg Val
 50 55 60
 Thr Val Ser Val Asp Glu Val Ala Arg Thr Ile Thr Val Ser Asp Arg
 65 70 75 80
 45 Gly Val Gly Met Thr Glu Glu Glu Val Glu Lys Tyr Ile Asn Gln Ile
 85 90 95
 Ala Phe Ser Ser Ala Glu Glu Phe Leu Glu Lys Tyr Lys Asp Asp Lys
 100 105 110
 50 Ala Ala Ile Ile Gly His Phe Gly Leu Gly Phe Tyr Ser Ala Phe Met
 115 120 125
 Val Ser Glu Arg Val Asp Val Ile Thr Arg Ser Phe Arg Glu Asp Ala
 130 135 140
 Thr Ala Val Lys Trp Ser Cys Asp Gly Ser Pro Glu Tyr Thr Leu Glu
 145 150 155 160
 55 Pro Ala Asp Lys Ala Asp Arg Gly Thr Asp Ile Val Met His Ile Asp
 165 170 175
 Glu Glu Asn Ser Glu Phe Leu Lys Lys Glu Lys Ile Glu Gly Leu Leu
 180 185 190
 60 Gly Lys Tyr Cys Lys Phe Leu Thr Val Pro Ile Ile Phe Gly Lys Lys
 195 200 205
 Gln Glu Trp Lys Asp Gly Lys Met Gln Asp Thr Asp Glu Asp Asn Gln
 210 215 220
 Ile Asn Asp Thr His Pro Ala Trp Thr Lys Lys Pro Ala Asp Leu Lys
 225 230 235 240
 65 Asp Glu Asp Tyr Lys Glu Phe Tyr Arg Ser Leu Tyr Pro Met Ser Glu
 245 250 255
 Glu Pro Leu Phe Trp Ile His Leu Asn Val Asp Tyr Pro Phe Asn Leu
 260 265 270
 70 Thr Gly Ile Leu Tyr Phe Pro Lys Ile Lys Asn Asn Leu Asp Leu Gln
 275 280 285
 Arg Asn Lys Ile Gln Leu Tyr Cys Asn Gln Val Tyr Val Thr Asp Glu
 290 295 300
 Val Gln Gly Ile Val Pro Asp Phe Leu Thr Leu Leu His Gly Val Ile
 305 310 315 320
 75 Asp Ser Pro Asp Ile Pro Leu Asn Val Ser Arg Ser Tyr Leu Gln Ser

201/ 490

325 330 335
 Asp Ala Asn Val Lys Lys Ile Ser Ser His Ile Thr Lys Lys Val Ala
 340 345 350
 5 Asp Arg Leu Glu Glu Ile Phe Lys Asn Asp Arg Pro Thr Phe Glu Glu
 355 360 365
 Lys Trp Asp Ser Leu Lys Leu Phe Val Glu Tyr Gly Met Leu Thr Asp
 370 375 380
 Glu Lys Phe Tyr Glu Arg Ala Ala Lys Phe Phe Leu Phe Thr Asp Met
 385 390 395 400
 10 Asp Gly His Lys Tyr Thr Phe Asp Glu Tyr Arg Thr Leu Val Glu Gly
 405 410 415
 Val Gln Thr Asp Lys Asp Gly Gln Val Val Tyr Leu Tyr Ala Thr Asp
 420 425 430
 15 Lys His Gly Gln Tyr Ser His Val Lys Arg Ala Ser Asp Lys Gly Tyr
 435 440 445
 Ser Val Met Leu Leu Asp Gly Gln Leu Asp Pro His Ile Val Ser Leu
 450 455 460
 Leu Glu Gln Lys Leu Glu Lys Thr His Phe Val Arg Val Asp Ser Asp
 465 470 475 480
 20 Thr Ile Asn Asn Leu Ile Arg Lys Glu Glu Arg Ala Glu Val Lys Leu
 485 490 495
 Ser Asp Thr Glu Arg Ala Thr Leu Val Lys Leu Phe Glu Ala Arg Leu
 500 505 510
 25 Pro Arg Asp Glu Lys Lys His Phe Asn Val Ala Phe Glu Ser Leu Gly
 515 520 525
 Ala Glu Gly Glu Ala Ile Leu Ile Thr Gln Ala Glu Phe Met Arg Arg
 530 535 540
 Met Arg Asp Met Ala Gln Leu Gln Pro Gly Met Ser Phe Tyr Gly Glu
 545 550 555 560
 30 Leu Pro Asp Ser Tyr Asn Leu Val Leu Asn Thr Asp His Pro Leu Ile
 565 570 575
 Asp Arg Val Leu Ser Gly Glu Lys Glu Ser Val Glu Pro Ser Leu Thr
 580 585 590
 35 Glu Leu Arg Ala Lys Ile Ala Glu Leu Lys Ala Glu Glu Ala Lys Leu
 595 600 605
 Leu Asp Glu Glu Lys Gly Lys Lys Pro Glu Glu Ile Pro Val Ala Thr
 610 615 620
 Lys Glu Ala Lys Glu Asn Asn Ala Val Glu Gln Ala Lys Thr Glu Gly
 625 630 635 640
 40 Ser Ile Asn Asp Gln Leu Thr Lys Tyr Ala Gln Asp Asn Glu Leu Ile
 645 650 655
 Gly Gln Leu Ile Asp Leu Ala Leu Leu Gly Ser Gly Leu Leu Thr Gly
 660 665 670
 45 Glu Ala Leu Ala Glu Phe Ile Arg Arg Ser Gln Arg Leu Leu
 675 680 685

(2) INFORMATION FOR SEQ ID NO:284

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 482 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

 55 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 60 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...482
 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:284

Asp Ile Arg Gln Lys Arg Pro Cys Phe Asn Ala Asn Leu Tyr Phe Tyr
 1 5 10 15
 70 Arg Ala Met Glu Lys Leu Ile Asp Ile Leu Val Val Asp Asp Asp Val
 20 25 30
 Ala Val Cys Ala Ala Leu Arg Leu Val Leu Lys Arg Ala Gly Tyr Asn
 35 40 45
 Pro Val Ile Ala Asn Ser Pro Asp Glu Ala Leu Ser Ile Met Arg Asn
 50 55 60
 75 Pro Asp Gly Gly Cys Lys Pro Ala Val Ile Leu Met Asp Met Asn Phe

	65					70				75						80
	Ser	Leu	Ser	Thr	Ser	Gly	Arg	Glu	Gly	Leu	Glu	Leu	Leu	Glu	Lys	Met
					85					90					95	
5	Gln	Ile	Phe	Thr	Ser	Cys	Pro	Val	Ile	Leu	Met	Thr	Ala	Trp	Ala	Ser
				100					105					110		
	Ile	Pro	Leu	Ala	Val	Glu	Gly	Met	Arg	Leu	Gly	Ala	Phe	Asp	Phe	Ile
			115					120					125			
	Gly	Lys	Pro	Trp	Asp	Asn	Asp	Arg	Leu	Leu	Arg	Thr	Ile	Asp	Thr	Ala
		130				135						140				
10	Leu	His	Leu	Ala	Ala	Pro	Ser	Ala	Val	Ala	Asn	Pro	Ser	Glu	Gln	Ser
		145				150					155					160
	Asp	Arg	Asp	Thr	Ala	Arg	Gln	Pro	Lys	Ala	Thr	Val	Gln	Glu	Asn	Asp
				165						170					175	
15	Pro	Cys	Ala	His	Ile	Ile	Gly	Arg	Ser	Asp	Ala	Ile	Cys	Lys	Ile	Lys
				180					185					190		
	Glu	Arg	Ile	Arg	Arg	Ile	Ala	Pro	Thr	His	Ala	Ser	Val	Leu	Ile	Thr
			195					200					205			
	Gly	Glu	Ser	Gly	Thr	Gly	Lys	Glu	Leu	Ile	Ala	Glu	Ala	Leu	His	Arg
		210				215						220				
20	Gly	Ser	Lys	Arg	Ala	Ser	Ala	Pro	Phe	Val	Lys	Val	Asn	Leu	Gly	Gly
		225				230					235				240	
	Ile	Pro	Glu	Ser	Leu	Phe	Glu	Ser	Glu	Leu	Phe	Gly	His	Lys	Lys	Gly
				245					250					255		
25	Ala	Phe	Thr	Asn	Ala	Phe	Ser	Asp	Arg	Lys	Gly	Arg	Phe	Glu	Leu	Ala
			260						265					270		
	Asp	Gly	Gly	Thr	Ile	Phe	Leu	Asp	Glu	Ile	Gly	Glu	Leu	Pro	Val	Gly
			275					280					285			
	Asn	Gln	Val	Lys	Leu	Leu	Arg	Val	Leu	Gln	Glu	Gln	Thr	Phe	Glu	Pro
		290					295					300				
30	Leu	Gly	Glu	Ser	Val	Ser	His	Arg	Val	Asp	Ile	Arg	Val	Val	Ser	Ala
		305				310					315				320	
	Thr	Asn	Ala	Ser	Leu	Glu	Arg	Met	Val	Ala	Glu	Gly	Arg	Phe	Arg	Glu
				325						330					335	
35	Asp	Leu	Tyr	Tyr	Arg	Ile	Asn	Leu	Ile	His	Leu	His	Leu	Pro	Pro	Leu
			340						345					350		
	Arg	Glu	Arg	Gln	Glu	Asp	Ile	Gln	Leu	Leu	Val	Glu	Ala	Phe	Ser	Glu
			355					360					365			
	Ala	Phe	Ala	Gln	Ser	Asn	Gly	Leu	Pro	His	Ala	Val	Trp	Ser	Ala	Glu
		370					375					380				
40	Ala	Met	Arg	Arg	Ile	Cys	Ala	Met	Pro	Leu	Pro	Gly	Asn	Val	Arg	Glu
		385				390					395				400	
	Leu	Lys	Asn	Val												

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 263 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Porphyromonas gingivalis*

```
(ix) FEATURE:
      (A) NAME/KEY: misc_feature
      (B) LOCATION 1...263
```

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:285

Arg Ser Leu Gln Ser Phe Gln Asn Lys Lys His Ser Ser Met Leu Lys

[illegible]

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35      (2) INFORMATION FOR SEQ ID NO:286

          (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 462 amino acids
              (B) TYPE: amino acid
              (D) TOPOLOGY: linear

          (ii) MOLECULE TYPE: protein

          (iii) HYPOTHETICAL: YES

45      (vi) ORIGINAL SOURCE:
              (A) ORGANISM: Porphyromonas gingivalis

          (ix) FEATURE:
              (A) NAME/KEY: misc_feature
              (B) LOCATION 1...462

50      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:286

```

55	Ser Met Ala Lys Glu Lys Thr Ile Tyr Val Cys Arg Ser Cys Gly Thr 1 5 10 15	Lys Tyr Ala Lys Trp Gln Gly Asn Cys Asn Ala Cys Gly Glu Trp Asn 20 25 30
	Cys Ile Asp Glu Glu Lys Val Pro Ala Pro Ala Ser Gly Lys His Ala 35 40 45	Ala Lys Ser Phe Met Pro Arg Glu Gln Asp Asn Arg Pro Arg Leu Leu 50 55 60
60	Gln Asp Val Glu Ser Gly Asp Glu Glu Arg Ile Arg Leu Gly Asp Glu 65 70 75	Glu Phe Asp Arg Val Leu Gly Gly Gly Ile Val Lys Gly Ala Phe Val 80 85 90 95
	Leu Leu Gly Gly Glu Pro Gly Ile Gly Lys Ser Thr Leu Ile Leu Gln 100 105 110	Thr Val Leu Arg Leu Pro Gln Leu Arg Thr Leu Tyr Val Ser Gly Glu 115 120 125
70	Glu Ser Ala Arg Gln Leu Lys Met Arg Ala Glu Arg Leu Gly Gln Ala 130 135 140	Ile Asn Gly Cys Tyr Val Tyr Cys Glu Thr Asn Ile Glu Arg Ile Leu 145 150 155
	Ser Arg Ala Glu Glu Leu Thr Pro Asp Leu Leu Val Ile Asp Ser Ile 160 165 170	
75		

204/ 490

165 170 175
Gln Thr Val Tyr Thr Glu Glu Met Glu Ser Ser Ala Gly Ser Val Gly
180 185 190
5 Gln Ile Arg Glu Cys Ala Ala Leu Leu Leu Lys Tyr Cys Lys Thr Thr
195 200 205
Gly Ile Pro Val Ile Val Ile Gly His Ile Thr Lys Glu Gly Ser Ile
210 215 220
Ala Gly Pro Lys Val Leu Glu His Ile Val Asp Thr Val Leu Leu Phe
225 230 235 240
10 Asp Gly Asp Lys His His Leu Tyr Arg Ile Leu Arg Gly Gln Lys Asn
245 250 255
Arg Tyr Gly Ser Thr Ser Glu Leu Gly Ile Tyr Glu Met Arg Gln Asp
260 265 270
15 Gly Leu Arg Gly Val Glu Asn Pro Ser Glu His Leu Ile Thr Arg Asn
275 280 285
Arg Glu Asp Leu Ser Gly Ile Ala Ile Ala Val Ala Met Glu Gly Ile
290 295 300
Arg Pro Ile Leu Ile Glu Ala Gln Ala Leu Val Ser Ser Ala Ile Tyr
305 310 315 320
20 Ala Asn Pro Gln Arg Ser Ala Thr Gly Phe Asp Ile Arg Arg Met Asn
325 330 335
Met Leu Leu Ala Val Leu Glu Lys Arg Ala Gly Phe Lys Leu Ile Gln
340 345 350
25 Lys Asp Val Phe Leu Asn Ile Ala Gly Gly Ile Lys Ile Ala Asp Pro
355 360 365
Ala Thr Asp Leu Ala Val Ile Ser Ala Val Leu Ala Ser Ser Leu Asp
370 375 380
Ile Val Ile Pro Pro Ala Val Cys Met Thr Gly Glu Val Gly Leu Ser
385 390 395 400
30 Gly Glu Ile Arg Pro Val Ser Arg Ile Glu Gln Arg Ile Thr Glu Ala
405 410 415
Arg Arg Ile Gly Phe Lys Glu Ile Leu Val Pro Ala Asp Asn Phe Arg
420 425 430
35 Gln Glu Asp Ala Gly Arg Phe Gly Ile Arg Leu Val Pro Val Arg Lys
435 440 445
Val Glu Glu Ala Phe Arg His Leu Phe Ser Lys Gly Arg Glu
450 455 460

(2) INFORMATION FOR SEQ ID NO:287

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 373 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287

60 Gly Ser Cys Gly Ser Ser Pro Ala Ile Gly Arg Ser Gly Cys Ser Arg
1 5 10 15
Cys Asp Arg Arg Ile Gly His Gly Leu Ser Thr Ser Ala Phe Arg Thr
20 25 30
Tyr Ala Gly Leu Val Cys His Ser Arg Leu Arg Asp Gln Ser Ser Cys
35 40 45
65 Arg Val Cys Gly Met Arg Pro Ile Gly Gln Leu Phe Phe Pro Ser Cys
50 55 60
Pro Arg Arg Ser Ala Ser Asp Ala Gly Arg Thr Glu Arg Ile Gln Ser
65 70 75 80
70 Pro Leu Gln Asn Leu Leu Gln Glu Met Gln Phe Ser Pro Thr Asn Arg
85 90 95
Arg Asn Pro Phe Asp Asn Met Asn Ser Arg His Leu Thr Ile Thr Ile
100 105 110
Ile Ala Gly Leu Ser Leu Phe Val Leu Thr Leu Gly Gly Cys Ser Val
115 120 125
75 Ala Gln Gln Asp Thr Gln Trp Thr Leu Gly Gly Lys Leu Phe Thr Ser

205 / 490

130 135 140
 Ala Trp Ile Gln Arg Ser Ala Glu Tyr Gln Ala Leu Cys Ile Gln Ala
 145 150 155 160
 Tyr Asn Ile Ala Thr Glu Arg Val Asp Ala Leu Pro Ala Glu Arg Lys
 165 170 175
 Gln Gly Asp Arg Pro Tyr Ala Ile Val Thr Asp Ile Asp Glu Thr Ile
 180 185 190
 Leu Asp Asn Thr Pro Asn Ser Val Tyr Gln Ala Leu Arg Gly Lys Asp
 195 200 205
 10 Tyr Asp Glu Glu Thr Trp Gly Lys Trp Cys Ala Gln Ala Asp Ala Asp
 210 215 220
 Thr Leu Ala Gly Ala Leu Ser Phe Phe Leu His Ala Ala Asn Lys Gly
 225 230 235 240
 Ile Glu Val Phe Tyr Val Thr Asn Arg Arg Asp Asn Leu Arg Glu Ala
 245 250 255
 15 Thr Leu Gln Asn Leu Gln Arg Tyr Gly Phe Pro Phe Ala Asp Glu Glu
 260 265 270
 His Leu Leu Thr Thr His Gly Pro Ser Asp Lys Glu Pro Arg Arg Leu
 275 280 285
 20 Lys Ile Gln Glu Gln Tyr Glu Ile Val Leu Leu Ile Gly Asp Asn Leu
 290 295 300
 Gly Asp Phe His His Phe Phe Asn Thr Lys Glu Glu Ser Gly Arg Lys
 305 310 315 320
 Gln Ala Leu Gly Leu Thr Ala Gly Glu Phe Gly Arg His Phe Ile Met
 325 330 335
 25 Leu Pro Asn Pro Asn Tyr Gly Ser Trp Glu Pro Ala Trp Tyr Gly Gly
 340 345 350
 Lys Tyr Pro Pro Leu Pro Glu Arg Asp Lys Ala Leu Lys Gln Leu His
 355 360 365
 30 Ser Gln Asn Ser Arg
 370

(2) INFORMATION FOR SEQ ID NO:288

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 426 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 40 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 45 (iv) ORIGINAL SOURCE:
 (A) ORGANISM: *Porphyromonas gingivalis*
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (D) LOCATION 1...426
 50 (xii) SEQUENCE DESCRIPTION: SEQ ID NO:288

Arg Trp Gly Phe Ser Asn Phe Val Ala Met Ser Thr Asn Ile Asp Val
 1 5 10 15
 55 Gln Gln Ile Lys Gln Arg Phe Gly Ile Ile Gly Ser Ser Pro Leu Met
 20 25 30
 Glu His Ala Ile Arg Val Ala Ala Gln Val Ala Pro Thr Asp Met Ser
 35 40 45
 60 Val Leu Val Thr Gly Glu Ser Gly Ser Gly Lys Glu Phe Phe Pro Gln
 50 55 60
 Ile Ile His Tyr Tyr Ser Ala Arg Lys His His Ser Tyr Ile Ala Val
 65 70 75 80
 Asn Cys Gly Ala Ile Pro Glu Gly Thr Ile Asp Ser Glu Leu Phe Gly
 85 90 95
 65 His Arg Lys Gly Ser Phe Thr Gly Ala Val Ser Asp Arg Lys Gly Tyr
 100 105 110
 Phe Glu Glu Ala Ser Gly Gly Thr Ile Phe Leu Asp Glu Val Gly Glu
 115 120 125
 70 Leu Pro Leu Pro Thr Gln Ala Arg Leu Leu Arg Val Leu Glu Thr Gly
 130 135 140
 Glu Phe Ile Pro Val Gly Ala Ser Gln Ser Gln Lys Thr Asp Val Arg
 145 150 155 160
 Ile Val Ala Ala Thr Asn Val Asn Leu Lys Glu Ala Val Ala Asn Gly
 165 170 175
 75 Lys Phe Arg Glu Asp Leu Phe Phe Arg Leu Asn Thr Val Pro Ile Glu

206/ 490

180 185 190
 Val Pro Ala Leu Arg Met Arg Pro Asp Asp Val Pro Leu Leu Phe Arg
 195 200 205
 Arg Phe Ala Ala Asp Ser Ala Glu Lys Tyr Arg Met Pro Pro Leu Arg
 210 215 220
 Leu Ser Asp Glu Ala Arg Thr Ile Leu Met Arg Tyr Arg Trp Pro Gly
 225 230 235 240
 Asn Val Arg Glu Leu Arg Asn Ile Thr Asp Arg Leu Ser Ile Leu Glu
 245 250 255
 10 Glu Glu Arg Thr Val Ser Ala Glu Thr Ile Thr Arg Tyr Leu Asp Ala
 260 265 270
 Glu Gly Met Gln Asp Leu His Pro Val Val Ile Arg Arg Asn Glu Thr
 275 280 285
 15 Thr Glu Ala Asp Lys Gln Ile Pro His Tyr Glu Arg Glu Ile Ile Tyr
 290 295 300
 Gln Val Leu Tyr Asp Met Lys Lys Glu Ile Ala Asp Leu Lys Gly Met
 305 310 315 320
 Met Asn Arg Leu Ala His His Glu Gln Pro Ser Trp Pro Val Gly Ser
 325 330 335
 20 Asp Val Trp Gly Asn Asp Asp Lys Arg Thr Ala Asp Pro Lys Trp Gly
 340 345 350
 Val Ser Thr His Lys Ala Pro Ile Ala Asn Ala Ala Glu Pro Val Glu
 355 360 365
 25 Pro Ile Gln Glu Ala Ser Glu Tyr Thr Glu Asp Pro Val Ser Leu Glu
 370 375 380
 Glu Val Glu Lys Lys Met Ile Ser Leu Ala Leu Glu Arg His Gly Gly
 385 390 395 400
 Arg Arg Lys Gln Thr Ala Glu Glu Leu Lys Ile Ser Glu Arg Thr Leu
 405 410 415
 30 Tyr Arg Lys Ile Lys Glu Tyr Gly Leu Glu
 420 425

(2) INFORMATION FOR SEQ ID NO:289

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 653 amino acids
 (B) TYPE: amino acid
 (C) TOPOLOGY: linear
 40 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 45 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1...653
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:289

Lys Asn Leu Pro Arg Tyr Ala Pro Ala Phe Gly Arg Asn Arg Lys Arg
 1 5 10 15
 55 Glu Gln Pro Asp Pro Asp Asn Asp Asp Ser Arg Gly Arg Ser His Arg
 20 25 30
 Gln Ser Gly Arg Ala Val Thr Val Val Cys Arg Arg Ile Gln Thr Pro
 35 40 45
 60 Leu Pro His Met Ile Leu Leu Phe Gly Gly Thr Thr Glu Gly Arg Ala
 50 55 60
 Ala Ala Arg Val Leu Asp Glu Ala Gly Ser Pro Phe Phe Tyr Ser Thr
 65 70 75 80
 Lys Gly Asn Leu Gln Glu Ile Gln Ser Ser His Gly His Arg Leu Thr
 85 90 95
 65 Gly Ala Met Thr Val Ala Asp Met Val Ser Phe Cys Arg Lys Glu Glu
 100 105 110
 Ile Arg Leu Ile Val Asp Ala Ala His Pro Phe Ala Glu Glu Leu His
 115 120 125
 70 Ala Ser Val Ala Glu Ala Ser Glu Gln Thr Gly Ile Pro Val Val Arg
 130 135 140
 Tyr Glu Arg Gln Tyr Pro Pro Arg Glu Glu Gly Ile Val Trp Cys Ala
 145 150 155 160
 Asn Tyr Asp Thr Ala Ala Glu Arg Met Leu Gly Asp Gly Val Gln Arg
 165 170 175
 75 Leu Leu Met Leu Thr Gly Val Asn Thr Ile Pro Lys Leu Ala Ala Phe

207/ 490

180 185 190
 Trp Lys Glu Arg Thr Thr Phe Cys Arg Ile Leu Lys Arg Asp Glu Ser
 195 200 205
 5 Val Ala Leu Ala Glu Lys Asn Gly Phe Pro Ala Glu Arg Ile Val Phe
 210 215 220
 Phe Glu Pro His Ala Asp Glu Leu Met Gln Ala Val Arg Pro Asp
 225 230 235 240
 Ala Ile Ile Thr Lys Glu Ser Gly Glu Ser Gly Tyr Phe Arg Glu Lys
 245 250 255
 10 Ile Glu Ala Ala Arg Arg Met Gly Ile Arg Ile Tyr Ala Val Arg
 260 265 270
 Pro Pro Leu Pro Pro Ser Phe Ile Pro Val Gly Gly Pro Val Gly Leu
 275 280 285
 15 Arg Arg Ala Val Glu Arg Leu Val Pro Gly Phe Phe Ser Leu Arg Ser
 290 295 300
 Gly Phe Thr Thr Gly Thr Thr Ala Thr Ala Val Val Ala Ala Met
 305 310 315 320
 Tyr Arg Leu Met Gly Leu Gly Ser Leu Ala Glu Ala Pro Val Glu Leu
 325 330 335
 20 Pro Ser Gly Glu Ile Val Ser Leu Pro Ile Ala Glu Ile Arg Glu Glu
 340 345 350
 Glu Asp Ala Val Val Ser Ala Val Leu Lys Asp Ala Gly Asp Asp Pro
 355 360 365
 25 Asp Val Thr Asn Gly Met Ala Val Cys Ala Thr Ile Arg Leu Asn Pro
 370 375 380
 Glu His Glu Glu Val Arg Phe Leu Gln Gly Glu Gly Val Gly Val Val
 385 390 395 400
 Thr Leu Pro Gly Leu Gly Leu Glu Val Gly Gly Pro Ala Ile Asn Leu
 405 410 415
 30 Val Pro Arg Arg Met Met Thr Ala Glu Val Arg Arg Leu Tyr Ala Gln
 420 425 430
 Gly Gly Val Asp Ile Thr Ile Ser Val Pro Glu Gly Arg Glu Ala Ala
 435 440 445
 35 Thr Gln Thr Phe Asn Pro Arg Leu Gly Ile Arg Asp Gly Ile Ser Ile
 450 455 460
 Ile Gly Thr Ser Gly Val Val Lys Pro Phe Ser Ala Glu Ala Phe Val
 465 470 475 480
 Gly Ala Ile Arg Lys Gln Val Gly Ile Ala Thr Ala Leu Gly Ala Asn
 485 490 495
 40 His Ile Val Leu Asn Ser Gly Ala Lys Ser Glu Arg Tyr Val Lys Gly
 500 505 510
 Ala Tyr Pro Ala Leu Ile Pro Gln Ala Phe Val Gln Tyr Gly Asn Phe
 515 520 525
 45 Val Gly Glu Ser Leu Ser Cys Val Ala Ser Phe Pro Ser Val Arg Ser
 530 535 540
 Val Thr Val Gly Ile Met Leu Gly Lys Ala Val Lys Leu Ala Glu Gly
 545 550 555 560
 Tyr Leu Asp Thr His Ser Lys Lys Val Val Met Asn Arg Asp Phe Leu
 565 570 575
 50 His Glu Leu Ala Arg Gln Ala Gly Cys Ser Glu Asp Ile His Ala Ile
 580 585 590
 Ile Asp Ser Leu Asn Leu Ala Arg Glu Leu Trp Thr Met Pro Ser Ala
 595 600 605
 55 Glu Asp Ser Asp Arg Leu Leu Arg Lys Ile Ala Glu Arg Ser Trp Glu
 610 615 620
 Thr Cys Arg Pro Ser Val Pro Ser Ala Glu Leu Glu Leu Leu Ile
 625 630 635 640
 Asp Glu Ser Gly Ala Ile Arg Phe Arg Ile Gly Gly Glu
 645 650

(2) INFORMATION FOR SEQ ID NO:290

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 451 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

208/490

(A) NAME/KEY: misc_feature
(B) LOCATION 1...451

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:290

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Gln Gln Arg Pro His Arg Ile Ile Met Leu Arg Thr Phe Arg Ile Gly
1 5 10 15
Gly Ile His Pro Pro Glu Asn Lys Leu Ser Ala Gly Lys Pro Val Glu
20 25 30
Val Leu Pro Ile Pro Ser Gln Val Val Ile Pro Leu Gly Gln His Ile
35 40 45
Gly Ala Pro Ala Thr Ala Thr Val Lys Lys Gly Asp Glu Val Lys Val
50 55 60
Gly Thr Ile Ile Ala Gln Ala Gly Gly Phe Val Ser Ala Asn Ile His
65 70 75 80
Ser Ser Val Ser Gly Lys Val Leu Lys Ile Asp Asn Val Tyr Asp Ser
85 90 95
Ser Gly Tyr Pro Lys Pro Ala Val Phe Ile Ser Val Glu Gly Asp Glu
100 105 110
Trp Glu Glu Gly Ile Asp Arg Ser Pro Ala Ile Val Lys Glu Cys Asn
115 120 125
Leu Asp Ala Lys Glu Ile Val Ala Lys Ile Ser Ala Ala Gly Ile Val
130 135 140
Gly Leu Gly Gly Ala Thr Phe Pro Thr His Val Lys Leu Ser Pro Pro
145 150 155 160
Pro Gly Asn Lys Ala Glu Ile Leu Ile Ile Asn Ala Val Glu Cys Glu
165 170 175 180
Pro Tyr Leu Thr Ser Asp His Val Leu Met Leu Glu His Gly Glu Glu
185 190 195
Ile Met Ile Gly Val Ser Ile Leu Met Lys Ala Ile Gln Val Asn Lys
200 205 210
Ala Val Ile Gly Val Glu Asn Asn Lys Lys Asp Ala Ile Ala His Leu
215 220 225
Thr Lys Leu Ala Thr Ala Tyr Pro Gly Ile Glu Val Met Pro Leu Lys
230 235 240
Val Gln Tyr Pro Gln Gly Gly Glu Lys Gln Leu Ile Asp Ala Val Ile
245 250 255
Arg Lys Gln Val Lys Ser Gly Ala Leu Pro Ile Ser Thr Gly Ala Val
260 265 270 275
Val Gln Asn Val Gly Thr Val Phe Ala Val Tyr Glu Ala Val Gln Lys
280 285 290
Asn Lys Pro Leu Val Glu Arg Ile Val Thr Val Thr Gly Lys Lys Leu
295 300 305
Ser Arg Pro Ser Asn Leu Leu Val Arg Ile Gly Thr Pro Ile Ala Ala
310 315 320
Leu Ile Glu Ala Ala Gly Gly Leu Pro Glu Asn Thr Gly Lys Ile Ile
325 330 335
Gly Gly Gly Pro Met Met Gly Arg Ala Leu Leu Ser Pro Asp Val Pro
340 345 350 355
Val Thr Lys Gly Ser Ser Gly Val Leu Ile Leu Asp Arg Glu Glu Ala
360 365 370
Val Arg Lys Pro Met Arg Asp Cys Ile Arg Cys Ala Lys Cys Val Gly
375 380 385
Val Cys Pro Met Gly Leu Asn Pro Ala Phe Leu Met Arg Asp Thr Leu
390 395 400
Tyr Lys Ser Trp Glu Thr Ala Glu Lys Gly Asn Val Val Asp Cys Ile
405 410 415
Glu Cys Gly Ser Cys Ser Phe Thr Cys Pro Ala Asn Arg Pro Leu Leu
420 425 430
Asp Tyr Ile Arg Gln Ala Lys Lys Thr Val Met Gly Ile Gln Arg Ala
435 440 445
Arg Lys Gln
450

(2) INFORMATION FOR SEQ ID NO:291

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 489 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

WO 99/29870

PCT/AU98/01023

210/ 490

(A) LENGTH: 384 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

- 5 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
10 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION: 1...384
15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:292

20 Asp Met Ala Glu Lys Arg Asp Tyr Tyr Glu Val Leu Gly Val Ser Lys
1 5 10 15
Asn Ala Thr Asp Asp Glu Leu Lys Lys Ala Tyr Arg Lys Lys Ala Ile
20 25 30
Gln Tyr His Pro Asp Lys Asn Pro Gly Asp Lys Glu Ala Glu Glu His
35 40 45
Phe Lys Glu Val Ala Glu Ala Tyr Asp Val Leu Ser Asp Pro Gln Lys
25 50 55 60
Arg Ser Gln Tyr Asp Gln Phe Gly His Ala Gly Leu Gly Gly Ala Ala
65 70 75 80
Gly Gly Gly Phe Ser Gly Gly Gly Met Ser Met Glu Asp Ile Phe Ser
85 90 95
30 Arg Phe Gly Asp Leu Phe Gly Gly Phe Gly Gly Phe Gly Gly Phe Ser
100 105 110
Asp Met Gly Gly Gly Ser Arg Arg Arg Val Arg Arg Gly Ser Asp Leu
115 120 125
35 Arg Val Arg Val Lys Leu Ser Leu Ala Asp Ile Ser Lys Gly Val Glu
130 135 140
Lys Lys Val Lys Val Lys Lys Gln Val Val Cys Ser Lys Cys Arg Gly
145 150 155 160
Asp Gly Thr Glu Glu Ala Asn Gly Lys Thr Thr Cys Gln Thr Cys His
165 170 175
40 Gly Thr Gly Val Val Thr Arg Val Ser Asn Thr Phe Leu Gly Ala Met
180 185 190
Gln Thr Gln Ser Thr Cys Pro Thr Cys His Gly Glu Gly Glu Ile Ile
195 200 205
45 Thr Lys Pro Cys Ser Lys Cys Lys Gly Glu Gly Val Glu Ile Gly Glu
210 215 220
Glu Val Ile Ser Phe His Ile Pro Ala Gly Val Ala Glu Gly Met Gln
225 230 235 240
Met Ser Val Asn Gly Lys Gly Asn Ala Ala Pro Arg Gly Gly Val Asn
245 250 255
50 Gly Asp Leu Ile Val Val Ile Ala Glu Glu Pro Asp Pro Asn Leu Ile
260 265 270
Arg Asn Gly Asn Asp Leu Ile Tyr Asn Leu Leu Ile Ser Val Pro Leu
275 280 285
55 Ala Ile Lys Gly Gly Ser Val Glu Val Pro Thr Ile Asp Gly Arg Ala
290 295 300
Lys Ile Arg Ile Glu Ala Gly Thr Gln Pro Gly Lys Met Leu Arg Leu
305 310 315 320
Arg Asn Lys Gly Leu Pro Ser Val Asn Gly Tyr Gly Met Gly Asp Gln
325 330 335
60 Leu Val Asn Val Asn Val Tyr Ile Pro Glu Ser Ile Asp Ala Lys Asp
340 345 350
Glu Gln Ala Ile Ala Ala Met Glu Asn Ser Asp Ser Phe Lys Pro Thr
355 360 365
65 Asp Ala Ala Arg Lys Asp Ile Asp Lys Lys Tyr Arg Glu Met Leu Asp
370 375 380

- (2) INFORMATION FOR SEQ ID NO:293
70 (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
75 (ii) MOLECULE TYPE: protein

WO 99/29870

PCT/AU98/01023

211/ 490

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293

Arg Phe Asp Ser Thr Thr Asn Val Ser Gln Ile Asn Leu Arg Thr Glu
1 5 10 15
Met Lys Lys Leu Ile Leu Ala Thr Leu Gly Leu Met Ala Ile Ala Met
20 25 30
Leu Ser Cys Ser Ser Asn Asn Lys Asp Leu Glu Asn Lys Gly Glu Ala
35 40 45
Thr Leu Leu Val Thr Phe Gly Ser Ser Tyr Lys Ala Pro Arg Glu Thr
50 55 60
Tyr Ala Lys Ile Glu Lys Thr Phe Ala Ala Tyr Pro Asp Gln Arg
65 70 75 80
Ile Ser Trp Thr Tyr Thr Ser Ser Ile Ile Arg Lys Lys Leu Ala Gln
85 90 95
Gln Gly Ile Tyr Ile Asp Ala Pro Asp Glu Ala Leu Glu Lys Leu Ala
100 105 110
Arg Leu Gly Tyr Lys Lys Ile Asn Val Gln Ser Leu His Val Ile Pro
115 120 125
Gly Arg Glu Tyr Asp Glu Met Ile Asp Phe Val Asn Lys Phe Lys Ala
130 135 140
Ala His Ser Asp Ile Thr Val Lys Val Gly Ala Pro Leu Phe Asp Thr
145 150 155 160
Asp Glu Asp Met Arg Glu Val Ala Glu Ile Leu His Lys Arg Phe Gln
165 170 175
Gln Thr Ile Glu Lys Gly Glu Ala Ile Val Phe Met Gly His Gly Thr
180 185 190
Glu His Ala Ala Asn Asp Arg Tyr Ala Arg Ile Asn Lys Ile Met Lys
195 200 205
Asn Tyr Ser Lys Phe Met Ile Val Gly Thr Val Glu Ser Asp Pro Ser
210 215 220
Ile Asn Asp Val Ile Ala Glu Leu Lys Glu Thr Gly Ala Thr Ala Val
225 230 235 240
Thr Met Met Pro Leu Met Ser Val Ala Gly Asp His Ala Thr Asn Asp
245 250 255
Met Ala Gly Asp Glu Asp Asp Ser Trp Lys Thr Leu Leu Thr Asn Ala
260 265 270
Gly Tyr Thr Val Ser Ile Asp Lys Leu Asp Asn Gly Asn Phe Ser Ala
275 280 285
Leu Gly Asp Ile Glu Glu Ile Arg Asn Ile Trp Leu Lys His Met Lys
290 295 300
Ala Thr Ser Ala Arg
305

(2) INFORMATION FOR SEQ ID NO:294

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 491 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294

Arg Arg Asp Ala Arg Arg Gln Leu Val Arg Arg Arg Arg Lys Glu Leu
1 5 10 15
Ser Gly Thr Ala Asn Thr Arg Cys Arg Arg Arg Val Phe Pro Glu Arg

WO 99/29870

PCT/AU98/01023

212/ 490

20 25 30
 Arg Ser Ala Ile Arg Trp Cys Phe Pro Arg Leu Arg Asp Gly Leu Gln
 35 40 45
 5 Pro Ile Arg Phe Gly Ser Leu Leu Ala Asn Pro Gln Gln Leu Ser Arg
 50 55 60
 Gly Val Arg Leu Arg Ser Phe Glu Ser Arg Arg Gln Pro Ile Cys Arg
 65 70 75 80
 Phe Gln Gly Ile Gln Gly Lys Arg Arg Asp Ile Leu Gln Pro Glu Gly
 85 90 95
 10 Asn Ser Leu Leu Arg Thr His Ala His Ala Ser Arg Leu Gly Ala Gly
 100 105 110
 Arg Ser Tyr Arg Tyr Leu Ala Pro Arg Thr Thr Ser Arg Pro Pro Thr
 115 120 125
 15 Ala Phe Leu Leu Phe Ala Pro Met Thr Ser Val Ser His Leu Arg Thr
 130 135 140
 Ile Ser Val Ala Gly Ile Leu Ala Ala Leu Gly Ala Val Leu Ile
 145 150 155 160
 Leu Phe Gly Val Asn Leu Phe Leu Gly Ser Val Ala Ile Pro Met Ser
 165 170 175
 20 Glu Ile Phe Arg His Leu Phe Ser Asp Arg Pro Glu Gly Gly Glu Ala
 180 185 190
 Leu Val His Tyr Asn Ile Leu Trp Lys Ser Arg Leu Pro Glu Ala Leu
 195 200 205
 Thr Ala Ala Phe Ala Gly Ala Gly Leu Ser Val Ser Gly Leu Gln Met
 210 215 220
 25 Gln Thr Val Phe Arg Asn Pro Leu Ala Gly Pro Ser Val Leu Gly Ile
 225 230 235 240
 Ser Ser Gly Ala Ser Leu Gly Val Ala Leu Val Val Leu Leu Ser Gly
 245 250 255
 30 Ser Leu Gly Gly Val Ala Leu Ser Ser Leu Gly Tyr Met Gly Glu Val
 260 265 270
 Ala Met Asn Ile Ala Ala Ala Val Gly Ser Leu Ala Val Met Gly Leu
 275 280 285
 35 Ile Val Phe Val Ser Thr Lys Val Arg Ser His Val Thr Leu Leu Ile
 290 295 300
 Ile Gly Val Met Ile Gly Tyr Val Ala Thr Ala Val Ile Gly Val Phe
 305 310 315 320
 Lys Phe Phe Ser Ile Glu Glu Asp Ile Arg Ala Tyr Val Ile Trp Gly
 325 330 335
 40 Leu Gly Ser Phe Ser Arg Ala Thr Asp Ser Gln Leu Ser Phe Phe Ala
 340 345 350
 Ile Leu Met Leu Ile Phe Ile Pro Ala Gly Met Leu Leu Val Lys Gln
 355 360 365
 45 Leu Asn Leu Leu Leu Gly Glu Ser Tyr Ala Arg Asn Leu Gly Leu
 370 375 380
 Asn Thr Arg Arg Ala Arg Leu Leu Val Ile Ser Ser Ala Gly Leu Leu
 385 390 395 400
 Ile Ala Thr Val Thr Ala Tyr Cys Gly Pro Ile Gly Phe Leu Gly Met
 405 410 415
 50 Ala Val Pro His Leu Ala Arg Val Ile Phe His Thr Ser Asp His Arg
 420 425 430
 Ile Leu Met Pro Ala Thr Cys Leu Ile Gly Ser Ala Leu Ala Leu Phe
 435 440 445
 55 Cys Asn Ile Ile Ala Arg Met Pro Gly Phe Glu Gly Ala Leu Pro Val
 450 455 460
 Asn Ser Val Thr Ala Leu Val Gly Ala Pro Ile Ile Val Thr Val Leu
 465 470 475 480
 Phe Arg Arg Arg Arg Phe Lys Glu Glu Thr Asp
 485 490

(2) INFORMATION FOR SEQ ID NO:295

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 763 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

WO 99/29870

PCT/AU98/01023

214/ 490

Pro Gln Met Ser Asp Tyr Tyr Ala Leu Gly Leu Glu Tyr Asn Gln Gly
565 570 575
Pro Ile Ser Phe Ser Ala Thr Val Tyr Asp Asn Glu Leu Arg Asn Leu
580 585 590
5 Ile Ser Phe Met Asp Ile Pro Thr Ser Pro Glu His Glu Ala Gln Gly
595 600 605
Ile Lys Lys Thr Lys Gln Tyr Ala Asn Ile Gly Lys Ala Arg Ser Arg
610 615 620
10 Gly Leu Asp Val Leu Cys Asp Ala Ser Ile Gly Trp Gly Ile Lys Leu
625 630 635 640
Gly Ala Gly Tyr Ser Leu Val Glu Ala Lys Asn Leu Gln Thr Asp Glu
645 650 655
Trp Leu Glu Gly Ala Ala Arg His Arg Ala Asn Val His Ala Asp Trp
660 665 670
15 Val His Tyr Trp Gly Gln Tyr Arg Leu Gly Val Ser Leu Phe Gly Arg
675 680 685
Ile Gln Ser Glu Arg Tyr Tyr Lys Asp Gly Asn Ala Pro Asp Tyr Thr
690 695 700
20 Leu Trp Arg Leu Ala Thr Ser His Arg Phe Ala His Phe Arg His Ile
705 710 715 720
Ile Leu Asp Gly Thr Leu Gly Ile Asp Asn Leu Phe Asp Tyr Val Asp
725 730 735
Asp Arg Pro Met Gly Val Asn Tyr Ala Thr Val Thr Pro Gly Arg Thr
740 745 750
25 Phe Phe Ala Gln Ile Ala Ile Arg Phe Asn Asn
755 760

(2) INFORMATION FOR SEQ ID NO:296

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 365 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
35 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
40 (A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...365
45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:296

Cys Cys Ala Arg Leu Arg Asp Thr Ser Pro Arg Lys Lys Ser Phe Arg
1 5 10 15
50 Asn Asp Thr Val Phe Pro Tyr Phe Val Ile His Leu Ile Lys His Ile
20 25 30
Ile Ile Met Thr Asp Asn Lys Gln Arg Asn Ile Val Phe Pro Ala Phe
35 40 45
55 Leu Leu Leu Leu Gly Val Ile Ala Val Val Thr Ile Val Gly Phe Phe
50 55 60
Met Leu Arg Pro Ala Glu Ile Ile Gln Gly Gln Ile Glu Val Thr
65 70 75 80
Glu Tyr Arg Val Ser Ser Lys Val Pro Gly Arg Ile Lys Glu Leu Arg
85 90 95
60 Val Ser Glu Gly Gln Gln Val Gln Ala Gly Asp Thr Leu Ala Val Ile
100 105 110
Glu Ala Pro Asp Val Ala Ala Lys Met Glu Gln Ala Lys Ala Ala Glu
115 120 125
Ala Ala Ala Gln Ala Gln Asn Ala Lys Ala Leu Lys Gly Ala Arg Ser
130 135 140
65 Glu Gln Ile Gln Ala Ala Tyr Glu Met Trp Gln Lys Ala Gln Ala Gly
145 150 155 160
Val Ala Ile Ala Thr Lys Thr His Gln Arg Val Gln Asn Leu Tyr Asp
165 170 175
70 Gln Gly Val Val Pro Ala Gln Lys Leu Asp Glu Ala Thr Ala Gln Arg
180 185 190
Asp Ala Ala Ile Ala Thr Gln Lys Ala Ala Glu Ala Gln Tyr Asn Met
195 200 205
75 Ala Arg Asn Gly Ala Glu Arg Glu Asp Lys Leu Ala Ala Ser Ala Leu
210 215 220

216/490

Ile Asn Gln Asn Asn Val Asn Val Trp Leu Ser Val Thr Ser Thr
 290 295 300
 Leu Val Ser Ile Ser Thr Leu Thr Ile Thr Ile Ile Asp Lys Thr Lys
 305 310 315 320

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(2) INFORMATION FOR SEQ ID NO:298

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 502 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

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(ix) FEATURE:

(A) NAME/KEY: misc feature
 (B) LOCATION 1...502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298

25

Ser Lys Ile Val Leu Arg Lys Phe Cys Thr Leu Ala Arg Met Lys Lys
 1 5 10 15
 Thr Asn Leu Phe Leu Ser Leu Leu Val Ile Phe Ile Thr Gly Ser Phe
 20 25 30
 Met Thr Ala Cys Ala Gln Lys Ser Lys Thr Asn Lys Leu Thr Glu Glu
 35 40 45
 Asp Arg Ser Arg Asn Glu Tyr Val Gln Ser Met Asp Val Leu Ser Asn
 50 55 60
 Ile Ile Gly Asn Val Arg Leu Tyr Phe Val Asp Thr Ile Ser Ile Lys
 65 70 75 80
 His Met Thr Arg Arg Gly Ile Asp Ala Met Leu Gly Gly Leu Asp Pro
 85 90 95
 Tyr Thr Glu Tyr Ile Pro Tyr Glu Glu Met Asp Glu Leu Lys Leu Met
 100 105 110
 Thr Thr Gly Glu Tyr Ala Gly Val Gly Ala Ile Ile Ser Gln Arg Pro
 115 120 125
 Asp Ser Ala Val Ile Ile Gln Arg Pro Met Glu Gly Met Pro Ala Asp
 130 135 140
 Glu Ala Gly Leu Ile Ala Gly Asp Arg Ile Leu Thr Ile Asp Gly Lys
 145 150 155 160
 Asp Phe Arg Lys Ser Thr Thr Pro Lys Val Ser Gln Ala Leu Lys Gly
 165 170 175
 Ile Ala Gly Thr Val Ala Lys Val Thr Val Met Arg Tyr Gly Glu Thr
 180 185 190
 Lys Pro Arg Thr Phe Ser Val Lys Arg Gln Lys Val Ile Met Asn Ser
 195 200 205
 Val Thr Tyr Ser Gly Met Leu Asp Gly Ser Ile Gly Tyr Ile Arg Leu
 210 215 220
 Asn Asn Phe Thr Asp Lys Ser Ala Glu Glu Val Arg Thr Ala Leu Leu
 225 230 235 240
 Asp Leu Arg Asp Lys Gln Gly Ala Lys Gly Leu Ile Leu Asp Leu Arg
 245 250 255
 Gly Asn Gly Gly Leu Met Gln Ala Ala Ile Glu Ile Val Asn Leu
 260 265 270
 Phe Val Pro Lys Gly Lys Glu Val Val Thr Thr Lys Gly Arg Ile Ala
 275 280 285
 Glu Ser Ala Ser Val Phe Arg Thr Leu Thr Glu Pro Ile Asp Thr Lys
 290 295 300
 Leu Pro Ile Val Val Leu Ile Asp Gly Gln Ser Ala Ser Ser Ser Glu
 305 310 315 320
 Ile Val Ala Gly Ala Leu Gln Asp Met Asp Arg Ala Val Leu Met Gly
 325 330 335
 Gln Lys Ser Tyr Gly Lys Gly Leu Val Gln Thr Thr Arg Gln Leu Pro
 340 345 350
 Tyr Asn Gly Val Ile Lys Leu Thr Thr Ala Lys Tyr Tyr Ile Pro Ser
 355 360 365
 Gly Arg Cys Ile Gln Arg Leu Asp Tyr Ser Arg Thr Asn Arg Thr Gly
 370 375 380
 Met Ala Thr Ala Ile Pro Asp Ser Leu His Lys Ile Phe Tyr Thr Ala
 385 390 395 400

75

WO 99/29870

PCT/AU98/01023

217/490

Ala Gly Arg Arg Val Glu Asp Ala Gly Gly Ile Leu Pro Asp Ile Glu
405 410 415
Val Lys Gln Asp Thr Ala Ala Thr Leu Leu Tyr Tyr Met Ala Ile Asn
420 425 430
5 Asn Asp Val Phe Asp Phe Val Thr Gly Tyr Val Leu Lys His Lys Thr
435 440 445
Ile Ala Lys Pro Glu Asp Phe Ser Ile Thr Asn Glu Asp Tyr Ala Ala
450 455 460
10 Phe Cys Lys Met Met Glu Glu Lys Lys Phe Asp Tyr Asp Arg Gln Ser
465 470 475 480
Gly Lys Met Leu Asp Lys Leu Glu Glu Leu Ala Lys Ile Glu Gly Tyr
485 490 495
Leu Pro Glu Ala Asn Ser Glu Leu Lys Ala Leu Arg Glu Lys Leu Lys
500 505 510
15 Pro Asn Leu Ser Arg Asp Leu Leu Arg Phe Lys Lys Glu Ile Thr Asn
515 520 525
Tyr Leu Asn Asn Glu Ile Val Thr Arg Tyr Tyr Tyr Glu Arg Gly Ser
530 535 540
20 Ile Arg Gln Ser Leu Pro Glu Asp Lys Val Val Lys Glu Ala Ile Lys
545 550 555 560
Leu Leu Lys Asp His Pro Glu Gln Ile Arg Gln Ile Leu Ala Ala Pro
565 570 575
Lys Ala Glu Asn Lys Gly
580
25
(2) INFORMATION FOR SEQ ID NO:299
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 985 amino acids
30 (B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
35 (iii) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
40 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...985
45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:299
Val Thr Asp Lys Met Gln Asn Lys Gly Phe Val Ile Val Ile Thr Ser
1 5 10 15
Ala Leu Ala Ile Ile Cys Ala Phe Tyr Leu Ser Phe Ser Phe Val Thr
20 25 30
50 Asn Arg Tyr Glu Lys Lys Ala Lys Ala Met Gly Asp Val Ala Gly Met
35 40 45
Ala Tyr Leu Asp Ser Met Ser Asn Glu Lys Val Trp Phe Gly Tyr Thr
50 55 60
Leu Lys Glu Ala Gln Ala Gln Gln Ile Gly Leu Gly Leu Asp Leu Lys
65 70 75 80
Gly Gly Met Asn Val Ile Leu Lys Leu Asn Ala Ser Asp Leu Leu Arg
85 90 95
Asn Leu Ser Asn Lys Ser Leu Asp Pro Asn Phe Asn Lys Ala Leu Glu
100 105 110
60 Asn Ala Ala Lys Ser Thr Glu Gln Ser Asp Phe Ile Asp Ile Phe Val
115 120 125
Lys Glu Tyr Arg Lys Leu Asp Pro Asn Gly Arg Leu Ala Val Ile Phe
130 135 140
Gly Ser Gly Asp Leu Arg Asp Gln Ile Thr Ala Lys Ser Thr Asp Ala
145 150 155 160
65 Asp Val Val Arg Leu Leu Lys Glu Lys Tyr Asn Ser Ala Val Glu Ala
165 170 175
Ser Phe Asn Val Leu Arg Ala Arg Ile Asp Ala Phe Gly Val Val Ala
180 185 190
70 Pro Asn Leu Gln Arg Leu Glu Gly Gln Gly Arg Ile Leu Val Glu Leu
195 200 205
Pro Gly Val Lys Asp Pro Glu Arg Val Arg Thr Leu Leu Gln Arg Ser
210 215 220
75 Ala Asn Leu Gln Phe Trp Arg Thr Tyr Lys Phe Glu Glu Val Ser Gly
225 230 235 240

SUBSTITUTE SHEET (Rule 26) (RO/AU)

WO 99/29870

PCT/AU98/01023

219/490

5 Thr Thr Phe Cys Ile Ile Ala Leu Tyr Ala Leu Leu Trp Lys Ile Leu
850 855 860
Pro Phe Thr Met Glu Ile Asp Gln Asn Phe Ile Ala Ala Ile Leu Ala
865 870 875 880
Ile Ile Gly Tyr Ser Leu Asn Asp Thr Val Val Val Phe Asp Arg Ile
885 890 895
Arg Glu Thr Met Lys Leu Tyr Pro Asn Arg Asp Arg Tyr Gln Val Ile
900 905 910
10 Asn Asp Ala Leu Asn Ser Thr Leu Gly Arg Thr Leu Asn Thr Ser Leu
915 920 925
Thr Thr Phe Ile Val Met Leu Val Ile Phe Ile Phe Gly Gly Ala Thr
930 935 940
Met Arg Ser Phe Thr Phe Ser Ile Leu Leu Gly Ile Val Ile Gly Thr
945 950 955 960
15 Tyr Ser Thr Leu Phe Val Ala Thr Pro Leu Ala Tyr Glu Ile Gln Lys
965 970 975
Arg Lys Leu Asn Lys Ala Ala Lys Lys
980 985
20
(2) INFORMATION FOR SEQ ID NO:300
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1046 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1046
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300
40 Asp Phe Pro Trp Val Arg Val Lys Pro Glu Lys Lys Arg Lys Gln His
1 5 10 15
Asn Ser Asn Asn Phe Lys Phe Asn Ala Lys Glu Lys Ser Met Lys Arg
20 25 30
45 Met Thr Leu Phe Phe Leu Cys Leu Leu Thr Ser Ile Gly Trp Ala Met
35 40 45
Ala Gln Asn Arg Thr Val Lys Gly Thr Val Ile Ser Ser Glu Asp Asn
50 55 60
50 Glu Pro Leu Ile Gly Ala Asn Val Val Val Val Gly Asn Thr Thr Ile
65 70 75 80
Gly Ala Ala Thr Asp Leu Asp Gly Asn Phe Thr Leu Ser Val Pro Ala
85 90 95
Asn Ala Lys Met Leu Arg Val Ser Tyr Ser Gly Met Thr Thr Lys Glu
100 105 110
55 Val Ala Ile Ala Asn Val Met Lys Ile Val Leu Asp Pro Asp Ser Lys
115 120 125
Val Leu Glu Gln Val Val Val Leu Gly Tyr Gly Thr Gly Gln Lys Leu
130 135 140
60 Ser Thr Val Ser Gly Ser Val Ala Lys Val Ser Ser Glu Lys Leu Ala
145 150 155 160
Glu Lys Pro Val Ala Asn Ile Met Asp Ala Leu Gln Gly Gln Val Ala
165 170 175
Gly Met Gln Val Met Thr Thr Ser Gly Asp Pro Thr Ala Val Ala Ser
180 185 190
65 Val Glu Ile His Gly Thr Gly Ser Leu Gly Ala Ser Ser Ala Pro Leu
195 200 205
Tyr Ile Val Asp Gly Met Gln Thr Ser Leu Asp Val Val Ala Thr Met
210 215 220
70 Asn Pro Asn Asp Phe Glu Ser Met Ser Val Leu Lys Asp Ala Ser Ala
225 230 235 240
Thr Ser Ile Tyr Gly Ala Arg Ala Ala Asn Gly Val Val Phe Ile Gln
245 250 255
Thr Lys Lys Gly Lys Met Ser Glu Arg Gly Arg Ile Thr Phe Asn Ala
260 265 270
75 Ser Tyr Gly Ile Ser Gln Ile Leu Asn Thr Lys Pro Leu Asp Asn Met

WO 99/29870

PCT/AU98/01023

222/ 490

	Lys	Thr	Glu	Val	Trp	Ile	Cys	Pro	Leu	Thr	Asn	Pro	Asp	Gly	Ala	Tyr
				260					265					270		
	Arg	Ala	Gly	Asn	His	Thr	Val	Gln	Gly	Ala	Thr	Arg	Tyr	Asn	Ala	Asn
			275					280					285			
5	Asn	Val	Asp	Leu	Asn	Arg	Asn	Phe	Lys	Asp	Asp	Val	Ala	Gly	Asp	His
		290					295					300				
	Pro	Asp	Gly	Lys	Pro	Trp	Gln	Pro	Glu	Ala	Thr	Ala	Phe	Met	Asp	Leu
		305				310					315				320	
10	Glu	Gly	Asn	Thr	Ser	Phe	Val	Leu	Gly	Ala	Asn	Ile	His	Gly	Gly	Thr
				325							330				335	
	Glu	Val	Val	Asn	Tyr	Pro	Trp	Asp	Asn	Lys	Lys	Glu	Arg	His	Ala	Asp
				340					345					350		
	Asp	Glu	Trp	Tyr	Lys	Leu	Ile	Ser	Arg	Asn	Tyr	Ala	Ala	Cys	Gln	
		355					360						365			
15	Ser	Ile	Ser	Ala	Ser	Tyr	Met	Thr	Ser	Glu	Thr	Asn	Ser	Gly	Ile	Ile
		370					375					380				
	Asn	Gly	Ser	Asp	Trp	Tyr	Val	Ile	Arg	Gly	Ser	Arg	Gln	Asp	Asn	Ala
		385				390				395					400	
20	Asn	Tyr	Phe	His	Arg	Leu	Arg	Glu	Ile	Thr	Leu	Glu	Ile	Ser	Asn	Thr
				405						410					415	
	Lys	Leu	Val	Pro	Ala	Ser	Gln	Leu	Pro	Lys	Tyr	Trp	Asn	Leu	Asn	Lys
				420					425					430		
	Glu	Ser	Leu	Leu	Ala	Leu	Ile	Glu	Glu	Ser	Leu	Tyr	Gly	Ile	His	Gly
		435						440					445			
25	Thr	Val	Thr	Ser	Ala	Ala	Asn	Gly	Gln	Pro	Leu	Lys	Cys	Gln	Ile	Leu
		450					455					460				
	Ile	Glu	Asn	His	Asp	Lys	Arg	Asn	Ser	Asp	Val	Tyr	Ser	Asp	Ala	Thr
		465				470				475					480	
30	Thr	Gly	Tyr	Tyr	Val	Arg	Pro	Ile	Lys	Ala	Gly	Thr	Tyr	Thr	Val	Lys
				485						490					495	
	Tyr	Lys	Ala	Glu	Gly	Tyr	Pro	Glu	Ala	Thr	Arg	Thr	Ile	Thr	Ile	Lys
				500					505					510		
	Asp	Lys	Glu	Thr	Val	Ile	Met	Asp	Ile	Ala	Leu	Gly	Asn	Ser	Val	Pro
			515					520					525			
35	Leu	Pro	Val	Pro	Asp	Phe	Thr	Ala	Ser	Pro	Met	Thr	Ile	Ser	Val	Gly
		530					535					540				
	Glu	Ser	Val	Gln	Phe	Gln	Asp	Gln	Thr	Thr	Asn	Asn	Pro	Thr	Asn	Trp
		545				550				555					560	
40	Glu	Trp	Thr	Phe	Glu	Gly	Gly	Gln	Pro	Ala	Met	Ser	Thr	Glu	Gln	Asn
				565						570					575	
	Pro	Leu	Val	Ser	Tyr	Ser	His	Pro	Gly	Gln	Tyr	Asp	Val	Thr	Leu	Lys
				580					585					590		
	Val	Trp	Asn	Ala	Ser	Gly	Ser	Asn	Thr	Ile	Thr	Lys	Glu	Lys	Phe	Ile
		595					600						605			
45	Thr	Val	Asn	Ala	Val	Met	Pro	Val	Ala	Glu	Phe	Val	Gly	Thr	Pro	Thr
		610					615					620				
	Glu	Ile	Glu	Glu	Gly	Gln	Thr	Val	Ser	Phe	Gln	Asn	Gln	Ser	Thr	Asn
		625				630				635					640	
50	Ala	Thr	Asn	Tyr	Val	Trp	Ile	Phe	Asp	Gly	Gly	Thr	Pro	Ala	Thr	Ser
				645						650					655	
	Glu	Asp	Glu	Asn	Pro	Thr	Val	Leu	Tyr	Ser	Lys	Ala	Gly	Gln	Tyr	Asp
				660					665					670		
	Val	Thr	Leu	Lys	Ala	Ile	Ser	Ala	Ser	Gly	Glu	Thr	Val	Lys	Thr	Lys
		675					680						685			
55	Glu	Lys	Tyr	Ile	Thr	Val	Lys	Lys	Ala	Pro	Val	Pro	Ala	Pro	Val	Ala
		690					695					700				
	Asp	Phe	Glu	Gly	Thr	Pro	Arg	Lys	Val	Lys	Lys	Gly	Glu	Thr	Val	Thr
		705				710				715					720	
60	Phe	Lys	Asp	Leu	Ser	Thr	Asn	Asn	Pro	Thr	Ser	Trp	Leu	Trp	Val	Phe
				725						730					735	
	Glu	Gly	Gly	Ser	Pro	Ala	Thr	Ser	Thr	Glu	Gln	Asn	Pro	Val	Val	Thr
				740					745					750		
	Tyr	Asn	Glu	Thr	Gly	Lys	Tyr	Asp	Val	Gln	Leu	Thr	Ala	Thr	Asn	Glu
		755					760						765			
65	Gly	Gly	Ser	Asn	Val	Lys	Lys	Ala	Glu	Asp	Tyr	Ile	Glu	Val	Ile	Leu
		770					775					780				
	Asp	Asp	Ser	Val	Glu	Asp	Ile	Val	Ala	Gln	Thr	Gly	Ile	Val	Ile	Arg
		785				790				795					800	
70	Pro	Gln	Asn	Gly	Thr	Lys	Gln	Ile	Leu	Ile	Glu	Ala	Asn	Ala	Ala	Ile
				805						810					815	
	Lys	Ala	Ile	Val	Leu	Tyr	Asp	Ile	Asn	Gly	Arg	Val	Val	Leu	Lys	Thr
				820					825					830		
	Thr	Pro	Asn	Gln	Leu	Arg	Ser	Thr	Val	Asp	Leu	Ser	Ile	Leu	Pro	Glu
		835					840						845			
75	Gly	Ile	Tyr	Thr	Ile	Asn	Ile	Lys	Thr	Glu	Lys	Ser	Ala	Arg	Thr	Glu

WO 99/29870

PCT/AU98/01023

223/490

850
Lys Ile His Ile Gly
865

855

860

5 (2) INFORMATION FOR SEQ ID NO:302

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302

25 Leu Ser Tyr Ser Gly Glu Ser Asp Ala Lys Glu Ser Asp Gln Asn Cys
1 5 10 15
Arg Lys Cys Thr Phe Ile Gly Phe Glu Lys Arg Val Asn Thr Met Arg
20 25 30
30 Leu Ile Lys Ala Phe Leu Val Gln Leu Leu Leu Leu Pro Ile Phe Phe
35 40 45
Tyr Lys Arg Phe Ile Ser Pro Leu Thr Pro Pro Ser Cys Arg Phe Thr
50 55 60
Pro Ser Cys Ser Ser Tyr Ala Ile Glu Ala Leu Arg Lys Tyr Gly Pro
65 70 75 80
35 Gly Lys Gly Leu Leu Ser Ile Lys Arg Ile Leu Arg Cys His Pro
85 90 95
Trp Gly Gly Ser Gly Tyr Asp Pro Val Pro
100 105

40 (2) INFORMATION FOR SEQ ID NO:303

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 861 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303

60 Leu Glu Met Ala Tyr Asp Phe Thr Gln Thr Phe Arg Asn Ser Leu Glu
1 5 10 15
Tyr Ser Tyr Gln Glu Ala Thr Arg Leu Gly Val Val Ala Val Thr Gln
20 25 30
65 Asp Met Leu Val Leu Gly Ile Ile Arg Asp Gly Asp Asn Gly Ala Ile
35 40 45
Asp Ile Met Arg His Tyr Gly Ile Asn Leu Tyr Glu Leu Lys Arg Leu
50 55 60
Ile Glu Leu Glu Ala Ile Ala Glu Ser Leu Pro Ala Ser Pro Glu Gly
65 70 75 80
70 Ser Pro Ile Phe Thr Pro Ser Ala Arg Glu Ala Ile Asp Asp Ala Thr
85 90 95
Asp Ile Cys Ala Asp Met Glu Asp Glu Ala Val Ser Pro Val His Leu
100 105 110
75 Leu Leu Ser Ile Leu Asn Ser Thr Gln Glu Ser Leu Val Gln Lys Ile
115 120 125

WO 99/29870

PCT/AU98/01023

224/ 490

	Phe	Met	Lys	Gln	Gly	Ile	Lys	Tyr	Asp	Thr	Ile	Leu	Ser	Asp	Tyr	Phe
	130						135					140				
	Gly	Gln	Arg	Asn	Pro	Ser	Glu	Gly	Lys	Ser	Pro	Ser	Glu	Met	Glu	Ile
	145					150					155				160	
5	Leu	Asp	Gly	Tyr	Gln	Asp	Asn	Asp	Phe	Asp	Asp	Glu	Glu	Asp	Glu	Ser
					165					170					175	
	Ser	Pro	Pro	Ser	Gly	Asn	Ser	Gly	Thr	Gly	Gly	Gly	Ser	Gly	Asp	Ala
				180					185					190		
10	Pro	Glu	Gln	Asn	Thr	Gly	Gly	Gly	Asp	Thr	Thr	Thr	Thr	Thr	Arg	Ser
				195				200						205		
	Gly	Gly	Asp	Thr	Pro	Ala	Leu	Asp	Thr	Phe	Gly	Thr	Asp	Ile	Thr	Ala
				210			215					220				
	Met	Ala	Ala	Ala	Gly	Lys	Leu	Asp	Pro	Val	Val	Gly	Arg	Glu	Gln	Glu
	225				230						235				240	
15	Ile	Glu	Arg	Val	Ile	Gln	Ile	Leu	Ser	Arg	Arg	Lys	Lys	Asn	Asn	Pro
				245						250				255		
	Val	Leu	Ile	Gly	Glu	Pro	Gly	Val	Gly	Lys	Ser	Ala	Ile	Val	Glu	Gly
				260				265					270			
20	Leu	Ala	Glu	Arg	Ile	Val	Asn	Arg	Lys	Val	Ser	Arg	Ile	Leu	Phe	Asp
			275				280						285			
	Lys	Arg	Ile	Ile	Ser	Leu	Asp	Leu	Ala	Gln	Met	Val	Ala	Gly	Thr	Lys
			290				295					300				
	Tyr	Arg	Gly	Gln	Phe	Glu	Glu	Arg	Leu	Lys	Ala	Val	Leu	Asp	Glu	Leu
	305				310						315				320	
25	Lys	Lys	Asn	Pro	Gln	Ile	Ile	Leu	Phe	Ile	Asp	Glu	Ile	His	Thr	Ile
				325						330				335		
	Val	Gly	Ala	Gly	Ser	Ala	Ala	Gly	Ser	Met	Asp	Thr	Ala	Asn	Met	Leu
				340					345				350			
30	Lys	Pro	Ala	Leu	Ala	Arg	Gly	Gln	Val	Gln	Cys	Ile	Gly	Ala	Thr	Thr
		355					360					365				
	Leu	Asp	Glu	Tyr	Arg	Lys	Asn	Ile	Glu	Lys	Asp	Gly	Ala	Leu	Glu	Arg
		370					375					380				
	Arg	Phe	Gln	Lys	Val	Pro	Ile	Ala	Pro	Ser	Thr	Ala	Glu	Glu	Thr	Leu
	385					390					395				400	
35	Thr	Ile	Leu	Gln	Asn	Ile	Lys	Glu	Lys	Tyr	Glu	Asp	Tyr	His	Gly	Val
				405						410				415		
	Arg	Tyr	Thr	Asp	Glu	Ala	Ile	Lys	Ala	Ala	Val	Glu	Leu	Thr	Asp	Arg
				420					425					430		
40	Tyr	Val	Ser	Asp	Arg	Phe	Phe	Pro	Asp	Lys	Ala	Ile	Asp	Ala	Met	Asp
			435					440					445			
	Glu	Ala	Gly	Ala	Ser	Val	His	Ile	Thr	Asn	Val	Val	Ala	Pro	Lys	Glu
			450				455					460				
	Ile	Glu	Ile	Leu	Glu	Ala	Glu	Leu	Ala	Ser	Val	Arg	Glu	Asn	Lys	Leu
	465					470					475				480	
45	Ser	Ala	Val	Lys	Ala	Gln	Asn	Tyr	Glu	Leu	Ala	Ala	Ser	Phe	Arg	Asp
				485						490				495		
	Gln	Glu	Arg	Arg	Thr	Gln	Gln	Gln	Ile	Ala	Glu	Glu	Lys	Lys	Lys	Trp
				500					505				510			
50	Glu	Glu	Gln	Met	Ser	Lys	His	Arg	Glu	Thr	Val	Asp	Glu	Asn	Val	Val
			515					520					525			
	Ala	His	Val	Val	Ala	Leu	Met	Thr	Gly	Val	Pro	Ala	Glu	Arg	Leu	Ser
			530				535					540				
	Thr	Gly	Glu	Gly	Glu	Arg	Leu	Arg	Thr	Met	Ala	Asp	Asp	Leu	Lys	Thr
	545					550					555				560	
55	Lys	Val	Val	Gly	Gln	Asp	Thr	Ala	Ile	Glu	Lys	Met	Val	His	Ala	Ile
				565						570				575		
	Gln	Arg	Asn	Arg	Leu	Gly	Leu	Arg	Asn	Glu	Lys	Lys	Pro	Ile	Gly	Ser
				580					585					590		
60	Phe	Leu	Phe	Leu	Gly	Pro	Thr	Gly	Val	Gly	Lys	Thr	Tyr	Leu	Ala	Lys
				595				600					605			
	Lys	Leu	Ala	Glu	Tyr	Leu	Phe	Glu	Asp	Glu	Asn	Ala	Met	Ile	Arg	Val
				610			615					620				
	Asp	Met	Ser	Glu	Tyr	Met	Glu	Lys	Phe	Ser	Val	Ser	Arg	Leu	Val	Gly
	625					630					635				640	
65	Ala	Pro	Pro	Gly	Tyr	Val	Gly	Tyr	Glu	Glu	Gly	Gly	Gln	Leu	Thr	Glu
				645						650				655		
	Arg	Val	Arg	Arg	Lys	Pro	Tyr	Ser	Val	Val	Leu	Leu	Asp	Glu	Ile	Glu
				660				665					670			
70	Lys	Ala	His	Ala	Asp	Val	Phe	Asn	Leu	Leu	Leu	Gln	Val	Met	Asp	Glu
				675				680					685			
	Gly	Gln	Leu	Thr	Asp	Ser	Leu	Gly	Arg	Arg	Val	Asn	Phe	Lys	Asn	Thr
				690			695					700				
	Val	Ile	Ile	Ile	Thr	Ser	Asn	Val	Gly	Thr	Arg	Gln	Leu	Lys	Asp	Phe
	705					710					715				720	
75	Gly	Gln	Gly	Ile	Gly	Phe	Arg	Ser	Glu	Lys	Asp	Glu	Glu	Ala	Asn	Lys

WO 99/29870

PCT/AU98/01023

226/ 490

290 295 300
 Trp Gln Lys Arg Ile Asn Thr Thr Val Phe Val Pro Glu Ser Met Tyr
 305 310 315 320
 Ala Asn Lys Leu Met Arg Leu Leu Met Gln Arg Lys Lys Ser Ile Ala
 325 330 335
 5 Ile Val Ile Asp Glu Leu Gly Gly Thr Ala Gly Met Val Thr Leu Glu
 340 345 350
 Asp Leu Val Glu Glu Ile Phe Gly Asp Ile Glu Asp Glu His Asp Thr
 355 360 365
 10 Arg Lys Ile Ile Ala Lys Gln Leu Gly Pro His Thr Tyr Leu Val Ser
 370 375 380
 Gly Arg Met Glu Ile Asp Asp Val Asn Glu Arg Phe Gly Leu Ser Leu
 385 390 395 400
 15 Pro Glu Ser Asp Asp Tyr Leu Thr Val Ala Gly Phe Ile Leu Asn Ser
 405 410 415
 His Gln Asn Ile Pro Gln Ala Asn Glu Val Val Glu Ile Ala Pro Tyr
 420 425 430
 Thr Phe Thr Ile Leu Arg Ser Ser Ser Thr Lys Ile Glu Leu Val Lys
 435 440 445
 20 Met Ser Ile Asp Asp Gln Ser Asn
 450 455

(2) INFORMATION FOR SEQ ID NO:305

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 299 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 30 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 35 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...299
 40 (x1) SEQUENCE DESCRIPTION: SEQ ID NO:305

Leu Lys Lys Glu Ile Thr Met Lys Gln Asn Tyr Phe Lys Arg Val Cys
 1 5 10 15
 45 Ser Leu Leu Trp Leu Val Leu Pro Met Leu Ile Met Pro Leu Glu Val
 20 25 30
 Ala Ala Gln Glu Ile Ile Pro Asn Glu Glu Val Leu Glu Ser Leu Thr
 35 40 45
 50 Phe Val Ala Pro Val Glu Glu Thr Asp Ala Ile Glu Ala Glu Val Glu
 50 55 60
 Ala Leu Gln Glu Ile Val Ala Thr Glu Glu Ile Ala Glu Gln Ala Val
 65 70 75 80
 Arg Ser Tyr Thr Tyr Thr Val Tyr Arg Asp Gly Val Lys Ile Ala Ser
 85 90 95
 55 Gly Leu Thr Glu Pro Thr Phe Leu Asp Glu Asp Val Pro Ala Gly Glu
 100 105 110
 His Thr Tyr Cys Val Glu Val Gln Tyr Gln Gly Gly Val Ser Asp Lys
 115 120 125
 60 Val Cys Val Asp Val Glu Val Lys Asp Phe Lys Pro Val Thr Asn Leu
 130 135 140
 Thr Gly Thr Ala Ser Asn Asp Glu Val Ser Leu Asp Trp Asp Gly Val
 145 150 155 160
 Glu Glu Lys Ala Glu Glu Pro Ala Ser Asp Lys Ala Val Ser Tyr Asn
 165 170 175
 65 Val Tyr Lys Asn Gly Thr Leu Ile Gly Asn Thr Ala Glu Thr His Tyr
 180 185 190
 Val Glu Thr Gly Val Ala Asn Gly Thr Tyr Ile Tyr Glu Val Glu Val
 195 200 205
 70 Lys Tyr Pro Asp Gly Val Ser Pro Lys Val Ala Val Thr Val Thr Val
 210 215 220
 Thr Asn Ser Ser Leu Ser Asn Val Asp Gly Gln Ala Pro Tyr Thr Leu
 225 230 235 240
 Arg Val Glu Gly Lys Lys Ile Ile Ala Glu Ala His Gly Met Ile Thr
 245 250 255
 75 Leu Tyr Asp Ile Asn Gly Arg Thr Val Ala Val Ala Pro Asn Arg Leu

WO 99/29870

PCT/AU98/01023

227/ 490

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260 265 270
 Glu Tyr Met Ala Gln Thr Gly Phe Tyr Ala Val Arg Phe Asp Val Gly
 275 280 285
 Asn Lys His His Val Ser Lys Ile Gln Val Arg
 290 295

(2) INFORMATION FOR SEQ ID NO:306

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 377 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306

Leu Phe Asn His Lys Lys Ser Trp Tyr Glu Thr Phe Gln Phe Tyr Leu
 1 5 10 15
 Val Val Phe Arg Ser Gly Phe Ile Leu Cys Glu Asn Thr Leu Ala
 20 25 30
 Gln Gln Lys Thr Glu Glu Phe Ala Pro Val Ser Asp Leu Arg Ala Glu
 35 40 45
 Ala Tyr Gly Ser Thr Val Phe Leu His Trp Thr Pro Pro Tyr Asp Asn
 50 55 60
 Pro Met Ile Pro Leu Ser Glu Ser Phe Glu Ser Gly Ile Pro Ala Ile
 65 70 75 80
 Trp Lys Thr Ile Asp Ala Asp Gly Asp Gly Tyr Asn Trp Met His Leu
 85 90 95
 Thr Asn Phe Thr Gly Gln Ser Gly Leu Cys Val Ser Ser Ala Ser Tyr
 100 105 110
 Ile Gly Gly Val Gly Ala Leu Thr Pro Asp Asn Tyr Leu Ile Thr Pro
 115 120 125
 Glu Leu Lys Leu Pro Thr Asp Ala Leu Val Glu Ile Ile Tyr Trp Val
 130 135 140
 Cys Thr Gln Asp Leu Thr Ala Pro Ser Glu His Tyr Ala Val Tyr Ser
 145 150 155 160
 Ser Ser Thr Gly Asn Asn Ala Ala Asp Phe Val Asn Leu Leu Tyr Glu
 165 170 175
 Glu Thr Leu Thr Ala Lys Arg Ile Gln Ser Pro Glu Leu Ile Arg Gly
 180 185 190
 Asn Arg Thr Gln Gly Val Trp Tyr Gln Arg Lys Val Val Leu Pro Asn
 195 200 205
 Asp Thr Lys Tyr Val Ala Phe Arg His Phe Asn Ser Thr Asp Asn Phe
 210 215 220
 Trp Leu Asn Leu Asp Glu Val Ser Ile Leu Tyr Thr Pro Leu Pro Arg
 225 230 235 240
 Arg Ala Pro Cys Pro His Pro Gly Gly Tyr Thr Tyr Ser Val Phe Arg
 245 250 255
 Asp Gly Gln Lys Ile Ala Ser Gly Leu Ser Ala Leu Ala Tyr Ile Asp
 260 265 270
 Thr Asp Val Pro Tyr Gly Thr Gln Asp Tyr Cys Val Gln Val Asn Tyr
 275 280 285
 Leu Gln Gly Asp Ser Tyr Lys Val Cys Lys Asn Ile Val Val Ala Asn
 290 295 300
 Ser Ala Asn Ile Tyr Gly Ala Asp Lys Pro Phe Ala Leu Thr Val Val
 305 310 315 320
 Gly Lys Thr Ile Val Ala Ser Ala Phe Lys Gly Glu Ile Thr Leu Tyr
 325 330 335
 Asp Ile Arg Gly Arg Leu Ile Ala Ser Gly Cys Asp Thr Leu Arg Tyr
 340 345 350
 Lys Ala Glu Asn Gly Phe Tyr Leu Ile Lys Ile Gln Val Asn Gly Thr
 355 360 365
 Val Tyr Thr Glu Lys Ile Gln Ile Gln
 370 375

WO 99/29870

PCT/AU98/01023

229/ 490

5 Gly Tyr Arg Leu Asn Lys Ala Asp Gly Glu Val Ile Glu Val Lys Thr
435 440 445
450 455 460
Ser Ser Ile Asn Ile Ser Trp Tyr Gly Tyr Gly Glu His Pro Glu Ser
465 470 475 480
Phe Ser Leu Ala Pro Asn Gln Leu Ser Gln Gly Ile Asn Thr Ile Thr
485 490 495
Leu Leu Tyr Arg Arg Thr Gly Thr Glu Gln Trp Glu Pro Val Arg His
500 505 510
10 Ala Gln Gly Gly Tyr Val Asn Ser Ile Lys Val Asn Thr Thr Asp Pro
515 520 525
Asn Asn Val Val Val Thr Val Asp Asn Asn Glu Gly Lys Leu Ser Ile
530 535 540
Val Pro Asn Ser Phe Val Ala Asp Leu Asn Ser Tyr Glu His Ser Thr
545 550 555 560
15 Ile Thr Val Gln Phe Asn Ser Asp Ser Pro Asp Glu Ile Arg Thr Pro
565 570 575
Val Ala Phe Ala Leu Ser Thr Gly Ala Thr Ala Asp Asp Val Ile Ser
580 585 590
20 Leu Gly Trp Val Met Ala Glu Val Pro Gly Gly Ser Ser Asn Tyr Pro
595 600 605
Val Val Trp Ser Lys Asp Val Leu Thr Leu Ser Glu Gly Asp Tyr Thr
610 615 620
25 Leu Tip Tyr Arg Phe Ser Ile Asn Asn Gln Lys Asp Glu Trp Lys Lys
625 630 635 640
Thr Gly Ser Val Ser Val Lys Thr Pro Thr Glu Tyr Thr His Pro Leu
645 650 655
Phe Glu Val Gly His Asn Gln Thr Ser Thr Tyr Thr Leu Asp Met Ala
660 665 670
30 His Asn Arg Val Leu Pro Asp Phe Thr Leu Lys Asn Leu Gly Leu Pro
675 680 685
Phe Asn Gly Glu Leu Val Val Val Phe Arg Gln Thr Gln Ser Ser Ser
690 695 700
35 Gly Ser Leu Trp Ala Ala Gln Glu Thr Val His Ile Lys Gln Gly Glu
705 710 715 720
Thr Phe Val Tyr Lys Pro Val Val Glu Gly Pro Ile Pro Asp Gly Ser
725 730 735
Tyr Arg Ala Thr Leu His Ala Phe Val Asn Gly Gln Gln Gln Leu Tyr
740 745 750
40 Leu Lys Gly Lys Arg Asn Tyr Thr Val Lys Ile Val Asn Gly Thr Ala
755 760 765
Val Glu Ala Ile Glu Ser Ser Glu Glu Ile Arg Val Phe Pro Asn Pro
770 775 780
45 Ala Arg Asp Tyr Val Glu Ile Ser Ala Pro Cys Ile Pro Gln Glu Thr
785 790 795 800
Ser Ile Ile Leu Phe Asp Leu Ser Gly Lys Ile Val Met Lys Asn Ser
805 810 815
Leu Ser Ala Gly His Gly Arg Met Asp Val Ser Arg Leu Pro Asn Gly
820 825 830
50 Ala Tyr Ile Leu Lys Val Asp Gly Tyr Thr Thr Lys Ile Asn Ile Val
835 840 845
His

55 (2) INFORMATION FOR SEQ ID NO:308

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 295 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

65 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

70 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308

75 Thr Lys Lys Thr Leu Met Lys Lys Leu Phe Leu Ser Leu Thr Ser Leu

WO 99/29870

PCT/AU98/01023

230/ 490

1 Val Met Val Phe Ala Val Ala Ser Cys Asp Ile Ile Asp Lys Asp Gln
20 25 30
5 Thr Leu Leu Pro Ala Pro Thr Asn Val Thr Pro Asp Asn Pro Asp Asp
35 40 45
Asn Pro Ser Glu Ile Asp Ile Thr Gln Thr His Thr Glu Lys Tyr Val
50 55 60
Leu Ala Glu Glu Phe Thr Gly Gln Lys Cys Leu Asn Cys Pro Lys Gly
65 70 75 80
10 His Arg Lys Leu Ala Ala Leu Lys Glu Gln Tyr Gly Lys Arg Leu Thr
85 90 95
Val Val Gly Ile His Ala Gly Pro Gly Ser Leu Val Pro Pro Leu Phe
100 105 110
15 Arg Thr Glu Ala Gly Asp Ala Tyr Tyr Ser Lys Phe Ala Asn Asn Thr
115 120 125
Pro Leu Pro Ala Leu Met Val Ser Arg Lys Lys Phe Gly Ser Ser Tyr
130 135 140
Val Tyr Asp Lys Ser Tyr Lys Thr Trp Asp Val Pro Ile Ala Glu Gln
145 150 155 160
20 Met Glu Gln Lys Ala Lys Ile Asn Ile Phe Ala Val Ala Glu Tyr Thr
165 170 175
Asp Thr Gln Lys Ile Lys Val Thr Val Lys Gly Lys Ile Leu Glu Gly
180 185 190
25 Asn Thr Leu Pro Lys Ser Met Val Gln Val Tyr Leu Leu Glu Asp Lys
195 200 205
Leu Ile Ala Pro Gln Val Asp Gly Asn Thr Thr Val Glu Asn Tyr Glu
210 215 220
His Asn His Val Leu Arg Gly Ala Val Asn Gly Ile Trp Gly Glu Glu
225 230 235 240
30 Phe Val Asn Leu Lys Asp Tyr Leu Tyr Thr Tyr Ala Val Glu Pro Leu
245 250 255
Ser Gly Met Ser Phe Val Ala Glu Asn Tyr Ser Ile Val Ala Phe Val
260 265 270
35 Tyr Asp Val Gln Thr Phe Glu Val Tyr Asp Val Val His Val Lys Ile
275 280 285
Asn Pro Gln Ser Asp Gly Lys
290 295

(2) INFORMATION FOR SEQ ID NO:309

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 230 amino acids
(E) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...230

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:309

1 Thr Asn Lys Lys Glu Glu Thr Met Lys Lys Ser Ser Val Val Ala Ser
5 10 15
Val Leu Ala Val Ala Leu Val Phe Ala Gly Cys Gly Leu Asn Asn Met
20 25 30
Ala Lys Gly Gly Leu Ile Gly Ala Gly Val Gly Gly Ala Ile Gly Ala
35 40 45
65 Gly Val Gly Asn Val Ala Gly Asn Thr Ala Val Gly Ala Ile Val Gly
50 55 60
Thr Ala Val Gly Gly Ala Ala Gly Ala Leu Ile Gly Lys Lys Met Asp
65 70 75 80
Lys Gln Lys Lys Glu Leu Glu Ala Ala Val Pro Asp Ala Thr Ile Gln
85 90 95
70 Thr Val Asn Asp Gly Glu Ala Ile Leu Val Thr Phe Asp Ser Gly Ile
100 105 110
Leu Phe Ala Thr Asn Ser Ser Thr Leu Ser Pro Asn Ser Arg Thr Ala
115 120 125
75 Leu Thr Lys Phe Ala Ala Asn Met Asn Lys Asn Pro Asp Thr Asp Ile

WO 99/29870

PCT/AU98/01023

231/ 490

130 135 140
Arg Ile Val Gly His Thr Asp Asn Thr Gly Ser Asp Lys Ile Asn Asp
145 150 155 160
Pro Leu Ser Glu Arg Arg Ala Ala Ser Val Tyr Ser Phe Leu Asn Ser
5 Gln Gly Val Ser Met Ser Arg Met Ala Ala Glu Gly Arg Gly Ser His
180 185 190
Glu Pro Val Ala Asp Asn Ser Thr Val Ala Gly Arg Ser Ala Asn Arg
195 200 205
10 Arg Val Glu Val Tyr Ile Leu Pro Asn Ala Lys Met Ile Glu Gln Ala
210 215 220
Gln Gln Gly Thr Leu Lys
225 230

15 (2) INFORMATION FOR SEQ ID NO:310

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 342 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

25

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

30

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310

35 Asn Arg Asn Arg Asn Met Ser Lys Lys Ser Ile Leu Leu Leu Cys Cys
1 5 10 15
Ser Leu Cys Phe Ile Ser Ala Thr Lys Ala Val Thr Pro Val Arg Asn
20 25 30
40 Val Arg Asn Ser Gln Val Asn Ser Lys Ala Lys Thr Glu Arg Thr Lys
35 40 45
Pro Ser Asp Ser Val Arg Tyr Ile Ser Asn Met Ile Ala Asp Arg Leu
50 55 60
Glu Phe Arg Asn Lys Ile Ser Ser Glu Lys Glu Val Arg Lys Ala Glu
65 70 75 80
45 Tyr Glu Asn Arg Leu Ala Met Glu Ala Leu Asn Tyr Pro Ala Ile Asp
85 90 95
Leu Tyr Gly Glu Asp Ser Trp Ser Glu Tyr Val Asn Pro Phe Val Gly
100 105 110
Ala Gly Thr Asp Val Glu Ile Pro Asn Ser Tyr Asp Ile Asp Cys Ser
50 115 120 125
Ser Phe Val Met Pro Val Glu Asp Lys Gln Val Thr Ser Gln Phe Gly
130 135 140
Tyr Arg Arg Arg Phe Gly Arg Met His Tyr Gly Ile Asp Leu Ser Val
145 150 155 160
55 Asn Arg Gly Asp Thr Ile Arg Ala Ala Phe Asp Gly Lys Val Arg Val
165 170 175
Arg Ser Tyr Glu Ala Arg Gly Tyr Gly Tyr Tyr Ile Val Leu Arg His
180 185 190
60 Pro Asn Gly Leu Glu Thr Val Tyr Gly His Met Ser Arg Gln Leu Val
195 200 205
Asp Glu Asn Gln Ile Val Arg Ala Gly Gln Pro Ile Gly Leu Gly Gly
210 215 220
Ser Thr Gly Arg Ser Thr Gly Pro His Leu His Phe Glu Thr Arg Phe
225 230 235 240
65 Met Gly Ile Pro Ile Asn Pro Ser Thr Ile Ile Asp Phe Asp Asn Gly
245 250 255
Val Pro Leu Arg Asp Ile Tyr Thr Phe Lys Arg Gly Ser Asn Ser Arg
260 265 270
70 Tyr Ala Lys Ala Ser Lys Thr Ser Ser Arg Tyr Ala Lys Lys Gly Lys
275 280 285
Lys Gly Arg Gln Ala Ser Ser Pro Met Thr Tyr Arg Ile Lys Lys Gly
290 295 300
Asp Thr Leu Glu Thr Ile Ala Lys Arg His Gly Thr Ser Val Gln Lys
305 310 315 320
75 Leu Cys Ala Thr Asn Gly Ile Gly Lys Ser Lys Ile Leu Thr Pro Gly

WO 99/29870

PCT/AU98/01023

233/490

Ser Leu Ser Val Gly Lys Tyr His Ser Pro Phe Phe Ala Thr Arg Leu
 85 90 95
 Gln Ile Asn Gly Gly Gln Ala His Thr Phe Leu Gly Lys Asn Gly Glu
 100 105 110
 5 Gln Glu Ile Asn Thr Asn Phe Gly Ala Ala His Phe Asp Phe Met Phe
 115 120 125
 Asp Val Val Asn Tyr Phe Ala Pro Tyr Arg Glu Asn Arg Phe Phe His
 130 135 140
 10 Leu Ile Pro Trp Val Gly Val Gly Tyr Gln His Lys Phe Ile Gly Ser
 145 150 155 160
 Glu Trp Ser Lys Asp Asn Val Glu Ser Leu Thr Ala Asn Val Gly Val
 165 170 175
 Met Met Ala Phe Arg Leu Gly Lys Arg Val Asp Phe Val Ile Glu Ala
 180 185 190
 15 Gln Ala Ala His Ser Asn Leu Asn Leu Ser Arg Ala Tyr Asn Ala Lys
 195 200 205
 Lys Thr Pro Val Phe Glu Asp Pro Ala Gly Arg Tyr Tyr Asn Gly Phe
 210 215 220
 20 Gln Gly Met Ala Thr Ala Gly Leu Asn Phe Arg Leu Gly Ala Val Gly
 225 230 235 240
 Phe Asn Ala Ile Unk Pro Met Asp Tyr Ala Leu Ile Asn Asp Leu Asn
 245 250 255
 Gly Gln Ile Asn Arg Leu Arg Ser Glu Val Glu Glu Leu Ser Lys Arg
 260 265 270
 25 Pro Val Ser Cys Pro Glu Cys Pro Glu Val Thr Pro Val Thr Lys Thr
 275 280 285
 Glu Asn Ile Leu Thr Glu Lys Ala Val Leu Phe Arg Phe Asp Ser His
 290 295 300
 30 Val Val Asp Lys Asp Gln Leu Ile Asn Leu Tyr Asp Val Ala Gln Phe
 305 310 315 320
 Val Lys Glu Thr Asn Glu Pro Ile Thr Val Val Gly Tyr Ala Asp Pro
 325 330 335
 Thr Gly Asn Thr Gln Tyr Asn Glu Lys Leu Ser Glu Arg Arg Ala Lys
 340 345 350
 35 Ala Val Val Asp Val Leu Thr Gly Lys Tyr Gly Val Pro Ser Glu Leu
 355 360 365
 Ile Ser Val Glu Trp Lys Gly Asp Ser Thr Gln Pro Phe Ser Lys Lys
 370 375 380
 40 Ala Trp Asn Arg Val Val Ile Val Arg Ser Lys
 385 390 395

(2) INFORMATION FOR SEQ ID NO:313

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 387 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 50 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 55 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...387
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:313

Tyr Lys Met Thr Tyr Arg Ile Met Lys Ala Lys Ser Leu Leu Leu Ala
 1 5 10 15
 65 Leu Ala Gly Leu Ala Cys Thr Phe Ser Ala Thr Ala Gln Glu Ala Thr
 20 25 30
 Thr Gln Asn Lys Ala Gly Met His Thr Ala Phe Gln Arg Asp Lys Ala
 35 40 45
 Ser Asp His Trp Phe Ile Asp Ile Ala Gly Gly Ala Gly Met Ala Leu
 50 55 60
 70 Ser Gly Trp Asn Asn Asp Val Asp Phe Val Asp Arg Leu Ser Ile Val
 65 70 75 80
 Pro Thr Phe Gly Ile Gly Lys Trp His Glu Pro Tyr Phe Gly Thr Arg
 85 90 95
 75 Leu Gln Phe Thr Gly Phe Asp Ile Tyr Gly Phe Pro Gln Gly Ser Lys
 100 105 110

WO 99/29870

PCT/AU98/01023

234/ 490

5 Glu Arg Asn His Asn Tyr Phe Gly Asn Ala His Leu Asp Phe Met Phe
115 120 125
Asp Leu Thr Asn Tyr Phe Gly Val Tyr Arg Pro Asn Arg Val Phe His
130 135 140
11 Ile Ile Pro Trp Ala Gly Ile Gly Phe Gly Tyr Lys Phe His Ser Glu
145 150 155 160
Asn Ala Asn Gly Glu Lys Val Gly Ser Lys Asp Asp Met Thr Gly Thr
165 170 175
10 Val Asn Val Gly Leu Met Leu Lys Phe Arg Leu Ser Arg Val Val Asp
180 185 190
Phe Asn Ile Glu Gly Gln Ala Phe Ala Gly Lys Met Asn Phe Ile Gly
195 200 205
Thr Lys Arg Gly Lys Ala Asp Phe Pro Val Met Ala Thr Ala Gly Leu
210 215 220
15 Thr Phe Asn Leu Gly Lys Thr Glu Trp Thr Glu Ile Val Pro Met Asp
225 230 235 240
Tyr Ala Leu Val Asn Asp Leu Asn Asn Gln Ile Asn Ser Leu Arg Gly
245 250 255
20 Gln Val Glu Glu Leu Ser Arg Arg Pro Val Ser Cys Pro Glu Cys Pro
260 265 270
Glu Pro Thr Gln Pro Thr Val Thr Arg Val Val Val Asp Asn Val Val
275 280 285
Tyr Phe Arg Ile Asn Ser Ala Lys Ile Asp Arg Asn Gln Glu Ile Asn
290 295 300
25 Val Tyr Asn Thr Ala Glu Tyr Ala Lys Thr Asn Asn Ala Pro Ile Lys
305 310 315 320
Val Val Gly Tyr Ala Asp Glu Lys Thr Gly Thr Ala Ala Tyr Asn Met
325 330 335
30 Lys Leu Ser Glu Arg Arg Ala Lys Ala Val Ala Lys Met Leu Glu Lys
340 345 350
Tyr Gly Val Ser Ala Asp Arg Ile Thr Ile Glu Trp Lys Gly Ser Ser
355 360 365
Glu Gln Ile Tyr Glu Glu Asn Ala Trp Asn Arg Ile Val Val Met Thr
370 375 380
35 Ala Ala Glu
385

(2) INFORMATION FOR SEQ ID NO:314

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 195 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
45 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
50 (A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...195
55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:314

60 Val Ile Gly Ile Ile Met Glu Phe Phe Met Leu Phe Ile Ala Ala Val
1 5 10 15
Phe Val Asn Asn Val Val Leu Ser Gln Phe Leu Gly Ile Cys Pro Phe
20 25 30
Leu Gly Val Ser Lys Lys Val Asp Thr Ser Ile Gly Met Gly Ala Ala
35 40 45
65 Val Thr Phe Val Leu Ala Leu Ala Thr Leu Val Thr Phe Leu Ile Gln
50 55 60
Lys Phe Val Leu Asp Arg Phe Gly Leu Gly Phe Met Gln Thr Ile Ala
65 70 75 80
Phe Ile Leu Val Ile Ala Ala Leu Val Gln Met Val Glu Ile Ile Leu
85 90 95
70 Lys Lys Val Ser Pro Pro Leu Tyr Gln Ala Leu Gly Val Phe Leu Pro
100 105 110
Leu Ile Thr Thr Asn Cys Cys Val Leu Gly Val Ala Ile Leu Val Ile
115 120 125
75 Gln Lys Asp Tyr Thr Leu Leu Gln Ser Phe Val Tyr Ala Ile Ser Thr
130 135 140

WO 99/29870

PCT/AU98/01023

235/ 490

Ala Ile Gly Phe Thr Leu Ala Met Val Thr Phe Ala Gly Ile Arg Glu
145 150 155 160
Gln Leu Asp Met Thr Asn Leu Pro Lys Ala Met Lys Gly Ile Pro Ser
165 170 175
5 Ala Leu Leu Ala Ala Gly Ile Leu Ala Met Ala Phe Met Gly Phe Ser
180 185 190
Gly Ile Ala
195

10 (2) INFORMATION FOR SEQ ID NO:315

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 876 amino acids
(E) TYPE: amino acid
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

20 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...876

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:315

30 Tyr Arg Ser Tyr Arg Gly Ile Gly Ser Gly Thr His Ser Pro Asn Leu
1 5 10 15
Lys Asn Arg Leu Lys Arg Ile Gly Ile Arg Ile Pro Asn Arg His Tyr
20 25 30
35 Ile His Ile Lys Pro Ile Lys Pro Lys Asn Lys Met Lys Gln Leu Asn
35 40 45
Ile Ile Ser Phe Ile Ile Ala Phe Leu Phe Leu Gly Thr Ser Ala Ser
50 55 60
Ala Gln Gln Ser Gly Gly Ser Val Thr Gly Thr Val Val Asp Lys Ser
65 70 75 80
40 Ser Lys Glu Pro Ile Ala Tyr Val Gln Val Phe Val Lys Gly Thr Thr
85 90 95
Leu Gly Thr Ser Thr Asp Ala Asn Gly Asn Tyr Ser Ile Lys Gly Ile
100 105 110
45 Pro Ser Gly Asn Gln Thr Ile Val Ala Arg Leu Met Gly Tyr Ser Thr
115 120 125
Cys Glu Glu Lys Val His Ile Glu Lys Gly Gly Ser Arg His Val Asp
130 135 140
Leu Tyr Leu Thr Glu Glu Ile Leu Ser Leu Asp Gly Val Val Val Ser
145 150 155 160
50 Ala Asn Arg Asn Glu Thr Phe Arg Arg Gln Ala Pro Ser Leu Val Thr
165 170 175
Val Leu Ser Pro Glu Leu Phe Leu Lys Thr Asn Ser Thr Asn Leu Ser
180 185 190
55 Gln Gly Leu Lys Phe Gln Pro Gly Leu Arg Val Glu Asp Asn Cys Gln
195 200 205
Asn Cys Gly Phe Asn Gln Val Arg Ile Asn Gly Leu Glu Gly Ala Tyr
210 215 220
Ser Gln Ile Leu Ile Asp Ser His Pro Ile Phe Ser Ser Leu Ala Gly
225 230 235 240
60 Val Tyr Gly Leu Glu Gln Met Pro Ala Asn Met Ile Glu Arg Val Glu
245 250 255
Val Ile Arg Gly Gly Gly Ser Ala Leu Phe Gly Ser Asn Ala Val Gly
260 265 270
65 Gly Val Ile Asn Val Ile Thr Lys Glu Pro Leu Arg Asn Ser Ala Glu
275 280 285
Ile Ser His Ser Thr Met Thr Phe Asp His Ala Lys Gly Trp Gly Ser
290 295 300
Phe Gln Asn Thr Thr Gln Phe Asn Gly Ser Met Leu Thr Glu Asp Arg
305 310 315 320
70 Lys Ala Gly Val Met Val Phe Gly Gln His Asn Tyr Arg Pro Gly Gln
325 330 335
Asp Ile Asp Gly Asp Asn Phe Thr Glu Leu Pro Asn Leu Arg Asn Arg
340 345 350
75 Ser Leu Gly Phe Arg Ser Tyr Tyr Lys Thr Gly Leu Tyr Ser Lys Ala
355 360 365

236/ 490

Thr Leu Glu Tyr His Ser Met Gln Glu Tyr Arg Arg Gly Gly Asp Arg
 370 375 380
 Leu Asp Asn Pro Pro Phe Glu Ala Gln Ile Ala Glu Tyr Leu Gln His
 385 390 395 400
 5 Tyr Ile Asn Gly Gly Ser Phe Lys Phe Asp Gln Gly Phe Ser Gly Gly
 405 410 415
 Lys Asp Phe Phe Ser Leu Tyr Ala Ser Ala Gln Asp Val Gln Arg Arg
 420 425 430
 10 Ser Tyr Tyr Gly Gly Gly Asp Tyr Thr Glu Asn Leu Leu Asn Gly Ala
 435 440 445
 Val Gln Ser Gly Ser Thr Glu Ser Asp Glu Tyr Asn Asp Ala Phe Thr
 450 455 460
 Ala Leu Thr Ser Tyr Gly Thr Thr Lys Gly Phe Asp Leu Gln Gly Gly
 465 470 475 480
 15 Gly Met Tyr Arg His Thr Phe Gly Glu Asn Trp Asp Phe Thr Gly Gly
 485 490 495
 Leu Glu Tyr Ile Tyr Gly Gln Leu Asp Asp Arg Ser Gly Tyr Arg Pro
 500 505 510
 20 Ser Lys Ile Asp Gln Asn Thr Ser Thr Phe Ser Gln Tyr Asp Gln Leu
 515 520 525
 Glu Tyr Lys Thr Glu Lys Leu Ser Ala Leu Ile Gly Ala Arg Ile Asp
 530 535 540
 Tyr Val Leu Leu Asn Gln Asp Gly Lys Arg Tyr Ile Asp Pro Leu Phe
 545 550 555 560
 25 Ile Phe Ser Pro Arg Ala Asn Val Arg Tyr Asn Pro Asn Lys Asn Leu
 565 570 575
 Ser Phe Arg Leu Ser Tyr Ser Glu Gly Phe Arg Ala Pro Gln Tyr Phe
 580 585 590
 30 Acp Glu Asp Leu His Val Glu Leu Ala Gly Gly Thr Pro Ile Ser Arg
 595 600 605
 Val Leu Ser Pro Asn Leu Lys Glu Glu Arg Ser Arg Ser Ile Ser Ala
 610 615 620
 Ser Phe Asp Tyr Tyr His Arg Ala Asp Glu Trp Gln Phe Asn Ile Met
 625 630 635 640
 35 Gly Glu Ala Phe Ser Thr Phe Ile Ser Asn Gln Phe Lys Pro Ser Asp
 645 650 655
 Lys Val Glu Thr Thr Ser Asp Gly Lys Glu Trp Ile Ile Arg Thr Ile
 660 665 670
 40 Tyr Asn Asp Lys Asp Gly Val Ser Lys Val Tyr Gly Val Asn Leu Glu
 675 680 685
 Gly Arg Ile Ala Tyr Asn Lys Ser Phe Asp Leu Gln Leu Gly Gly Thr
 690 695 700
 Trp Gln Arg Ser Arg Tyr Gly Ser Ile Tyr Thr Ala Val Glu Ala Asp
 705 710 715 720
 45 Lys Thr Thr Gly Gln Ala Glu Ile Ser Val Lys Asp Tyr Val Arg Thr
 725 730 735
 Pro Asn Leu Tyr Gly Tyr Phe Val Ala Thr Val Arg Pro Thr Glu His
 740 745 750
 50 Phe Ala Ile Asn Leu Ser Gly Thr Phe Thr Gly Lys Met Asp Val Val
 755 760 765
 His Glu Ala Tyr Glu Gly Asp Ile Pro Ala Glu His Ile Ala Pro Asp
 770 775 780
 Gly Ser Phe Asp Phe Glu Met Asn Gly Gln Gln Phe Lys Gly Leu Ala
 785 790 795 800
 55 Glu Gly His Ala Lys Leu Val Lys Thr Pro Ala Phe Ala Asp Ile Asp
 805 810 815
 Leu Lys Leu Ser His Asp Phe His Leu Ala Ser Thr Met Thr Leu Glu
 820 825 830
 60 Leu Asn Ala Gly Ile Gln Asn Ile Phe Asn Ser Tyr Gln Lys Asp Thr
 835 840 845
 Asp Lys Gly Pro Gly Arg Ala Ser Thr Tyr Val Tyr Gly Pro Met Gln
 850 855 860
 Pro Arg Arg Ile Phe Val Gly Thr Lys Ile Asn Phe
 865 870 875

(2) INFORMATION FOR SEQ ID NO:316

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 899 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

WO 99/29870

PCT/AU98/01023

238/490

515 520 525
Lys Tyr Tyr Gln Gln Tyr Ser Val Thr Phe Met Asp Pro Trp Phe Gly
530 535 540
Gly Lys Arg Pro Asp Met Phe Ser Phe Ser Ala Phe Tyr Ser Lys Thr
545 550 555 560
Thr Ala Ile Asp Ser Lys Phe Tyr Asn Ser Asn Ala Gly Asn Tyr Tyr
565 570 575
Asn Ala Tyr Tyr Asn Ser Tyr Tyr Asn Asn Tyr Asn Ser Tyr Tyr Asn
580 585 590
10 Gly Met Ser Asn Tyr Thr Gly Asp Leu Tyr Thr Gln Ala Ser Asp Pro
595 600 605
Asp Arg Ser Leu Gln Met Leu Gly Thr Ser Ile Gly Tyr Gly Lys Arg
610 615 620
15 Leu Thr Trp Pro Asp Asn Trp Phe Gln Ile Tyr Thr Ser Leu Asn Tyr
625 630 635 640
Thr Tyr Tyr Arg Leu Arg Asn Trp Ser Tyr Asn Thr Phe Gln Asn Phe
645 650 655
His His Gly Ser Ala Asn Asp Leu Asn Leu Glu Leu Arg Leu Ser Arg
660 665 670
20 Thr Ser Ile Asp Asn Pro Ile Tyr Thr Arg Ser Gly Ser Arg Phe Met
675 680 685
Val Ser Val Ala Ala Thr Leu Pro Tyr Ser Leu Trp Asp Asn His Asp
690 695 700
25 Tyr Ala Ser Gln Asn Leu Ser Val Ser Asp Arg Tyr Arg Phe Ile Glu
705 710 715 720
Tyr His Lys Trp Lys Phe Arg Gly Arg Val Phe Thr Pro Leu Leu Asn
725 730 735
Pro Ala Thr His Lys Tyr Thr Pro Val Leu Met Ser Arg Val Glu Gly
740 745 750
30 Ala Val Leu Gly Ser Tyr Asn Ser Asn Lys Lys Ser Pro Phe Gly Thr
755 760 765
Phe Tyr Met Gly Gly Asp Gly Met Ser Ser Tyr Tyr Gly Gly Tyr Met
770 775 780
35 Asn Glu Thr Ile Gly Leu Arg Gly Tyr Lys Asn Gly Ser Ile Ala Gly
785 790 795 800
Asn Asn Tyr Asp Tyr Ala Tyr Ala Tyr Met Arg Leu Thr Met Glu Leu
805 810 815
Arg Phe Pro Ile Leu Phe Glu Asn Ser Phe Asn Ala Trp Leu Leu Ala
820 825 830
40 Phe Ala Glu Ala Gly Asn Ala Trp Arg Ser Ile Asp Asn Tyr Asn Pro
835 840 845
Phe Asn Leu Lys Arg Ser Ala Gly Val Gly Leu Arg Val Thr Leu Pro
850 855 860
45 Met Val Gly Met Leu Gly Ile Asp Trp Gly Tyr Gly Phe Asp Arg Pro
865 870 875 880
Asp Asn Ser Leu Gln Arg Gly Gly Ser Asn Val His Phe Val Leu Gly
885 890 895
Gln Glu Phe

50

(2) INFORMATION FOR SEQ ID NO:317

55

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

60

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

65

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...177

70

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317

75

Gln Ile Asn Met Asn Gly Asp Met Lys Arg Phe Leu Ile Leu Ile Gly
1 5 10 15
Phe Ala Leu Ala Val Ala Phe Ser Gly Phe Ser Gln Lys Phe Ala Leu
20 25 30
Val Asp Met Glu Tyr Ile Leu Arg Asn Ile Pro Asp Tyr Glu Met Met

239/ 490

35 40 45
 Asn Glu Gln Leu Glu Gln Val Ser Lys Lys Trp Gln Asn Glu Ile Glu
 50 55 60
 5 Ala Leu Glu Asn Glu Ala Gln Ser Met Tyr Lys Lys Tyr Gln Ser Asp
 65 70 75 80
 Leu Val Phe Leu Ser Ala Ala Gln Lys Lys Thr Gln Glu Glu Ala Ile
 85 90 95
 Val Lys Lys Glu Gln Gln Ala Ser Glu Leu Lys Arg Lys Tyr Phe Gly
 100 105 110
 10 Pro Glu Gly Glu Leu Tyr Lys Lys Arg Ser Asp Leu Met Lys Pro Ile
 115 120 125
 Gln Asp Glu Ile Trp Asn Ala Ile Lys Glu Ile Ala Lys Arg Asn Asn
 130 135 140
 15 Tyr Gln Met Val Leu Asp Arg Gly Thr Ser Gly Ile Ile Phe Ala Ser
 145 150 155 160
 Pro Ser Ile Asp Ile Ser Asp Leu Val Leu Ser Lys Met Gly Phe Ser
 165 170 175
 Lys

20

(2) INFORMATION FOR SEQ ID NO:318

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: protein

30 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

35 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...170

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:318

Arg Ile Asn Lys Gln His Glu Met Lys Lys Phe Phe Leu Met Leu Leu
 1 5 10 15
 Met Ala Leu Pro Leu Ser Leu Leu Ala Gln Lys Val Ala Val Val Asn
 20 25 30
 45 Thr Glu Glu Ile Ile Ser Lys Met Pro Glu Gln Val Ala Ala Thr Lys
 35 40 45
 Gln Leu Asn Glu Leu Ala Glu Lys Tyr Arg Leu Asp Leu Lys Ser Met
 50 55 60
 Asp Asp Glu Phe Ala Lys Lys Thr Glu Glu Phe Val Lys Glu Lys Asp
 65 70 75 80
 Ser Leu Leu Glu Asn Ile Arg Asn Arg Arg Gln Gln Glu Leu Gln Asp
 85 90 95
 Ile Gln Thr Arg Tyr Gln Gln Ser Tyr Gln Thr Met Gln Glu Asp Leu
 100 105 110
 55 Gln Lys Arg Gln Gln Gln Leu Phe Ala Pro Ile Gln Gln Lys Val Ala
 115 120 125
 Asp Ala Ile Lys Lys Val Gly Asp Glu Glu Asn Cys Ala Tyr Ile Met
 130 135 140
 60 Glu Ala Gly Met Met Leu Tyr Thr Gly Ala Thr Ala Ile Asp Leu Thr
 145 150 155 160
 Ala Lys Val Lys Ala Lys Leu Gly Ile Lys
 165 170

65 (2) INFORMATION FOR SEQ ID NO:319

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 828 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

70 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

75 (vi) ORIGINAL SOURCE:

240/ 490

(A) ORGANISM: Porphyromonas gingivalis

(1X) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...828

5

(21) SEQUENCE DESCRIPTION: SEQ ID NO:319

10 Ile Met Lys Glu Ala Ile Pro Arg Lys Asn Lys Tyr Ile Lys Leu Asn
 1 5 15 25
 Gly Ile Tyr Arg Leu Ser Phe Ile Leu Leu Cys Cys Leu Leu Cys Ser
 20 25 30
 Gln Ala Ala Met Ala Gln Gly Val Arg Val Ser Gly Tyr Val Leu Asp
 35 40 45
 15 Arg Gly Glu Lys Pro Ile Pro Phe Ala Gly Val Lys Val Arg Gly Thr
 50 55 60
 Gly Thr Gly Ala Thr Thr Asn Leu Lys Gly Tyr Tyr Glu Phe Arg Met
 65 70 75 80
 20 Lys Ala Thr Thr Asp Ser Ile Thr Ile Glu Phe Ser Ser Met Gly Tyr
 85 90 95
 Gln Gly Val Ser Arg Ser Phe Pro Ser Leu Thr Lys Asp Thr Arg Leu
 100 105 110
 Asn Val Arg Leu Ala Glu Ala Glu Met Glu Leu Ser Ser Val Thr Val
 115 120 125
 25 Gln Ala Thr Lys Arg Arg Leu Asn Thr Met Glu Arg Val Asn Thr Arg
 130 135 140
 Asp Leu Arg Val Asn Ala Gly Pro Thr Gly Gly Val Glu Ser Leu Ile
 145 150 155 160
 Ser Thr Tyr Ala Gly Val Thr Gln Asn Asn Glu Leu Ser Ser Gln Tyr
 165 170 175
 30 Ser Val Arg Gly Gly Ser Tyr Asp Glu Asn Met Val Tyr Val Asn Gly
 180 185 190
 Val Glu Val Tyr Arg Pro Leu Leu Val Arg Ser Ala Gln Gln Glu Gly
 195 200 205
 35 Leu Ser Phe Val Asn Pro Asp Leu Thr Gln Ser Val Gln Phe Ser Ala
 210 215 220
 Gly Gly Phe Thr Ala Asp Tyr Gly Asp Lys Met Ser Ser Val Leu Asp
 225 230 235 240
 40 Ile Arg Tyr Lys Gln Pro Gln Glu Lys Glu Gly Ala Val Leu Leu Gly
 245 250 255
 Met Leu Gln Ser Ser Ala Tyr Tyr Gly Ser Ser Ala Gly Ala Phe Ser
 260 265 270
 Gln Ile Thr Gly Val Arg Tyr Lys Ser Ala Lys Ser Leu Leu Gly Thr
 275 280 285
 45 Thr Asp Thr Lys Ala Glu Tyr Asp Pro Ile Tyr Ala Asp Gly Gln Thr
 290 295 300
 Phe Met Thr Tyr Arg Phe Ser Pro Lys Leu Ser Val Ser Phe Leu Gly
 305 310 315 320
 50 Asn Ile Ser Gln Thr Arg Tyr Lys Phe Val Pro Gln Thr Arg Glu Thr
 325 330 335
 Ser Phe Gly Thr Leu Ser Asp Ala Lys Lys Leu Lys Ile Phe Phe Asp
 340 345 350
 Gly Gln Glu Gln Asp Arg Phe Leu Thr Tyr Phe Gly Ala Phe Ser Met
 355 360 365
 55 Asn Phe Val Pro Asp Asp Lys Gln Arg His Thr Val Thr Leu Ser Ala
 370 375 380
 Phe Asn Ser Asn Glu Arg Glu Thr Tyr Asp Ile Gln Gly Glu Tyr Phe
 385 390 395 400
 60 Leu Asn Asp Val Gln Leu Gly Ala Asp Gly Thr Ala Ser Met Ala Ser
 405 410 415
 Gly Ser Glu Asn Ser Asn Gly Leu Gly Ile Gly Arg Asn His Glu His
 420 425 430
 Ala Arg Asn Arg Leu Ser Tyr Arg Val Leu Asn Met Gly Tyr Arg Gly
 435 440 445
 65 Glu Met Lys Leu Asn Glu Lys His Arg Leu Gln Ala Gly Val Ser Ala
 450 455 460
 Gln Met Glu Lys Ile Ala Asp His Ile Ser Glu Trp Glu Arg Arg Asp
 465 470 475 480
 70 Ser Val Gly Tyr Asn Leu Pro His Ser Glu Thr Val Leu Leu Met Tyr
 485 490 495
 Asn Asn Leu Tyr Ala Asp Thr Gln Met Arg Gly Thr Arg Leu Ser Ala
 500 505 510
 Phe Val Gln Asp Arg Phe Asn Phe Ser Met Gly Gly Gly Thr Phe Ser
 515 520 525
 75 Leu Ile Pro Gly Ile Arg Ala Ser Trp Trp Ser Phe Asn Lys Glu Leu

WO 99/29870

PCT/AU98/01023

241/ 490

530 535 540
 Leu Val Ser Pro Arg Ile Ser Val Gly Tyr Ser Pro Glu Ser Asn Pro
 545 550 555
 Ala Leu Val Leu Arg Ala Ala Ala Gly Leu Tyr Tyr Gln Ala Pro Phe
 565 570 575
 Tyr Lys Glu Leu Arg Gln Thr His Lys Asp Ala Glu Gly Asn Asn Val
 580 585 590
 Val Val Leu Asn Glu Lys Ile Arg Ser Gln Gly Ala Phe His Ile Leu
 595 600 605
 10 Ala Gly Ala Asp Tyr Thr Phe Glu Met Gly Gly Arg Lys Tyr Lys Phe
 610 615 620
 Thr Ala Glu Ala Tyr Tyr Lys Ser Leu Phe Asn Ile Asn Pro Tyr Ile
 625 630 635
 15 Ile Glu Asn Val Lys Ile Arg Tyr Leu Gly Glu Asn Ile Gly Ser Gly
 645 650 655
 Tyr Ala Ala Gly Ile Asp Leu Lys Leu Phe Gly Glu Leu Val Pro Gly
 660 665 670
 Val Asp Ser Trp Leu Thr Ala Ser Ile Ile Lys Ala Arg Gln Lys Leu
 675 680 685
 20 Asp Gly Tyr Gly Ser Leu Pro Leu Met Asn Ala Pro Thr Tyr Asn Phe
 690 695 700
 Ser Phe Phe Leu Gln Glu Tyr Val Pro Gly Asn Lys Arg Ile Thr Ala
 705 710 715 720
 25 Thr Leu Arg Ala Ala Leu Ser Gly Gly Leu Pro Gln Leu Asn Pro Ser
 725 730 735
 Lys Gly Leu Ser Ser Pro Ala Phe Thr Ala Pro Ala Tyr Lys Arg Val
 740 745 750
 Asp Leu Gly Val Met Tyr Lys Trp Leu Asp Pro Asp Asp Ser Phe Ala
 755 760 765
 30 Gly Arg Ser Lys Trp Leu Met Gly Val Lys Gly Ala Tyr Ile Gly Ala
 770 775 780
 Asp Leu Phe Asn Leu Phe Asp Met Thr Asn Val Asn Ser Tyr Tyr Trp
 785 790 795 800
 35 Val Ser Asp Ala Tyr Gln Gln Gln Tyr Ala Val Pro Asn Tyr Leu Thr
 805 810 815
 Arg Arg Gln Phe Asn Leu Arg Leu Leu Val Glu Phe
 820 825

40 (2) INFORMATION FOR SEQ ID NO:320
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 679 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 45 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 50 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 55 (B) LOCATION 1...679
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:320

60 Pro Ile Pro Phe Leu Leu Asn Met Tyr Ser Gly His His Lys Ile His
 1 5 10 15
 Tyr Pro Phe Leu Ile Leu Leu Val Cys Leu Ala Phe Ala Ala Cys Lys
 20 25 30
 Ser Val Lys Leu Lys Asp Ala Glu Lys Ala His Asp Arg Gln Glu Tyr
 35 40 45
 65 Thr Lys Ala Ala Asp Met Tyr Asn Thr Leu Tyr Arg Arg Thr Arg Arg
 50 55 60
 Lys Gln Val Glu Met Lys Ala Tyr Thr Ala Phe Arg Ser Gly Glu Asn
 65 70 75 80
 70 Tyr Arg Ala Ala Gly Arg Gln Ala Lys Ala Leu Arg Gly Tyr Leu Asn
 85 90 95
 Ala Arg Arg Tyr Gly Tyr Pro Asp Ser Val Val Leu Leu Arg Leu Ala
 100 105 110
 Gln Thr Tyr Gln Gln Gly Gly Asn Tyr Lys Glu Ala Glu Val Leu Phe
 115 120 125
 75 Arg Gly Tyr Leu Glu Ala Tyr Pro Lys Ser Tyr Phe Ala Ala Ile Gly

242/ 490

130 135 140
 Leu Glu Gly Cys Leu Phe Ala Arg Gln Gln Lys Glu Tyr Pro Thr Arg
 145 150 155 160
 Tyr Arg Ile Arg Arg Ala Ala Glu Trp Asn Ser Ala Arg Gly Asp Phe
 165 170 175
 Gly Pro Ala Tyr Ala Pro Asp Ala Ser Ala Leu Tyr Phe Thr Ser Ser
 180 185 190
 Arg Ser Lys Asp Asp Gly Leu Asp Asn Ser Ser Ile Thr Gly Leu Lys
 195 200 205
 Pro Asn Asp Ile Tyr Ile Ile Lys Arg Asp Ala Gln Gly Arg Trp Gly
 210 215 220
 Arg Pro Asp Ser Val Ser Gly Gly Ile Asn Thr Pro Trp Asp Glu Gly
 225 230 235 240
 Val Pro Thr Ile Thr Pro Asp Gly Ser Thr Ile Tyr Tyr Thr Leu Ala
 245 250 255
 Gln Gln Gly Ala Asp Tyr Asp Arg Thr Val Gln Ile Tyr Ser Ala Ala
 260 265 270
 Arg Ser Gly Glu Gly Gly Trp Ser Asn Gly Ser Leu Val Asp Ile Met
 275 280 285
 Arg Asp Ser Leu Arg Met Ala Ala His Pro Ser Met Ser Ala Ser Gly
 290 295 300
 Asp Tyr Leu Tyr Phe Val Ser Asn Ile Gly Gly Ser Tyr Gly Gly Lys
 305 310 315 320
 Asp Ile Tyr Arg Val Lys Val Ser Asp Arg Ser Tyr Gly Ser Pro Glu
 325 330 335
 Asn Leu Gly Pro Asp Ile Asn Thr Pro Gly Asp Glu Met Phe Pro Phe
 340 345 350
 Ile Asp Gly Asp Ser Thr Leu Phe Phe Ala Ser Asp Gly His Ala Gly
 355 360 365
 Leu Gly Gly Leu Asp Ile Phe Lys Ala Thr Leu Asp Ser Thr Gly Gln
 370 375 380
 Trp His Val Val Asn Met Gly Gln Pro Val Asn Ser Ser Ala Asp Asp
 385 390 395 400
 Phe Gly Leu Ala Val Glu Pro Lys Gly Lys Asn Lys Glu Glu Ala Leu
 405 410 415
 Pro Asp Asn Gly Val Lys Gly Val Phe Cys Ser Asn Arg Gly Asp Ala
 420 425 430
 Arg Gly Trp Pro His Leu Phe His Phe Glu Leu Pro Ala Ile Tyr Thr
 435 440 445
 Glu Ile Gln Gly Tyr Val Met Asp Arg Glu Glu Asn Pro Ile Ala Gly
 450 455 460
 Ala Thr Val Arg Ile Val Gly Glu Arg Gly Pro Val Gly Gln Gly Phe
 465 470 475 480
 Val Thr Thr Arg Asp Asp Gly Ser Tyr Lys Met Ser Val Gln Gly Asp
 485 490 495
 Thr Arg Tyr Val Met Leu Ala Gly Ala Ser Gly Tyr Leu Asn Gln Tyr
 500 505 510
 Val Glu Leu Lys Thr Asp Thr Ala Lys Gln Ser Glu Thr Tyr Tyr Val
 515 520 525
 Asp Phe Phe Leu Ala Ser Arg Glu Lys Ala Glu Gly Leu Gln Asn Ile
 530 535 540
 Phe Tyr Asp Phe Asp Lys Ala Thr Leu Arg Pro Glu Ser Met Lys Ser
 545 550 555 560
 Leu Asp Glu Leu Ile Arg Ile Leu Thr Asp Asn Pro Asp Ile Arg Ile
 565 570 575
 Glu Leu Gly Ser His Ala Asp Arg Lys Gly Pro Asp Ala Tyr Asn Leu
 580 585 590
 Gly Leu Ser Asp Arg Arg Ala Lys Ser Val Val Asp Tyr Leu Thr Ser
 595 600 605
 Arg Gly Ile Ala Ala Asp Arg Leu Thr Trp Lys Gly Tyr Gly Lys Ser
 610 615 620
 Val Pro Lys Thr Val Thr Ala Lys Ile Ala Glu Arg His Asp Phe Leu
 625 630 635 640
 Lys Glu Gly Asp Val Leu Thr Glu Glu Phe Val Ala Pro Leu Thr Glu
 645 650 655
 Glu Gln Gln Ser Val Cys Asp Gln Leu Asn Arg Arg Thr Glu Phe Arg
 660 665 670
 Val Ile Glu Glu Glu Leu Arg
 675

(2) INFORMATION FOR SEQ ID NO:321

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 772 amino acids

(B) TYPE: amino acid

243/490

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

10 (ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321

15 Pro Ala Gln Pro Lys Thr Tyr Cys Ile Arg Tyr Phe Arg Arg Glu Val
1 5 10 15
Ser Pro Arg Arg Gln Thr Glu Arg Thr Leu Tyr Ala Asp Lys Met Arg
20 20 25 30
Arg His Ile Val Lys Cys Cys Pro Ser Ala Ser Ile Leu Leu Gln Glu
35 40 45
Tyr Ser Thr Thr Glu Leu Phe Ile His His Phe Asn Ile Ser Ile Ile
50 55 60
Met Lys Lys Phe Phe Phe Ala Leu Leu Ser Ile Gly Ile Ser Ala Gln
25 65 70 75 80
Ala Phe Ala Lys Thr Asp Asn Val Pro Thr Asp Ser Leu Arg Val His
85 90 95
Asn Leu Gln Thr Val Thr Val Tyr Ser Thr Arg Thr Ala Val Pro Leu
100 105 110
30 Lys Lys Ile Pro Ala Lys Met Glu Leu Ile Ser Ser Arg Asn Ile Lys
115 120 125
Gln Ser Gly Phe Asn Asn Met Thr Asp Ile Leu Lys Thr Gln Ser Ser
130 135 140
35 Leu Asp Val Ile Gln Tyr Pro Gly Phe Ser Ser Asn Ile Gly Ile Arg
145 150 155 160
Gly Phe Lys Pro Ser Gly Lys Tyr Val Thr Val Leu Val Asn Gly Ile
165 170 175
Pro Ala Gly Thr Asp Asn Ile Ser Thr Leu Asn Thr Ser Asn Ile Glu
180 185 190
40 Gln Ile Glu Ile Leu Lys Gly Pro Phe Ser Ser Ile Tyr Gly Thr Asn
195 200 205
Ala Met Gly Gly Val Val Asn Ile Ile Thr His Lys Ser Lys Asp Lys
210 215 220
45 Ile His Gly Asn Val Ser Leu Phe Gly Gly Ser Tyr Gln Thr Met Ala
225 230 235 240
Gly Ser Phe Asn Leu Gly Gly Arg Phe Glu Asp Ile Phe Ser Phe Asp
245 250 255
Leu Ser Leu Gly Leu Asp Lys Gln Asn Lys Asp Tyr Lys Thr Gly Ser
260 265 270
50 Asn Asn Phe Leu Ser Leu Ser Lys Leu Glu Glu Ala Ile Val Asp Val
275 280 285
Asn Ala Thr Lys Asn Lys Lys Met Lys Gly Ser Asp Tyr Thr Val Ala
290 295 300
55 Thr Gly Arg Leu Arg Phe Gly Ile Asp Phe Thr Pro Glu Trp Ser Leu
305 310 315 320
Asn Leu Tyr Gln Asn Val Phe Leu Gly Asp Ala Ile Pro Val Gly Gly
325 330 335
Ser Ile Trp Gly Val Tyr Gly Glu Ser Lys Lys Asn Leu Asn Arg Ser
340 345 350
60 Ser Thr Ser Phe Glu Leu Leu Gly Lys His Gly Cys His Thr Leu Gln
355 360 365
Phe Ser Pro Tyr Phe Asn Ile Glu Lys Ser Glu Asn Tyr Asn Asn Ala
370 375 380
65 Asp Pro Thr Gly Phe Ile Asn Tyr Lys Ser Asp Tyr Tyr Thr Tyr Gly
385 390 395 400
Ala Leu Leu Gln Asp Lys Ile Ser Phe Gly Gly Gln Asn Ile Val Leu
405 410 415
Gly Val Asp Ser Arg Asn Met Thr Met Glu Ser Glu Arg Phe Glu Gln
420 425 430
70 Ala Gly Val Asn Thr Lys Pro Tyr Asn Pro Gly Tyr Ala Thr Asn Asn
435 440 445
Ile Gly Leu Phe Gly Gln Ala Asn Phe Tyr Leu Leu Asn Asp Ala Leu
450 455 460
75 Ser Ile Ser Ala Gly Ala Arg Ala Asp Phe Met Phe Phe Asp Leu Lys
465 470 475 480

WO 99/29870

PCT/AU98/01023

244/ 490

Ala Asn Glu Tyr Leu Asn Asn Glu Ala Lys Gln Glu Thr His Asn Val
485 490 495
Ile Asn Pro Asn Val Gly Ile Lys Tyr Glu Phe Val Lys Gly Leu Thr
500 505 510
5 Ala His Gly Thr Phe Gly Ser Ala Phe Ser Ala Pro Asp Ala Phe Gln
515 520 525
Lys Ala Gly Gln Tyr Val Gly Pro Phe Gly Thr Thr Ile Gly Asn Pro
530 535 540
10 Asp Leu Lys Pro Glu Lys Ser Met Thr Trp Asp Phe Gly Ile Gly Tyr
545 550 555 560
Ser Asn Ala Arg Cys Gly Ile Gln Ala Asp Val Thr Leu Thr Tyr Phe
565 570 575
His Thr Asp His Lys Asp Leu Ile Leu Ser Ser Pro Asp Tyr Ala Asn
580 585 590
15 Asn Ile Thr Thr Tyr Ile Asn Ala Asp Lys Ala Arg Met Ser Gly Ile
595 600 605
Glu Ala Leu Leu Ser Tyr Asp Phe Gly Ser Leu Phe Ala Asn Lys Phe
610 615 620
20 Ser Leu Arg Ala Phe Ala Asn Ala Thr Ile Met Leu Asn Ser Glu Met
625 630 635 640
Lys Lys Ser Gln Thr Asp Ala Pro Trp Ser Glu Met Tyr Tyr Val Arg
645 650 655
Lys Gln Asn Ile Thr Phe Gly Ile Glu Tyr Arg Gly Lys Glu Gly Leu
660 665 670
25 Glu Val Met Leu Asn Gly Arg Phe Met Gly Arg Arg Ile Glu Gln Asn
675 680 685
Trp Tyr Ala Tyr Tyr Pro Glu Val Arg Pro Glu Leu Gln Gln Leu Leu
690 695 700
30 Ala Ala Glu Glu Pro Glu Leu Ala Ala Gln Gly Leu Leu Arg His Pro
705 710 715 720
Gln Ala Met Val Phe Asn Ala Ser Ala Tyr Tyr His Met Asn Lys Tyr
725 730 735
Leu Thr Phe Gly Val Asn Leu Asn Asn Ile Leu Asp Glu Leu Tyr Thr
740 745 750
35 Glu Lys Asp Gly Tyr His Met Pro Gly Arg Asn Ile Met Gly Lys Val
755 760 765
Met Val Asn Phe
770

40 (2) INFORMATION FOR SEQ ID NO:322

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 484 amino acids
(B) TYPE: amino acid
45 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
55 (B) LOCATION 1...484

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322

60 Gly Arg Ala Ser Ser Pro Tyr Arg Gln Met Asp Gly Ile Leu Asn Asp
1 5 10 15
Glu Tyr Arg Gln Ala Ser Met Asn Arg Phe Ser Asn His Trp Pro Cys
20 25 30
65 Ile Leu Val Gly Phe Val Leu Trp Phe Val Ser Ala Ser Arg Thr Val
35 40 45
Ala Gln Asn Ala Ser Glu Thr Thr Val Ser Tyr Asp Thr Asp Thr Ala
50 55 60
Val Leu Ser Glu Ala Asp Val Leu Arg Ile Ala Leu Ser Glu Asn Ala
65 70 75 80
70 Thr Val Lys Val Ala Asp Met Asp Val Arg Lys Gln Glu Tyr Ala Arg
85 90 95
Arg Ala Ala Arg Ala Asp Leu Phe Pro Lys Val Asp Leu Asn Gly Val
100 105 110
75 Tyr Ser His Thr Leu Lys Lys Gln Val Leu Tyr Ile Asp Met Pro Gly
115 120 125

WO 99/29870

PCT/AU98/01023

246/ 490

Leu Val Lys Val Ala Leu Ser Glu Ser Leu Pro Pro Gly Ala Lys Gln
 65 76 75 80
 Ile Arg Ile Gly Phe Ser Leu Pro Lys Glu Thr Glu Glu Lys Val Thr
 85 90 95
 5 Ala Leu Tyr Leu Leu Val Ser Asp Ser Leu Ala Val Arg Asp Leu Pro
 100 105 110
 Asp Tyr Lys Gly Arg Val Ser Tyr Asp Ser Phe Pro Ile Ser Lys Glu
 115 120 125
 10 Asp Arg Thr Thr Ala Leu Ser Ala Asp Ser Val Ala Gly Arg Arg Phe
 130 135 140
 Phe Tyr Leu Ala Ala Asp Ile Gly Pro Val Ala Ser Phe Ser Arg Ser
 145 150 155 160
 Asp Thr Leu Thr Ala Arg Val Glu Glu Val Ala Val Asp Gly Arg Pro
 165 170 175
 15 Leu Pro Leu Lys Glu Leu Ser Pro Ala Ser Arg Arg Leu Tyr Arg Gly
 190 195 200 205
 Tyr Glu Ala Leu Phe Val Pro Gly Asp Gly Gly Ser Arg Asn Tyr Arg
 210 215 220
 20 Ile Pro Ala Ile Leu Lys Thr Ala Asn Gly Thr Leu Ile Ala Met Ala
 225 230 235 240
 Asp Arg Arg Lys Tyr Asn Gln Thr Asp Leu Pro Glu Asp Ile Asp Ile
 245 250 255
 Val Met Arg Arg Ser Thr Asp Gly Gly Lys Ser Trp Ser Asp Pro Arg
 260 265 270
 25 Ile Ile Val Gln Gly Glu Gly Arg Asn His Gly Phe Gly Asp Val Ala
 275 280 285
 Leu Val Gln Thr Gln Ala Gly Lys Leu Leu Met Ile Phe Val Gly Gly
 290 295 300
 30 Val Gly Leu Trp Gln Ser Thr Pro Asp Arg Pro Gln Arg Thr Tyr Ile
 305 310 315 320
 Ser Glu Ser Arg Asp Glu Gly Leu Thr Trp Ser Pro Pro Arg Asp Ile
 325 330 335
 Thr His Phe Ile Phe Gly Lys Asp Cys Ala Asp Pro Gly Arg Ser Arg
 340 345 350
 35 Trp Leu Ala Ser Phe Cys Ala Ser Gly Gln Gly Leu Val Leu Pro Ser
 355 360 365
 Gly Arg Ile Thr Phe Val Ala Ala Ile Arg Glu Ser Gly Gln Glu Tyr
 370 375 380
 40 Val Leu Asn Asn Tyr Val Leu Tyr Ser Asp Asp Glu Gly Asp Thr Trp
 385 390 395 400
 Gln Leu Ser Asp Cys Ala Tyr Arg Arg Gly Asp Glu Ala Lys Leu Ser
 405 410 415
 45 Leu Met Pro Asp Gly Arg Val Leu Met Ser Ile Arg Asn Gln Gly Arg
 420 425 430
 Gln Glu Ser Arg Gln Arg Phe Phe Ala Leu Ser Ser Asp Asp Gly Leu
 435 440 445
 Thr Trp Glu Arg Ala Lys Gln Phe Glu Gly Ile His Asp Pro Gly Cys
 450 455 460
 50 Asn Gly Ala Met Leu Gln Val Lys Arg Asn Gly Arg Asp Gln Val Leu
 465 470 475 480
 His Ser Leu Pro Leu Gly Pro Asp Gly Arg Arg Asp Gly Ala Val Tyr
 485 490 495
 55 Leu Phe Asp His Val Ser Gly Arg Trp Ser Ala Pro Val Val Val Asn
 500 505 510
 Ser Gly Ser Ser Ala Tyr Ser Asp Met Thr Leu Leu Ala Asp Gly Thr
 515 520 525
 Ile Gly Tyr Phe Val Glu Glu Gly Asp Glu Ile Ser Leu Val Phe Ile
 530 535 540
 60 Arg Phe Val Leu Asp Asp Leu Phe Asp Val Arg Gln

(2) INFORMATION FOR SEQ ID NO:324

- 65 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 293 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 70 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
- 75

WO 99/29870

PCT/AU98/01023

247/ 490

(1.) FEATURE:
(A) NAME/KEY: misc_feature
(P) LOCATION: 1...293

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:324

Lys Ser Pro Ser Asp Ser Ala Leu Pro Ser Val Trp Ser Ala Asn Thr
1 5 10 15
Ile Ser Gly Leu Val Gly Gly Lys Arg Ile Thr Leu Leu Ile Leu Tyr
20 25 30
Ser Met Ala Ile Arg Ser Ser Asn Ile Glu Ser Ile Gln Cys Phe Val
35 40 45
Met Lys Lys Glu Lys Leu Trp Ile Ala Ile Val Ala Gly Leu Ala Phe
50 55 60
Val Leu Gly Leu Tyr Ala Leu Gly Arg Ser Val Ala Gln Leu Arg Arg
65 70 75 80
Ser Gln Pro Ser Val Thr Val Thr Gly Met Ala Glu Arg Asn Phe Lys
85 90 95
Ser Asp Leu Ile Val Trp Thr Ala Ser Tyr Gln Leu Gln Met Met Asp
100 105 110
Leu Glu Ser Ala Tyr Lys Ala Leu Lys Glu Lys Gln Ile Leu Val Ala
115 120 125
Asp Tyr Leu Lys Asn Lys Gln Leu Pro Asp Ser Ser Tyr Ile Phe Ser
130 135 140
Ser Val Ala Ile Ser Lys Glu Tyr Asn Tyr Tyr Tyr Asp Pro Arg Gln
145 150 155 160
Glu Gln Asn Val Arg Thr Phe Ala Gly Tyr Leu Leu Ser Gln Thr Val
165 170 175
Thr Val Thr Ser Gln Asp Ile Glu His Val Glu Lys Ile Ser Arg Asp
180 185 190
Ile Thr Glu Leu Ile Asn Gln Gly Val Glu Ile Thr Ser Asp Arg Pro
195 200 205
Ala Tyr Tyr Tyr Thr Lys Leu Asn Asp Leu Lys Val Glu Met Leu Arg
210 215 220
Asn Ala Ser Glu Asp Ala Phe Asn Arg Ala Ser Val Ile Ala Glu Gly
225 230 235 240
Ser Gly Ser Ser Val Gly Lys Met Leu Ser Ser Ser Met Gly Val Phe
245 250 255
Gln Ile Val Gly Leu Asn Ser Asn Glu Asp Tyr Ser Trp Gly Gly Ser
260 265 270
Phe Asn Thr Ser Ser Lys Met Lys Thr Ala Ser Ile Thr Val Lys Ala
275 280 285
Ser Phe Ala Leu Lys
290

45 (2) INFORMATION FOR SEQ ID NO:325

(i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 280 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

55 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

60 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...280

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:325

Gly Lys Leu Gln Met Lys Lys Thr Ile Ala Ile Ile Ala Ser Ala Leu
1 5 10 15
Leu Ala Leu Gly Ala Val Gly Cys Lys Lys Asn Ala Asp Thr Thr Ala
20 25 30
Val Ser Glu Lys Asp Ser Ile Ala Leu Ser Met Gly Ile Leu Tyr Gly
35 40 45
Gln Asp Phe Ala Asn Gln Phe Glu Met Ser Arg Leu Gln Gly Gln Pro
50 55 60
Ile Asp Ser Val Ala Phe Leu Asp Gly Phe Lys Tyr Gly Ile Asp Thr
65 70 75 80

248/ 490

Thr Arg Phe Ser Tyr Asn Leu Gly Ala Ile Tyr Ala Ser Asn Ile Ala
 85 90 95
 Arg Gln Leu Ala His Asp Ser Ile Asp Ile Asp Lys Phe Tyr Ala Ala
 100 105 110
 5 Met Arg Ala Ala Leu Leu Lys Asp Thr Val Ser Ile Ala Met Lys Pro
 115 120 125
 Ala Asp Ala Gln Ala Phe Met Gln Arg Ile Gln Ala Lys Lys Gln Arg
 130 135 140
 10 Glu Asn Asn Met Lys Gln Phe Gly Gln Asn Ile Glu Lys Gly Asn Glu
 145 150 155 160
 Tyr Ile Asp Thr Phe Lys Lys Glu Asp Gly Val Thr Val Thr Thr
 165 170 175
 Gly Leu Ala Tyr Lys Thr Leu Gln Glu Gly Thr Gly Ala Thr Pro Ser
 180 185 190
 15 Leu Ala Asp Thr Val Arg Val Lys Tyr Val Gly Thr Leu Val Asp Gly
 195 200 205
 Lys Glu Phe Asp Lys Asn Glu Glu Gly Ile Glu Phe Ala Val Thr Gly
 210 215 220
 20 Val Ile Lys Gly Trp Thr Glu Met Leu Gln Leu Met Lys Val Gly Gln
 225 230 235 240
 Lys Val Arg Val Val Ile Pro Gln Glu Leu Ala Tyr Gly Glu Thr Gly
 245 250 255
 Asn Tyr Thr Ile Glu Pro Phe Ser Thr Leu Thr Phe Glu Met Glu Leu
 260 265 270
 25 Ile Gly Ile Lys Pro Gly Lys Lys
 275 280

(2) INFORMATION FOR SEQ ID NO:326

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 803 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 35 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 40 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...803
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:326

Cys Arg Lys Gln Lys Leu Ser Asn Pro Lys Arg Ser Arg Tyr Pro Cys
 1 5 10 15
 50 Arg Arg Ile Ser Phe Arg Gln Ser Asp Lys Asn Pro Met Lys Val Leu
 20 25 30
 Arg Gln Val Phe Leu Pro Ile Leu Phe Val Leu Leu Thr Gly Ala Cys
 35 40 45
 55 Ser Thr Thr Lys Asn Leu Pro Glu Gly Glu Gln Leu Tyr Ile Gly Met
 50 55 60
 Gly Lys Thr Gln Ile Leu Arg Gln Asp Lys Ser His Ala Gly Gln Gln
 65 70 75 80
 Ala Leu Thr Glu Val Glu Ser Thr Leu Lys Val Thr Pro Asn Gly Ala
 85 90 95
 60 Ile Phe Gly Ser Ala Ser Ala Ser Leu Pro Lys Ile Pro Phe Gly Leu
 100 105 110
 Trp Leu Tyr Asn Ser Phe Val Gly Asp Ser Thr Val Ile Ser Lys Trp
 115 120 125
 65 Ile Phe Asp Lys Phe Ala Ala Lys Pro Val Phe Ile Ser Gln Val Lys
 130 135 140
 Ser Asp Ser Arg Ala Lys Val Ala Thr Asn Ile Leu Arg Glu His Gly
 145 150 155 160
 Tyr Phe Asp Ala Lys Val Lys Ser Ser Val Thr Thr Leu Lys Lys Asp
 165 170 175
 70 Ser Leu Lys Ala Lys Ile Ser Tyr Thr Val Asp Met Ala Ser Pro Tyr
 180 185 190
 His Tyr Asp Ser Ile Ile Pro Leu Pro Ile Ser Thr Phe Pro Asp Ser
 195 200 205
 75 Ile Leu Ala Tyr Arg Gln Thr Pro Ser Leu Ile Arg Lys Gly Asp Gln
 210 215 220

WO 99/29870

PCT/AU98/01023

249/ 490

5 Phe Asn Leu Ala Lys Leu His Glu Glu Arg Gln Thr Ile Ser Ala Leu
 235 230 235 240
 Leu Arg Arg Asn Gly Tyr Tyr Tyr Phe Arg Pro Gln Arg Ile Ile Tyr
 245 250 255
 Glu Ala Asp Thr Leu Leu Val Arg Gly Ala Val Cys Leu Arg Ala Lys
 260 265 270
 Leu Ser Glu Asp Thr Pro Pro Gln Ala Met Arg Pro Trp Arg Ile Gly
 275 280 285
 10 Lys Arg Thr Ala Val Leu Leu Gly Met Asn Gly Glu Ser Pro Thr Asp
 290 295 300
 Ser Leu Glu Val Glu Asp Met Lys Val Leu Tyr Tyr Arg Lys Met Pro
 305 310 315 320
 Val Arg Pro Lys Ile Leu Ala Lys Arg Phe Arg Phe Phe Ser Gly Asn
 325 330 335
 15 Leu Tyr Arg Gln Lys Asp Asp Glu Thr Thr Arg Lys Ser Leu Ala Arg
 340 345 350
 Leu Gly Ala Phe Ser Val Ile Asp Leu Asn Phe Leu Gln Arg Asp Ser
 355 360 365
 20 Ile Ser Gly Leu Leu Asp Val Arg Leu Leu Thr Thr Leu Asp Lys Pro
 370 375 380
 Trp Asp Ala Ser Leu Glu Thr Leu Phe Thr Ser Lys Ser Asn Asp Phe
 385 390 395 400
 Ile Gly Pro Gly Leu Asn Phe Ala Leu Ala Arg Arg Asn Val Phe Gly
 405 410 415
 25 Gly Gly Glu Asn Leu Ser Trp Asn Ile Gly Gly Ser Tyr Glu Trp Glu
 420 425 430
 Thr Gly Asn Arg Pro Glu Asn Ser Ser Asn Arg Leu Ile Asp Ile Asn
 435 440 445
 30 Ser Tyr Asn Met Asn Thr Ala Val Asn Leu Ser Phe Pro Ser Ile Val
 450 455 460
 Phe Pro Gly Leu Leu Asp Lys Tyr Tyr Tyr Tyr Pro Thr Thr Thr Thr
 465 470 475 480
 Phe Gln Ala Ser Ala Thr Ala Leu Asn Arg Ala His Tyr Phe Ser Met
 485 490 495
 35 Tyr Ser Phe Gly Phe Ser Thr Thr Tyr Glu Phe Gln Pro Ser Lys Glu
 500 505 510
 His Arg His Ala Ile Phe Pro Leu Lys Leu Asn Tyr Asn Leu Leu Gly
 515 520 525
 40 His Gln Thr Glu Thr Phe Gln Ala Ile Thr Ala Asn Asn Pro Pro Leu
 530 535 540
 Leu Leu Ser Leu Gln Ser Gln Phe Leu Ala Gln Met Gly Tyr Ile Tyr
 545 550 555 560
 Thr Phe Asn Lys Ser Val Ser Glu Lys Ser Pro His His Leu Trp Met
 565 570 575
 45 Gln Phe Gly Leu Ser Glu Ala Gly Asn Leu Leu Asn Leu Ile Tyr Leu
 580 585 590
 Ala Ala Gly Lys Lys Tyr Ser Asp Thr Lys Asn Phe Val Gly Val Pro
 595 600 605
 50 Phe Ser Gln Phe Ile Lys Ala Thr Gly Glu Leu Arg Tyr Ser Tyr Thr
 610 615 620
 Ile Asp Arg Asn Gln Ser Leu Ala Thr Arg Phe Gly Thr Gly Val Ile
 625 630 635 640
 Tyr Ser Tyr Gly Asn Met Arg Val Ala Pro Tyr Ser Glu Gln Phe Tyr
 645 650 655
 55 Val Gly Gly Ala Asn Ser Ile Arg Ala Phe Thr Val Arg Ser Ile Gly
 660 665 670
 Pro Gly Arg Phe Asn Pro Asp Ser Asp Asn Gln Tyr Ser Tyr Leu Asp
 675 680 685
 60 Gln Val Gly Glu Phe Lys Leu Glu Ala Asn Val Glu Tyr Arg Gly Lys
 690 695 700
 Leu Phe Gly Asp Leu His Ala Ala Val Phe Leu Asp Ala Gly Asn Val
 705 710 715 720
 Trp Leu Leu Arg Glu Asp Ser Ser Arg Pro Gly Gly Ala Leu Ser Glu
 725 730 735
 65 Val Gly Ser Val Ser Asn Phe Leu Asn Ser Ile Ala Leu Gly Thr Gly
 740 745 750
 Val Gly Leu Arg Tyr Asp Leu Ala Phe Leu Val Val Arg Val Asp Val
 755 760 765
 70 Gly Phe Gly Leu His Leu Pro Tyr Asn Thr Gly Lys Lys Gly Tyr Tyr
 770 775 780
 Asn Ile Pro Arg Phe Lys Asp Ala Ile Gly Phe His Leu Ala Val Gly
 785 790 795 800
 Tyr Pro Phe

WO 99/29870

PCT/AU98/01023

250/ 490

(C) INFORMATION FOR SEQ ID NO:327

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 783 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1...783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327

1	Ser	Leu	Ser	Pro	Tyr	Ile	Arg	Phe	Pro	Met	Ser	Ser	His	Ser	Val	Arg
5																
10	Tyr	Leu	Ile	Gly	Ile	Ala	Gly	Cys	Leu	Leu	Met	Leu	Ala	Ser	Ser	
15																
20	Cys	Ser	Val	Thr	Arg	Tyr	Val	Pro	Asp	Gly	Ser	Arg	Leu	Leu	Asp	Arg
25																
30	Val	Thr	Ile	Ala	Ser	Glu	Thr	Gly	Ser	Ile	Ala	Leu	Pro	Glu	Asp	Ile
35																
40	Arg	Asp	Tyr	Thr	Leu	Gln	Gln	Pro	Asn	Tyr	Arg	Leu	Phe	Gly	Met	Thr
45																
50	Arg	Trp	Leu	Leu	Arg	Val	Tyr	Ser	Ser	Ser	Asn	Pro	Asn	Ser	Asn	Ser
55																
60	Trp	Trp	Asn	Arg	Ser	Leu	Arg	Lys	Met	Gly	Glu	Pro	Pro	Val	Leu	Ile
65																
70	Asp	Ser	Val	Leu	Thr	Asp	Arg	Thr	Ala	Asn	Arg	Leu	Ala	Lys	Ala	Met
75																
80	Ala	Gly	Asp	Gly	Phe	Leu	Asp	Ala	Thr	Ala	Arg	Ala	Val	Val	Asp	Thr
85																
90	Gly	Leu	Tyr	Lys	Lys	Ala	Arg	Ile	Thr	Tyr	Leu	Ile	Gln	Pro	Gly	Ser
95																
100	Arg	Tyr	Tyr	Ile	Arg	Asn	Met	Ala	Leu	Asp	Val	Lys	Asn	Pro	Leu	Leu
105																
110	Pro	Pro	Val	Ala	Leu	Gly	Asn	Ser	Leu	Pro	Ser	Ala	Tyr	Lys	Val	Gly
115																
120	Ile	Ser	Glu	Gly	Ser	Pro	Leu	Ser	Pro	Ile	Val	Leu	Asp	Glu	Glu	Arg
125																
130	Lys	Ala	Ile	Ala	Arg	His	Met	Arg	Asn	Asn	Gly	Phe	Trp	Lys	Phe	Ser
135																
140	Ala	Glu	Asp	Val	Tyr	Tyr	Glu	Ala	Asp	Thr	Thr	Val	Ser	Gly	Gly	Ser
145																
150	Gly	Thr	Lys	Ser	Ala	Asp	Leu	Lys	Leu	Val	Val	Asn	Gly	Ile	Gly	Arg
155																
160	Tyr	Pro	Tyr	Arg	Ile	Gly	Arg	Val	Phe	Phe	His	Ala	Asp	Tyr	Asp	Pro
165																
170	Leu	Glu	Ser	Asp	Phe	Arg	Val	Gln	Glu	Leu	Pro	Arg	Ile	Asp	Ser	Ile
175																
180	Ser	Arg	Gly	Asp	Tyr	Thr	Val	Tyr	Tyr	Gly	Ser	Arg	Gly	Arg	Tyr	Ile
185																
190	Arg	Ala	Ser	Ala	Leu	Thr	Arg	Ser	Val	Ser	Val	Thr	Pro	Gly	Ala	Phe
195																
200	Phe	Cys	Glu	Asp	Asp	Val	Glu	Arg	Ser	Tyr	Ile	Lys	Leu	Asn	Ala	Leu
205																
210	Pro	Ile	Val	Arg	Asn	Val	Asn	Ile	Arg	Phe	Val	Glu	His	Asn	Gly	Lys
215																
220	Asp	Glu	Ile	Ala	Leu	Ala	Asp	Ser	Ser	Arg	Leu	Val	Asp	Cys	Tyr	Ile
225																
230	Leu	Thr	Val	Pro	Ala	Lys	Ser	Lys	Ser	Phe	Glu	Ala	Glu	Val	Leu	Gly
235																
240	Thr	Asn	Ser	Ala	Gly	Asp	Phe	Gly	Ala	Ala	Leu	Ser	Leu	Gly	Phe	Thr
245																
250	Asp	Arg	Asn	Leu	Phe	Arg	Gly	Ala	Glu	Met	Phe	Asn	Ile	Lys	Leu	Lys
255																
260	Gly	Ala	Tyr	Glu	Ala	Ile	Arg	Lys	Gly	Ser	His	Ser	Phe	Met	Glu	Tyr
265																
270	Gly	Val	Glu	Ser	Ser	Leu	Arg	Phe	Pro	Arg	Leu	Leu	Phe	Pro	Phe	Ile
275																

WO 99/29870

PCT/AU98/01023

251/490

5 Ser Asp 435 Thr Arg Arg Arg 440 Leu Arg Ala Ser Thr 445 Gln Trp Lys Ile
150 450 455 460
Gly Tyr Asn Tyr Gln Thr Arg Pro Glu Phe Asp Arg Val Ile Leu Ser
465 470 475 480
Ala Gln Leu Asn Tyr Ser Trp Gln Thr Tyr Leu His Asn Arg Leu Arg
485 490 495
His Thr Ile Arg Leu Leu Asp Val Asp Tyr Leu His Leu Pro Tyr Ile
500 505 510
10 Asp Pro Asp Phe Ala Gln Ser Leu Pro Pro Thr Thr Ala Leu Tyr Asn
515 520 525
Tyr Thr Glu Gln Phe Ile Leu Gly Ser Ala Tyr Ile Leu Asn Tyr Thr
530 535 540
15 Thr Ala Ser Ser Met Glu Arg Thr Val Ser Asn Pro Phe Thr Ala Arg
545 550 555 560
Phe Ser Ile Gln Thr Ala Gly Asn Leu Leu Gln Ala Ile Ser Tyr Leu
565 570 575
20 Thr Asp Ser Pro Lys Asp Glu His Gly Leu Tyr Lys Met Phe Gly Leu
580 585 590
His Tyr Ala Gln Phe Val Lys Leu Asp Leu Asp Leu Ala Lys Thr Val
595 600 605
Leu Leu Glu Lys Asp Asn Thr Leu Ala Leu His Leu Gly Phe Gly Leu
610 615 620
25 Ala Phe Pro Tyr Gly Asn Ala Arg His Ile Pro Phe Glu Leu Arg Tyr
625 630 635 640
Phe Ala Gly Gly Ser Asn Ser Val Arg Gly Trp Ser Val Arg Thr Leu
645 650 655
Gly Pro Gly Ser Met Lys Met Thr Pro Asp Lys Thr Phe Phe Asp Gln
660 665 670
30 Met Gly Asp Ile Arg Leu Asp Leu Asn Val Glu Tyr Arg Thr Lys Leu
675 680 685
Phe Trp Lys Phe Arg Ala Ala Phe Val Asp Ala Gly Asn Val Trp
690 695 700
35 Thr Ile Lys Glu Tyr Glu Asn Gln Glu Asp Gly Leu Phe Arg Phe Asp
705 710 715 720
Arg Phe Tyr Lys Glu Ile Ala Leu Ala Tyr Gly Leu Gly Leu Arg Leu
725 730 735
Asp Phe Asp Tyr Phe Leu Val Arg Leu Asp Ala Gly Leu Lys Ala Tyr
740 745 750
40 Asp Pro Gln Gln Thr Gly Arg Tyr Lys Trp Ala Ile Thr Arg Pro Asn
755 760 765
Leu Ser Ser Asn Phe Ala Trp His Ile Ala Val Gly Tyr Pro Phe
770 775 780

45 (2) INFORMATION FOR SEQ ID NO:328

(i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 875 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

55 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

60 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328

65 Val Glu Ser Lys Leu Leu Cys Leu Met Arg Lys Arg Ile Leu Gln Leu
1 5 10 15
Phe Leu Thr Ala Leu Leu Leu Ala Leu Gly Ser Ser Leu Ala Ile Ala
20 25 30
70 Gln Thr Val Val Thr Gly Lys Val Ile Asp Ser Glu Thr Ser Glu Pro
35 40 45
Leu Ile Gly Val Ser Val Ser Thr Gly Gln Gly Ala Ser Leu Arg Gly
50 55 60
Val Thr Thr Asp Met Asp Gly Gly Phe Arg Phe Glu Val Pro Ala Lys
65 70 75 80
75 Ser Val Leu Thr Phe Arg Cys Val Gly Tyr Ala Thr Val Thr Arg Ser

252 / 490

[illegible]

WO 99/29870

PCT/AU98/01023

253/490

5 His Cys Gly Val Glu Ala Glu Val Ser Tyr Arg Pro Ile Arg Gln Ile
690 695 700
Acp Leu Arg Gly Met Phe Ser Leu Gly Asp Trp Thr Trp Gln Asn Asn
705 710 715 720
Val Ser Tyr Thr Ser Tyr Asp Glu Ala Gly Asn Glu Thr Gly Gln Asp
725 730 735
Ile Thr Tyr Ile Lys Gly Leu His Val Gly Asp Ala Ala Gln Met Thr
740 745 750
10 Ala Ala Val Ser Ala Asp Ile Glu Leu Phe Lys Gly Phe His Val Ile
755 760 765
Gly Lys Tyr Asn Phe Leu Gly Lys Asn Tyr Ala Gly Phe Asn Pro Ala
770 775 780
Thr Arg Asn Ala Gln Gln Tyr Glu Ala Asp Gly Lys Glu Ile Val Glu
785 790 795 800
15 Ser Trp Lys Leu Pro Asp Val Gly Leu Phe Asp Leu Ser Ala Ser Tyr
805 810 815
Asn Phe Lys Leu Gly Ser Leu Ser Thr Thr Phe Tyr Phe Asn Met Asp
820 825 830
20 Asn Val Ala Asp Lys Arg Tyr Val Ser Asp Ala Asp Asp Asn Ile Ile
835 840 845
Gly Lys Lys His Asp Glu Ala Ser Ala Leu Val Trp Tyr Gly Phe Gly
850 855 860
Arg Thr Trp Ser Thr Gly Ile Arg Val Asn Phe
865 870 875

(2) INFORMATION FOR SEQ ID NO:329

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 460 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329

45 Asn Arg Cys Asn Pro Ser Arg Gln Tyr Phe His Leu Ser Gln Asn Asp
1 5 10 15
Val Gly Arg Ser Leu Arg Ala Phe Leu Ile His Leu Ser Met Lys Phe
20 25 30
50 Ser Ile Arg Leu Phe Leu Cys Ile Ile Phe Leu Leu Ser Ala Phe Ile
35 40 45
Leu Pro Ala Leu Gly Gln Lys Ser Lys Gln Val Gln Arg Leu Glu Lys
50 55 60
Gln Arg Lys Glu Ala Leu Lys Ala Ile Glu Lys Thr Asp Arg Glu Leu
65 70 75 80
Arg Asn Thr Lys Lys Asp Lys Gln Asp Lys Gln Lys His Leu Asn Leu
85 90 95
Leu Asn Lys Gln Val Ala Gln Arg Lys Gln Met Val Gln Leu Leu Asp
100 105 110
60 Asn Glu Val Lys Glu Leu Gln Ser Asp Ile Asp Ser Met Thr Gly Val
115 120 125
Cys His Gln Leu Ser Val Glu Glu Lys Ala Arg Ser Asp Glu Tyr Ala
130 135 140
Gln Ala Leu Gln Ser Met Gln Lys Arg Lys Arg Ser Leu Asp Arg Ile
145 150 155 160
65 Leu Phe Ile Ser Ser Ala Lys Ser Phe Asp Glu Gly Met Arg Arg Met
165 170 175
Arg Phe Leu Glu Gln Tyr Ala Ser Ala Tyr Lys Leu Ala Ser Val Arg
180 185 190
70 Leu Arg Asp Thr Arg Ser Lys Leu Glu Thr Glu Arg Ala Thr Val Glu
195 200 205
Asp Ala Lys Lys Glu Lys Gly His Leu Leu Val Ile Arg Glu Glu Glu
210 215 220
Lys Lys Lys Leu Glu Gly Gln Gln Ala Glu Gln Arg Arg Gln Val Gln
225 230 235 240

SUBSTITUTE SHEET (Rule 26) (RO/AU)

WO 99/29870

PCT/AU98/01023

254/ 490

Ala Leu Gly Ala Lys Gln Lys Asp Leu Glu Ala Gln Leu Arg Lys Gln
 245 250 255
 Lys Lys Gln Ala Glu Ala Leu Asn Arg Lys Ile Glu Lys Gln Ile Ala
 260 265 270
 5 Lys Glu Ile Glu Ala Ala Glu Arg Arg Ala Arg Glu Glu Arg Glu Arg
 275 280 285
 Leu Ala Arg Glu Ala Lys Ala Lys Gly Lys Pro Val Pro Ala Glu Pro
 290 295 300
 10 Glu Arg Lys Ala Glu Thr Lys Gly Gly Tyr Ala Met Asp Ala Ser Glu
 305 310 315 320
 Arg Ala Leu Ser Gly Ser Phe Ala Gln Asn Lys Gly Arg Leu Pro Gly
 325 330 335
 Pro Val Arg Gly Arg Tyr Arg Ile Val Ser Asp Phe Gly Val His Gln
 340 345 350
 15 His Ser Glu Leu Lys Lys Val Gln Val Asn Asn Gly Gly Ile Asp Ile
 355 360 365
 Ala Val Ala Thr Gly Ser Asp Ala Thr Ser Val Phe Asp Gly Val Val
 370 375 380
 20 Ser Ser Val Phe Val Ile Pro Gly Tyr Asn Ser Ala Val Met Val Arg
 385 390 395 400
 His Gly Asn Tyr Ile Thr Val Tyr Ala Asn Leu Ser Lys Val Tyr Val
 405 410 415
 Asn Ser Gly Thr Arg Val Lys Thr Gly Gln Ala Leu Gly Arg Ala Tyr
 420 425 430
 25 Thr Asp Pro Ser Asn Asn Gln Thr Ile Ile His Phe Glu Ile Trp Lys
 435 440 445
 Glu Arg Ser Lys Gln Asn Pro Arg Leu Trp Leu Arg
 450 455 460
 30 (2) INFORMATION FOR SEQ ID NO:330
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 342 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 35 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 40 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...342
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:330
 50 Ser Phe Tyr Gln Glu Ile Asp Arg Leu Met Lys Lys Tyr Leu Leu Tyr
 1 5 10 15
 Ala Ser Leu Leu Thr Ser Val Leu Leu Phe Ser Cys Ser Lys Asn Asn
 20 25 30
 55 Pro Asn Glu Pro Val Glu Asp Arg Ser Ile Glu Ile Ser Ile Arg Val
 35 40 45
 Asp Asp Phe Thr Lys Thr Gly Glu Ala Val Arg Tyr Glu Arg Asn Gln
 50 55 60
 Gly Ser Ala Ala Glu Arg Leu Ile Thr Asn Leu Tyr Leu Leu Phe
 65 70 75 80
 60 Asp Gln Ser Gly Ala Asn Pro Ala Lys Tyr Tyr Ile Thr Gly Asn Thr
 85 90 95
 Phe Thr Gly Gly Thr Trp Leu Pro Asp Asp Met Lys Val Lys Leu Asp
 100 105 110
 65 Met Thr Gln Ser Glu Ala Gly Glu Arg Lys Val Tyr Val Val Ala Asn
 115 120 125
 Val Asp Asn Ala Val Lys Thr Ala Leu Asp Ala Val Ala Asn Glu Ser
 130 135 140
 Asp Leu Gln Thr Val Lys Arg Thr Thr Ala Met Pro Trp Ser Thr Asp
 145 150 155 160
 70 Ile Ala Ser Pro Phe Leu Met Ser Gly Asn Lys Thr His Asp Phe Leu
 165 170 175
 Ala Asn Arg Leu Leu Asp Asn Val Pro Leu Val Arg Ala Ile Ala Lys
 180 185 190
 75 Val Glu Leu Asn Ile Ser Leu Ser Glu Lys Phe Gln Ile Val Pro Ile
 195 200 205

SUBSTITUTE SHEET (Rule 26) (RO/AU)

WO 99/29870

PCT/AU98/01023

255/ 490

Ile Val Asn Gly Ser Leu Ser Glu Phe Lys Phe Arg Tyr Val Asn Phe
 210 215 220
 Asp Lys Glu Thr Tyr Val Val Lys Pro Thr Thr Lys Pro Asp Asn Leu
 225 230 235 240
 5 Ile Ser Ser Ala Asn Gly Val Trp Pro Gln Ile Thr Asp Trp Thr Val
 245 250 255
 Trp Gly Ala Ser Leu Asn Thr Ser Pro Ala Pro Asp Ala Gly Thr Gly
 260 265 270
 10 Tyr Thr Leu Asp Ala Asn Gly Lys Val Thr Ala Leu Arg Ile Val Thr
 275 280 285
 Tyr Leu Asn Glu Arg Asp Ser Lys Gly Ala Thr Val Glu Val Ala Leu
 290 295 300
 Pro Arg Val Asp Asp Gly Thr Leu Pro Pro Pro Glu Phe Gly Pro Glu
 305 310 315 320
 15 Leu Tyr Arg Leu Pro Leu Pro Asp Lys Ile Leu Arg Asn His Trp Tyr
 325 330 335
 Lys Tyr Glu Val Glu Ile
 340

(2) INFORMATION FOR SEQ ID NO:331

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 329 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...329

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:331

Asn Leu Arg Thr Gln Pro Phe Phe Leu Val Asp Leu Gln Ser Met Ile
 1 5 10 15
 Arg Thr Ile Leu Ser Arg Tyr Val Ser Ser Asn Phe Trp Ser Arg Gly
 20 25 30
 45 Ala Thr Phe Phe Thr Ile Phe Pro Ala Phe Ile Leu Ala Ala Thr
 35 40 45
 Ala Leu Pro Ala Cys Gly Gly Thr Ala Ser Gly Ser Asp Arg Thr
 50 55 60
 Leu Ala Val Thr Ile Glu Pro Gln Lys Tyr Phe Ile Glu Ser Ile Ala
 65 70 75 80
 50 Asp Lys Ser Val Gln Val Val Ala Leu Val Pro Ala Gly Ser Asn Pro
 85 90 95
 Glu Glu Tyr Asp Pro Ser Pro Thr Val Met Lys Arg Leu Ser Glu Ala
 100 105 110
 55 Asp Ala Tyr Phe Tyr Ile Gly Gly Leu Gly Phe Glu Gln Arg Asn Leu
 115 120 125
 Ala Ala Ile Arg Asp Asn Asn Pro Lys Leu Pro Leu Phe Glu Met Gly
 130 135 140
 Lys Ala Leu Ala Asp Ala Gly Ser Ala Asp Leu His Gly Ser Cys Thr
 145 150 155 160
 60 Asp His Ser His Thr Asp Leu His Ala His Asp Pro His Tyr Trp Ser
 165 170 175
 Ser Val Val Gly Ala Lys Ala Leu Ser Arg Ala Ala Tyr Asp Ala Leu
 180 185 190
 65 Val Glu Leu Tyr Pro Asn Glu Lys Asp Lys Trp Asp Lys Gly His Asp
 195 200 205
 Arg Leu Asn Gly Arg Ile Asp Ser Val Lys Arg Leu Val Asp Thr Met
 210 215 220
 Phe Ala Asn Gly Lys Ala Asp Lys Ala Phe Val Ile Tyr His Pro Ser
 225 230 235 240
 70 Leu Ser Phe Phe Ala Gln Glu Phe Gly Leu Arg Gln Ile Val Ile Glu
 245 250 255
 Glu Asp Gly Lys Glu Pro Thr Ala Ala His Leu Arg Arg Val Ile Asp
 260 265 270
 75 Gln Ala Arg Ala Asp Gly Val Arg Ile Val Phe Ile Gln Pro Glu Phe
 275 280 285

258/490

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333

10 Lys Gln Ile Val Met Thr Val Lys Arg Ala Val Arg Ile Ala Leu Leu
 1 5 10 15
 Thr Leu Ile Gly Ile Leu Phe Ser Ser Pro Ser Leu Val Arg Ala Gln
 20 25 30
 Ser Leu Phe Ser Thr Glu His Val Leu Gln Leu Tyr Asn Lys Ile Leu
 35 40 45
 15 Tyr Gly Glu Ser Ala Ala Asp Thr Val Ala Glu Lys Thr Ala Gly Glu
 50 55 60
 Ser Ala Phe Pro Phe Ile Asp Lys Leu Ile Asn Leu Gly Arg Thr Phe
 65 70 75 80
 20 Leu Gly Lys Pro Tyr Arg Tyr Arg Gly Pro Ser Pro Trp Pro Met Asp
 85 90 95
 Cys Ser Gly Tyr Val Ser Tyr Leu Tyr Ser Lys Phe Asp Ile Lys Leu
 100 105 110
 Pro Arg Gly Ala Ala Ala Gln Ser Gln Tyr Thr Asn Pro Ile Glu Arg
 115 120 125
 25 Glu Asp Val Arg Pro Gly Asp Leu Leu Phe Phe Lys Gly Arg Asn Ala
 130 135 140
 Arg Ser Asn Arg Ile Gly His Val Ala Leu Val Ser Val Asp Glu
 145 150 155 160
 30 Asp Asp Ile Thr Met Met His Ser Arg Asn Ser Arg Gly Ile Val Ile
 165 170 175
 Glu Lys Leu Asn Arg Ser Ala Tyr Phe Ser Arg Arg Leu Val Ser Tyr
 180 185 190
 Gly Arg Val Pro Gly Ala Lys Arg Val Ile Pro Arg Lys Ser
 195 200 205

(2) INFORMATION FOR SEQ ID NO:334

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 467 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334

55 Lys Gly Thr Trp Asn Arg Lys Asn Arg Arg Glu Glu Met Lys Arg Thr
 1 5 10 15
 Ile Leu Leu Thr Ala Leu Thr Val Leu Ser Ser Leu Ser Leu Leu Arg
 20 25 30
 60 Ala Gln Asn Glu Ser Glu Ala Ser Thr Asn Pro Met Ser Gly Leu Ser
 35 40 45
 Leu Glu Asp Cys Ile Arg Ile Ala Lys Glu Arg Asn Leu Asn Leu Arg
 50 55 60
 Arg Gln Glu Ile Glu Gln Glu Asn Arg Ile Ile Ser Leu Asp Ala Ala
 65 70 75 80
 Arg His Ser Phe Leu Pro Ser Val Asn Ala Gly Ile Gly His Asn Tyr
 85 90 95
 Ser Phe Gly Arg Ser Lys Asp Lys Thr Gly Val Thr Val Asp Arg Ser
 100 105 110
 70 Ser Met Asn Thr Asn Leu Ser Ile Gly Ala Ser Val Glu Val Phe Ser
 115 120 125
 Gly Thr Arg Arg Leu His Asp Leu Lys Gln Gln Lys Tyr Asn Val Glu
 130 135 140
 Asp Gly Ile Ala Arg Leu Gln Lys Ala Arg Glu Asp Leu Ser Leu Gln
 145 150 155 160

WO 99/29870

PCT/AU98/01023

259/ 490

Ile Ala Ala Leu Tyr Ile Asn Leu Leu Phe Arg Gln Glu Met Thr Arg
 165 170 175
 Thr Ala Glu Thr Gln Leu Ala Leu Ile Arg Glu Gln Arg Asn Arg Thr
 180 185 190
 5 Ala Glu Met Val Arg Val Gly Lys Trp Ala Glu Gly Lys Leu Leu Asp
 195 200 205
 Ile Asn Ala Gln Met Ala Lys Asp Glu Gln Leu Leu Val Gln Tyr Arg
 210 215 220
 10 Ser Glu Glu Glu Leu Ala Arg Leu Asp Leu Gly Gln Ala Leu Glu Leu
 225 230 235 240
 Glu His Pro Glu Ser Ile Ala Val Lys Ala Pro Asp Thr Asp Val Leu
 245 250 255
 Val Ala Glu Arg Leu Gly Ser Leu Leu Ala Pro Glu Glu Ile Tyr Arg
 260 265 270
 15 Thr Ala Leu Gly Leu Lys Pro Ala Leu His Ser Ser Glu Leu Gln Ile
 275 280 285
 Ala Ser Ala Arg Glu Gly Leu Ala Ser Ala Arg Ala Tyr Phe Pro
 290 295 300
 20 Thr Leu Ser Leu Ser Ala Gly Tyr Ser Asn Gly Tyr Phe Arg Asp Leu
 305 310 315 320
 Gly Lys Glu Tyr Ala Ala Ile Asn Pro Ser Phe Ser Glu Gln Trp Lys
 325 330 335
 Asn Asn Gly Ser Tyr Ser Ile Gly Leu Ser Leu Asn Ile Pro Ile Phe
 340 345 350
 25 Ser Ala Met Gln Thr Gln Asp Arg Val Arg Ser Ser Arg Leu Gln Ile
 355 360 365
 Arg Ser Ser Glu Leu Arg Leu Val Glu Glu Lys Lys Ala Leu Tyr Lys
 370 375 380
 30 Glu Ile Arg Gln Ala Tyr Ser Asn Ala Val Ala Ala Asp Lys Ala Ile
 385 390 395 400
 Ala Ala Ala Glu Asn Ser Lys Ala Ala Thr Leu Lys Ala Tyr Glu Tyr
 405 410 415
 Ala Arg Asp Ser Phe Glu Ala Gly Arg Leu Ser Ala Tyr Glu Tyr Ala
 420 425 430
 35 Glu Ala Lys Thr Lys Tyr Ala Leu Ser Gln Val Glu Glu Leu Arg Ala
 435 440 445
 Lys Tyr Asp Phe Ile Tyr Lys Ala Lys Val Leu Asp Phe Tyr Gln Gly
 450 455 460
 40 Lys Asp Phe
 465

(2) INFORMATION FOR SEQ ID NO:335

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 451 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...451
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:335

Lys Thr Ser Tyr Arg Asn Asn Met Arg Phe Gln His Tyr Leu Ile Cys
 1 5 10 15
 65 Thr Ala Ala Val Ala Ala Leu Ala Ala Asn Pro Leu Thr Gly Gln Ser
 20 25 30
 Asn Met Thr Leu Glu Glu Cys Ile Asp Tyr Ala Arg Arg His Ser Ser
 35 40 45
 Ala Val Ala Leu Ser Ala Ala Glu Leu Glu Gln Ser Lys Ala Asp Tyr
 50 55 60
 70 Leu Gln Ala Val Gly Asn Phe Leu Pro Arg Val Ser Ala Gly Thr Gly
 65 70 75 80
 Ala Ser Trp Asn Phe Gly Arg Gly Leu Asp Ala Glu Thr Asn Thr Tyr
 85 90 95
 75 Thr Asp Ile Asn Ser Phe Asn Asn Ser Tyr Ser Ile His Ala Thr Met
 100 105 110

260/ 490

Thr Leu Phe Asp Gly Leu Gln Ser Val Tyr Arg Leu Arg Met Ala His
115 120 125
Ala Arg Arg Glu Ala Ser Arg Leu Ser Val Arg Glu Gln Gln Glu Leu
130 135 140
5 Ala Ala Leu Gly Thr Thr Glu Ala Tyr Tyr Asp Leu Val Tyr Ala Arg
145 150 155 160
Gln Met Gln Glu Leu Ala Met Gln Lys Tyr Glu Glu Ser Ser Arg Leu
165 170 175
10 His Arg Gln Thr Ala Arg Met Glu Glu Leu Gly Met Lys Ser Arg Pro
180 185 190
Asp Val Leu Glu Met Gln Ser Arg Met Ala Gly Asp Arg Leu Ala Leu
195 200 205
Thr Gln Ala Asp Asn Gln Cys Ile Ile Ala Leu Ile Arg Leu Lys Glu
210 215 220
15 Lys Met Asn Phe Pro Ile Asp Asp Glu Leu Val Val Asp Asp Met Pro
225 230 235 240
Ala Asp Ser Leu Ser Ala Asp Met Ala Glu Ser Asp Ser Ser Ala Gly
245 250 255
20 Val Phe Ala Arg Ala Ala His His His Pro Val Leu Leu Arg Ala Lys
260 265 270
Leu Asp Glu Gln Ala Ala Thr Asp Arg Leu Arg Ala Ala Arg Gly Ala
275 280 285
Phe Leu Pro Ser Val Ser Val Ser Gly Gly Trp Asn Thr Gly Phe Ser
290 295 300
25 Arg Phe Leu Asn Gly Ser Asp Tyr Thr Pro Phe Ser Glu Gln Phe Arg
305 310 315 320
Asn Arg Arg Gly Glu Tyr Val Ser Leu Asn Leu Ser Ile Pro Ile Phe
325 330 335
30 Ser Gly Phe Ser Leu Val Ser His Leu Arg Gln Ala Arg Ala Glu Arg
340 345 350
Arg Ala Ala Ile Val Arg Arg Gly Glu Ala Glu Arg Arg Leu Tyr Ser
355 360 365
Glu Ile Ala Gln Ala Met Ala Asp Arg Asp Ala Ala Leu Ala Ser Tyr
370 375 380
35 Arg Gln Ala Lys Glu His Thr Asp Ala Met Gln Thr Ala Tyr Glu Ala
385 390 395 400
Val Leu Gln Arg Tyr Glu Glu Gly Leu Asn Thr Ala Ile Asp Leu Thr
405 410 415
40 Thr Gln Ala Asn Arg Leu Leu Asp Ala Arg Val Gln Arg Leu Arg Ala
420 425 430
Ala Met Thr Tyr Arg Leu Lys Cys Lys Leu Ile Ala Tyr Tyr Gly Cys
435 440 445
Leu Ser Asp
450

45 (2) INFORMATION FOR SEQ ID NO:336
(1) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 962 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(11) MOLECULE TYPE: protein
55 (111) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
60 (1x) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...962
65 (x1) SEQUENCE DESCRIPTION: SEQ ID NO:336
Ala Ile Phe Val Val Ser Leu Gln Ile Glu Lys Ile Thr Glu Asn Lys
1 5 10 15
Tyr Asn Ser Asp Lys Ser Met Asn Lys Phe Tyr Lys Ser Leu Leu Gln
20 25 30
70 Ser Gly Leu Ala Ala Phe Val Ser Met Ala Thr Ala Leu Thr Ala Ser
35 40 45
Ala Gln Ile Ser Phe Gly Gly Glu Pro Leu Ser Phe Ser Ser Arg Ser
50 55 60
75 Ala Gly Thr His Ser Phe Asp Asp Ala Met Thr Ile Arg Leu Thr Pro
65 70 75 80

WO 99/29870

PCT/AU98/01023

261/ 490

	Asp	Phe	Asn	Pro	Glu	Asp	Leu	Ile	Ala	Gln	Ser	Arg	Trp	Gln	Ser	Gln
				85						90					95	
	Arg	Asp	Gly	Arg	Pro	Val	Arg	Ile	Gly	Gln	Val	Ile	Pro	Val	Asp	Val
				100					105					110		
5	Asp	Phe	Ala	Ser	Lys	Ala	Ser	His	Ile	Ser	Ser	Ile	Gly	Asp	Val	Asp
			115					120					125			
	Val	Tyr	Arg	Leu	Gln	Phe	Lys	Leu	Glu	Gly	Ala	Lys	Ala	Ile	Thr	Leu
			130				135					140				
10	Tyr	Tyr	Asp	Ala	Phe	Asn	Ile	Pro	Glu	Gly	Gly	Arg	Leu	Tyr	Ile	Tyr
			145			150					155				160	
	Thr	Pro	Asp	His	Glu	Ile	Val	Leu	Gly	Ala	Tyr	Thr	Asn	Ala	Thr	His
				165					170					175		
	Arg	Arg	Asn	Gly	Ala	Phe	Ala	Thr	Glu	Pro	Val	Pro	Gly	Ser	Glu	Leu
				180					185					190		
15	Ile	Met	Asp	Tyr	Glu	Val	Ser	Arg	Gly	Gly	Thr	Leu	Pro	Asp	Ile	Lys
			195					200					205			
	Ile	Ser	Gly	Ala	Gly	Tyr	Ile	Phe	Asp	Lys	Val	Gly	Gly	Arg	Pro	Val
			210				215					220				
20	Thr	Asp	Asn	His	Tyr	Gly	Ile	Gly	Glu	Asp	Asp	Ser	Asp	Ser	Asp	Cys
				225			230				235				240	
	Glu	Ile	Asn	Ile	Asn	Cys	Pro	Glu	Gly	Ala	Asp	Trp	Gln	Ala	Glu	Lys
				245					250					255		
	Asn	Gly	Val	Val	Gln	Met	Ile	Met	Val	Lys	Gly	Gln	Tyr	Ile	Ser	Met
				260					265					270		
25	Cys	Ser	Gly	Asn	Leu	Leu	Asn	Asn	Thr	Lys	Gly	Asp	Phe	Thr	Pro	Leu
			275					280					285			
	Ile	Ile	Ser	Ala	Gly	His	Cys	Ala	Ser	Ile	Thr	Thr	Asn	Phe	Gly	Val
			290				295					300				
30	Thr	Gln	Ser	Glu	Leu	Asp	Lys	Trp	Ile	Phe	Thr	Phe	His	Tyr	Glu	Lys
				305			310				315				320	
	Arg	Gly	Cys	Ser	Asn	Gly	Thr	Leu	Ala	Ile	Phe	Arg	Gly	Asn	Ser	Ile
				325					330					335		
	Ile	Gly	Ala	Ser	Met	Lys	Ala	Phe	Leu	Pro	Ile	Lys	Gly	Lys	Ser	Asp
				340					345					350		
35	Gly	Leu	Leu	Leu	Gln	Leu	Asn	Asp	Glu	Val	Pro	Leu	Arg	Tyr	Arg	Val
				355				360					365			
	Tyr	Tyr	Asn	Gly	Trp	Asp	Ser	Thr	Pro	Asp	Ile	Pro	Ser	Ser	Gly	Ala
				370			375					380				
40	Gly	Ile	His	His	Pro	Ala	Gly	Asp	Ala	Met	Lys	Ile	Ser	Ile	Leu	Lys
				385			390				395				400	
	Lys	Thr	Pro	Ala	Leu	Asn	Thr	Trp	Ile	Ser	Ser	Ser	Gly	Ser	Gly	Gly
				405					410					415		
	Thr	Asp	Asp	His	Phe	Tyr	Phe	Lys	Tyr	Asp	Gln	Gly	Gly	Thr	Glu	Gly
				420					425					430		
45	Gly	Ser	Ser	Gly	Ser	Ser	Leu	Phe	Asn	Gln	Asn	Lys	His	Val	Val	Gly
				435				440					445			
	Thr	Leu	Thr	Gly	Gly	Ala	Gly	Asn	Cys	Gly	Gly	Thr	Glu	Phe	Tyr	Gly
				450			455					460				
50	Arg	Leu	Asn	Ser	His	Trp	Asn	Glu	Tyr	Ala	Ser	Asp	Gly	Asn	Thr	Ser
				465			470				475				480	
	Arg	Met	Asp	Ile	Tyr	Leu	Asp	Pro	Gln	Asn	Asn	Gly	Gln	Thr	Thr	Ile
				485					490					495		
	Leu	Asn	Gly	Thr	Tyr	Arg	Asp	Gly	Tyr	Lys	Pro	Leu	Pro	Ser	Val	Pro
				500				505					510			
55	Arg	Leu	Leu	Gln	Ser	Thr	Gly	Asp	Gln	Val	Glu	Leu	Asn	Trp	Thr	
				515				520				525				
	Ala	Val	Pro	Ala	Asp	Gln	Tyr	Pro	Ser	Ser	Tyr	Gln	Val	Glu	Tyr	His
				530			535					540				
60	Ile	Phe	Arg	Asn	Gly	Lys	Glu	Ile	Ala	Thr	Thr	Lys	Glu	Leu	Ser	Tyr
				545			550				555				560	
	Ser	Asp	Ala	Ile	Asp	Glu	Ser	Ile	Ile	Gly	Ser	Gly	Ile	Ile	Arg	Tyr
				565					570					575		
	Glu	Val	Ser	Ala	Arg	Phe	Ile	Tyr	Pro	Ser	Pro	Leu	Asp	Gly	Val	Glu
				580					585					590		
65	Ser	Tyr	Lys	Asp	Thr	Asp	Lys	Thr	Ser	Ala	Asp	Leu	Ala	Ile	Gly	Asp
				595				600					605			
	Ile	Gln	Thr	Lys	Leu	Lys	Pro	Asp	Val	Thr	Pro	Leu	Pro	Gly	Gly	Gly
				610			615					620				
70	Val	Ser	Leu	Ser	Trp	Lys	Val	Pro	Phe	Leu	Ser	Gln	Leu	Val	Ser	Arg
				625			630				635				640	
	Phe	Gly	Glu	Ser	Pro	Asn	Pro	Val	Phe	Lys	Thr	Phe	Glu	Val	Pro	Tyr
				645					650					655		
	Val	Ser	Ala	Ala	Ala	Ala	Gln	Thr	Pro	Asn	Pro	Pro	Val	Gly	Val	Val
				660					665				670			
75	Ile	Ala	Asp	Lys	Phe	Met	Ala	Gly	Thr	Tyr	Pro	Glu	Lys	Ala	Ala	Ile

262/ 490

675 680 685
 Ala Ala Val Tyr Val Met Pro Ser Ala Pro Asp Ser Thr Phe His Leu
 690 695 700
 5 Phe Leu Lys Ser Asn Thr Asn Arg Arg Leu Gln Lys Val Thr Thr Pro
 705 710 715 720
 Ser Asp Trp Gln Ala Gly Thr Trp Leu Arg Ile Asn Leu Asp Lys Pro
 725 730 735
 Phe Pro Val Asn Asn Asp His Met Leu Phe Ala Gly Ile Arg Met Pro
 740 745 750
 10 Asn Lys Tyr Lys Leu Asn Arg Ala Ile Arg Tyr Val Arg Asn Pro Asp
 755 760 765
 Asn Leu Phe Ser Ile Thr Gly Lys Lys Ile Ser Tyr Asn Asn Gly Val
 770 775 780
 15 Ser Phe Glu Gly Tyr Gly Ile Pro Ser Leu Leu Gly Tyr Met Ala Ile
 785 790 795 800
 Lys Tyr Leu Val Val Asn Thr Asp Ala Pro Lys Ile Asp Met Ser Leu
 805 810 815
 Val Gln Glu Pro Tyr Ala Lys Gly Thr Asn Val Ala Pro Phe Pro Glu
 820 825 830
 20 Leu Val Gly Ile Tyr Val Tyr Lys Asn Gly Thr Phe Ile Gly Thr Gln
 835 840 845
 Asp Pro Ser Val Thr Thr Tyr Ser Val Ser Asp Gly Thr Glu Ser Asp
 850 855 860
 25 Glu Tyr Glu Ile Lys Leu Val Tyr Lys Gly Ser Gly Ile Ser Asn Gly
 865 870 875 880
 Val Ala Gln Ile Glu Asn Asn Asn Ala Val Val Ala Tyr Pro Ser Val
 885 890 895
 Val Thr Asp Arg Phe Ser Ile Lys Asn Ala His Met Val His Ala Ala
 900 905 910
 30 Ala Leu Tyr Ser Leu Asp Gly Lys Gln Val Arg Ser Trp Asn Asn Leu
 915 920 925
 Arg Asn Gly Val Thr Phe Ser Val Gln Gly Leu Thr Ala Gly Thr Tyr
 930 935 940
 35 Met Leu Val Met Gln Thr Ala Asn Gly Pro Val Ser Gln Lys Ile Val
 945 950 955 960
 Lys Gln

(2) INFORMATION FOR SEQ ID NO:337

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 702 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337

60 Trp Lys Lys Ser Asn Pro Gln Tyr Arg Gly Arg Thr Ala Asn Tyr Arg
 1 5 10 15
 Asp His Tyr Asn Thr Glu Ser Tyr Leu Ser Leu Arg Arg Asn Gln Thr
 20 25 30
 Met Lys Tyr Leu Ile Arg Leu Phe Leu Ser Leu Met Leu Leu Ser Leu
 35 40 45
 65 Trp Thr Gly Cys Thr His Glu Glu Leu Ser Ile Cys Asp Gly Glu Asn
 50 55 60
 Thr Leu Val Leu Arg Val Glu Thr Gly Lys Ala Pro Asn Ala Arg Ala
 65 70 75 80
 70 Thr Glu Pro Gly Gln Gly Ile Tyr Asn Glu Asn Lys Val Gly Ser Ile
 85 90 95
 Ser Val Leu Phe Tyr Leu Glu Gly Gln Leu Arg Trp Gln Val Lys Ser
 100 105 110
 Thr Asp Tyr Gln Ile His Glu Gly Ala Tyr Ile Ile Pro Val Lys Glu
 115 120 125
 75 Gln Met Arg Pro Leu Phe Asn Gly Asn Asn Asn Phe Ser Ile Tyr Val

WO 99/29870

PCT/AU98/01023

263/ 490

	130		135		140
	Val Ala Asn Leu Asp Phe Asn Ala Pro Ala Thr Glu Ala Ala Leu Ser				
	145		150		155
	Gln Phe Val Val Glu Lys Ser Ile Glu Val Ser Ser Thr Thr Ala Pro				
5		165		170	175
	Ala Asp Phe Val Met Leu Ala His Gly Asn Lys Gln Ile Asn Met Ala				
	180		185		190
	Thr Thr Glu Gly Lys Leu Leu Gly Asp Tyr Lys Leu Lys Arg Val Ala				
10		195		200	205
	Ala Lys Ile Arg Met Ile Lys Pro Thr Ile Asn Val Gln Gly Tyr Glu				
	210		215		220
	Val Val Gly Asn Ile Gln Ala Lys Phe Arg Asn Ser Val Thr Lys Gly				
	225		230		235
	Phe Leu Thr Thr Glu Ala Gln Glu Ile Pro Ala Ala Ala Ser Tyr Lys				
15		245		250	255
	Thr Ser Glu Tyr Leu Asp Ile Ala Glu Ser Ala Pro Ala Asn Ser Ile				
	260		265		270
	His Phe Tyr Ser Tyr Tyr Asn Lys Trp Thr Leu Ser Thr Pro Glu Lys				
	275		280		285
20		Arg Pro Glu Phe Phe Ile Met Val Lys Phe Lys Lys Thr Gly Gln Pro			
	290		295		300
	Asp Asn Thr Ala Lys Pro Tyr Tyr Arg Val Pro Leu Glu Ser Gln				
	305		310		315
	Asp Asn Gln Val Lys Ser Asn Val Leu Tyr Asn Leu Asn Val Lys Ile				
25		325		330	335
	Glu Ile Leu Gly Ser Leu Gln Glu Pro Glu Ala Val Ser Val Asn Gly				
	340		345		350
	Thr Leu Ala Ile Glu Glu Trp Ile Leu His Gln Asp Ala Phe Asn Leu				
	355		360		365
30		Pro Ala Thr Asn Tyr Leu Ile Val Glu Gln His Glu Ile Phe Met Asn			
	370		375		380
	Asn Val Asn Thr Tyr Ser Val Lys Tyr Gln Thr Ser Gln Lys Pro Ile				
	385		390		395
	Ser Ile Ser Ile Gln Ser Val Thr Phe Ser Tyr Val Ser Ser Asp Gly				
35		405		410	415
	Thr Gln His Asn Asp Leu Val Ala Ser Ser Ser Asp Gln Tyr Pro Thr				
	420		425		430
	Ile Thr Ser Asp Asn Thr Ser Ile Ile Thr Ser Lys Ile Pro Val				
	435		440		445
40		Asn Asn Val Pro Lys Lys Ile Val Phe Glu Val Thr Asn Gly Val Ala			
	450		455		460
	Gly Leu Lys Glu Thr Val Thr Val Leu Gln Tyr Pro Ala Gln Phe Ile				
	465		470		475
	Val Asn Thr Leu Gly Thr Ala Ser Ala Trp Arg Pro Asp Gly Ser Leu				
45		485		490	495
	Ala Pro Gly Leu Asn Asn Lys Ala Ile Tyr His Val Val Val Leu Val				
	500		505		510
	Pro Pro Glu Asn Leu Phe Glu Asp Gly Thr Gln Thr Ile Ile Gly Tyr				
	515		520		525
50		Pro Pro Thr Glu Thr Ile Ser Phe His Lys Lys Glu Asn Asn Thr Tyr			
	530		535		540
	Pro Ile Val Trp Ser Asp Thr Asn Thr Thr Lys Gln Asp Leu Glu Thr				
	545		550		555
	Ser Arg Met Ile Ser Pro Ser Phe Glu Leu Ala Ser Gln Leu Gly Ala				
55		565		570	575
	Thr Leu Pro Met Pro Tyr Leu Glu Tyr Trp Pro Gly Thr Ser Tyr Leu				
	580		585		590
	Leu Asp Tyr Ser Gly Asn Tyr Asn Asn Lys Arg Tyr Ala Leu Phe Asn				
	595		600		605
60		Cys Ala Phe Tyr Trp Glu Lys Arg Lys Val Asn Asn Glu Glu Ile Lys			
	610		615		620
	Phe Asp Asp Trp Arg Leu Pro Thr Glu Ala Glu Ile Lys Leu Ile Asp				
	625		630		635
	Lys Leu Gln His Asn Glu Gln Ser Ala Val Gln Ala Ile Met Thr Gly				
65		645		650	655
	Asn Tyr Tyr Trp Asp Ser Tyr Ser Ala Asn Gly Ser Tyr Lys Met Gln				
	660		665		670
	Gly Gly Gly Gln Gly Asn Ser Ser Lys Ala Tyr Val Arg Cys Val				
	675		680		685
70		Arg Asp Val Lys Lys Pro Ile Arg Asp Lys Lys Ser Gly Lys			
	690		695		700

(2) INFORMATION FOR SEQ ID NO:338

75

(1) SEQUENCE CHARACTERISTICS:

WO 99/29870

PCT/AU98/01023

264/ 490

(A) LENGTH: 1312 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
10 (A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1312

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:338

Lys Arg Val Asp Ser Tyr Glu Cys Arg Gln Lys Ala Cys Lys Cys Ala
1 5 10 15
20 Ile Cys Val Ile Gln Lys Phe Thr Asn Val Lys Leu Asn Asp Met Arg
20 25 30
Lys Ile Leu Ser Phe Leu Met Met Cys Ser Leu His Leu Gly Leu Gln
35 40 45
25 Ser Gln Thr Trp His Gly Asp Pro Asp Ser Val Ala Ala Leu Pro Ser
50 55 60
Ile Gly Ile Gln Glu Ser Ser Cys Thr Arg Ile Thr Phe Glu Val Val
65 70 75 80
Phe Pro Gly Phe Tyr Ser Val Glu Lys Arg Glu Gly Asn Gln Val Phe
85 90 95
30 Gln Arg Ile Ser Met Pro Gly Cys Gly Ser Phe Gly Asn Leu Gly Glu
100 105 110
Ala Glu Leu Pro Val Leu Lys Lys Met Ile Ala Val Pro Glu Phe Ser
115 120 125
35 Thr Ala Asn Val Ala Val Lys Ile Lys Glu Thr Glu Thr Phe Asp Asn
130 135 140
Tyr Asn Ile Tyr Pro Asn Pro Thr Tyr Val Val Glu Glu Leu Pro Glu
145 150 155 160
Gly Gly Thr Tyr Leu Val Glu Ala Phe Ala Ile Asn Asn Asp Tyr Tyr
165 170 175
40 Ser Gln Asn Val Ser Leu Pro Ser Thr His Tyr Val Tyr Ser Gln Asp
180 185 190
Gly Tyr Phe Arg Ser Gln Arg Phe Ile Glu Val Thr Leu Tyr Pro Phe
195 200 205
45 Arg Tyr Asn Pro Val Arg Gln Glu Ile Leu Phe Ala Lys Lys Ile Glu
210 215 220
Val Thr Ile Thr Phe Asp Asn Pro Gln Pro Pro Leu Gln Lys Asn Thr
225 230 235 240
Gly Ile Phe Asn Lys Val Ala Ser Ser Ala Phe Ile Asn Tyr Glu Ala
245 250 255
50 Asp Gly Lys Ser Ala Ile Glu Asn Asp Met Val Phe Ser Arg Gly Thr
260 265 270
Thr Thr Tyr Ile Ser Gly Asn Val Ala Ser Asn Leu Pro Gln Asn Cys
275 280 285
55 Asp Tyr Leu Val Ile Tyr Asp Asp Met Phe Asn Val Asn Gln Gln Pro
290 295 300
His Asp Glu Ile Lys Arg Leu Cys Glu His Arg Ala Phe Tyr Asn Gly
305 310 315 320
Phe Asp Val Ala Ala Val Ser Ile Lys Asp Val Leu Asn Ser Phe Pro
325 330 335
60 Ser Asn Ala Thr Ser Tyr Ile Asn Glu Thr Lys Leu Lys Asn Phe Ile
340 345 350
Arg Ser Val Tyr Asn Gln Ser Asn Ala Lys Arg Thr Leu Asp Gly Lys
355 360 365
Leu Gly Tyr Val Leu Leu Ile Gly Lys Pro Leu Ser Lys Tyr Leu Ala
370 375 380
65 Asp Thr Asp Asn Thr Lys Val Pro Thr Ser Phe Ile His Asn Val Ser
385 390 395 400
Leu Ile Pro Ser His Pro Thr Phe Gly Ser Ile Cys Ala Ser Asp Tyr
405 410 415
70 Phe Phe Ser Cys Val Ser Pro Leu Asp Thr Val Gly Asp Leu Phe Ile
420 425 430
Gly Arg Phe Ser Val Thr Asn Ala His Glu Leu His Asn Leu Ile Glu
435 440 445
75 Lys Thr Ile Asn Lys Glu Ile Ser Tyr Asn Pro Ile Ala His Lys Asn
450 455 460

266/ 490

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1060      1065      1070
Thr Tyr Pro Glu Ser Asp Phe Ala Ile Ala Ala Leu Lys Glu Leu Phe
1075      1080      1085
Arg Ile Glu Lys Met Ser Gly Asn Asp Tyr Glu Gly Leu Lys Asp Tyr
5 1090      1095      1100
Phe Arg Ser Asn Pro Thr Ile Ile Ser Ser Gln Asn Leu Phe Pro Thr
1105      1110      1115      1120
Ala Asp Phe Leu Ser Ala Arg Cys Asp Ile Val Cys Glu Asn Tyr Gln
1125      1130      1135
10  Ser Ala Ile Asp Trp Tyr Glu Asn Arg Leu Asn Ser Glu Ile Ser Tyr
1140      1145      1150
Gln Asp Ser Val Phe Ala Val Ile Asp Leu Gly Asp Ile Tyr Trp Asn
1155      1160      1165
15  Met Gln Leu Asp Ser Leu Arg Gly Thr Gly Ile Asp Leu Asn Ile Leu
1170      1175      1180
Ser Cys Glu Gln Arg Lys Ser Leu Glu Ser His Gln Asn Val Lys Asn
1185      1190      1195      1200
Tyr Leu Leu Ser Thr Leu Pro Glu Ser Thr Gly Thr Leu Leu Pro Pro
1205      1210      1215
20  Leu Glu Cys Asn Lys Ser Ser Leu Asp Lys Ser Lys Ile Ile Ser Ile
1220      1225      1230
Ser Pro Asn Pro Ala Lys Ala Val Val Thr Ile Ile Tyr Tyr Thr Asp
1235      1240      1245
25  Asn Pro Ser Cys Ser Val Ile Lys Ile Tyr Gly Ile Asn Gly Ala Ser
1250      1255      1260
Ala Asp Ile Thr Gly Leu Pro Lys His Leu Ser Glu Gly Tyr Tyr Ser
1265      1270      1275      1280
Ile Gln Phe Asn Thr Ser Asn Phe Asp Pro Gly Phe Tyr Leu Val Thr
1285      1290      1295
30  Leu Asn Val Asp Gln Lys Ile Ile Asp Thr Glu Lys Leu Arg Ile Lys
1300      1305      1310

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(2) INFORMATION FOR SEQ ID NO:339

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 938 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 40 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 45 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...938
- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:339

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Ser Glu Asn Tyr Arg Tyr Gly Lys Ile Thr Asn Gln Ile Met Ala Ile
1 5 10 15
55 Met Met Lys Ser Ile Val Phe Arg Ala Phe Leu Thr Ile Leu Leu Ser
20 25 30
Trp Ala Ala Ile Thr Asn Pro Thr Ala Gln Glu Ile Ser Gly Met Asn
35 40 45
60 Ala Ser Cys Leu Ala Ala Pro Ala Gln Pro Asp Thr Ile Leu Tyr Glu
50 55 60
Ser Phe Glu Asn Gly Pro Val Pro Asn Gly Trp Leu Glu Ile Asp Ala
65 70 75 80
Asp Ala Asp Gly Ala Thr Trp Gly Ser Pro Ser Gly Ser Phe Ser Val
85 90 95
65 Pro Tyr Gly His Asn Gly Leu Cys Thr Tyr Ser His Ile Arg Ser Gly
100 105 110
Ile Ser Thr Ala Gly Asn Tyr Leu Ile Thr Pro Asn Ile Glu Gly Ala
115 120 125
70 Lys Arg Val Lys Tyr Trp Val Cys Asn Gln Tyr Ser Thr Asn Pro Glu
130 135 140
His Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala Ile Glu Asp Phe
145 150 155 160
Val Leu Leu Phe Asp Asp Ser Ile Thr Gly Lys Pro Thr Pro Leu Val
165 170 175
75 Trp Arg Arg Arg Ile Val Asp Leu Pro Glu Gly Thr Lys Tyr Ile Ala

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268/ 490

Lys Pro Leu Gln Leu Thr Gly Tyr Asn Ile Tyr Ala Asn Gly Ser Leu
 785 790 795 800
 Leu Val His Ile Gln Asp Pro Thr Val Leu Glu Tyr Ile Asp Glu Thr
 805 810 815
 5 Tyr Ser Ser Arg Asp Gly Gln Val Glu Met Glu Tyr Cys Val Thr Ala
 820 825 830
 Val Tyr Asn Asp Asn Ile Glu Ser Gln Ser Val Cys Asp Lys Leu Asn
 835 840 845
 10 Tyr Thr Ile Thr Ser Leu Asp Asn Ile Gln Ser Asp Thr Ser Leu Lys
 850 855 860
 Ile Tyr Pro Asn Pro Ala Ser Tyr Val Val Arg Ile Glu Gly Leu Ser
 865 870 875 880
 Arg Ser Lys Ser Thr Ile Glu Leu Tyr Asn Ala Leu Gly Ile Cys Ile
 885 890 895
 15 Leu Arg Glu Glu Thr His Ser Glu Lys Thr Glu Ile Asp Val Ser Arg
 900 905 910
 Leu Asn Asp Gly Val Tyr Leu Ile Lys Val Val Gly Gly Asn Lys Thr
 915 920 925
 20 Thr Thr Glu Lys Val Glu Ile Lys Arg Pro
 930 935

(2) INFORMATION FOR SEQ ID NO:340

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 606 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Porphyromonas gingivalis*
 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...606
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:340

Ile Ile Phe Cys Thr Ile His His Ser Glu Leu Glu Ile Met Asn Ser
 1 5 10 15
 45 Ile Met Lys Tyr Gln Leu Tyr Thr Ala Val Ile Met Ala Leu Ser Val
 20 25 30
 Ser Ser Val Cys Gly Gln Thr Pro Arg Asn Thr Glu Thr Lys Arg Pro
 35 40 45
 Asp Thr Leu Arg Arg Glu Leu Thr Ile Val Asn Asp Gln Thr Val Glu
 50 55 60
 Met Glu His Ala Asp Pro Leu Pro Ala Ala Tyr Lys Ala Ile Glu Pro
 65 70 75 80
 Arg Leu Lys Pro Phe Arg Pro Glu Tyr Asn Lys Arg Thr Phe Gly Phe
 85 90 95
 55 Val Pro Glu Val Ser Ser Ser Gly Arg Asn Asn Leu Pro Asn Ile Leu
 100 105 110
 Pro Thr Glu Gly His Met Lys His Arg Gly Tyr Leu Asn Ile Gly Ile
 115 120 125
 Gly His Thr Leu Asn Gln Arg Met Asp Ala Gly Tyr Arg Leu Ile Asp
 130 135 140
 60 Ala Glu Gln Glu Arg Leu Asn Leu Phe Leu Ser Tyr Arg Gly Met Lys
 145 150 155 160
 Ser Ala Phe Asn Thr Gly Asp Phe Asp Gly Asp Arg Lys Asp Arg Arg
 165 170 175
 65 Met Met Ala Gly Val Asp Tyr Glu Gln Arg Arg Pro Ser Phe Val Leu
 180 185 190
 Ala Thr Gly Leu Tyr Tyr Ser Asn His Tyr Phe Asn Asn Tyr Gly Arg
 195 200 205
 Gly Ala Thr Thr Asn Val Gly Ser Ile Pro Gln Leu Ser Thr Pro Val
 210 215 220
 70 Thr Pro Gln Met Asp Asn Gly Thr His Asn Val Arg Val Tyr Leu Gly
 225 230 235 240
 Ala Lys Asn Asp Val Ile Asp Ala Arg Ile Asp Tyr Arg Phe Phe Arg
 245 250 255
 75 Ser Ile Pro Tyr Leu Gly Thr Asp Pro Met Lys Ala Leu Thr Glu His
 260 265 270

WO 99/29870

PCT/AU98/01023

269/ 490

5 Thr Pro Glu Leu Asn Val Thr Met Ser Asn Glu Leu Ser Asp Asp Ile
275 280 285
Lys Leu Gly Val Glu Val Arg Thr Gly Gly Leu Phe Phe Ala Lys Asn
290 295 300
Ser Glu Met Ile Gln Thr Gly Val Leu Ser Glu Thr Asp Arg Asn Leu
305 310 315 320
Tyr Tyr Val Glu Gly Ala Pro Thr Ile Gly Phe Val Gly Asp Ser Asp
325 330 335
10 Asn Met Gln Trp Asn Ile Gln Ala Gly Val Gly Ile Ser Ser His Phe
340 345 350
Gly Ala Lys Gly Arg Leu Phe Phe Trp Pro Lys Leu Asp Ala Ser Leu
355 360 365
Ser Ile Phe Pro Ser Trp Arg Val Tyr Ala Lys Ala Phe Gly Gly Val
370 375 380
15 Ile Arg Asn Gly Leu Ala Asp Val Met Gln Glu Glu Met Pro Tyr Leu
385 390 395 400
Met Pro Asn Thr Ile Val Leu Pro Ser Arg Asn Ala Leu Thr Ala Gln
405 410 415
20 Leu Gly Val Lys Gly Asn Ile Ala Asp Val Val Arg Met Glu Val Tyr
420 425 430
Gly Asp Phe Ser Lys Leu Thr Gly Val Pro Phe Tyr Thr Pro Thr Leu
435 440 445
Pro Leu Tyr Asn Pro Ser Asp Leu Tyr Gln Tyr Asn Val Ser Phe Leu
450 455 460
25 Pro Ile Tyr Ala Asp Gly Ser Arg Trp Arg Ala Gly Gly Lys Leu Glu
465 470 475 480
Tyr Ser Tyr Arg Asp Met Leu Arg Phe Leu Val Asp Ala Ser Tyr Gly
485 490 495
30 Lys Trp Asn Leu Asp Gly Gly Leu Val Ala Ser Met Gln Pro Asp Leu
500 505 510
Ile Leu Lys Ala Glu Val Gly Val His Pro Ile Ala Pro Leu Asp Val
515 520 525
Arg Leu Arg Tyr Thr Gln Leu Asn Gly Arg Tyr Arg Tyr Ser Phe Gly
530 535 540
35 Ser Ala Gly Ser Glu Ala Leu Gly Ile Gly Asn Val His Leu Leu Ser
545 550 555 560
Ala Asp Val Ser Tyr Lys Leu Lys Lys Asn Leu Ser Leu Tyr Leu Lys
565 570 575
40 Ile Asp Asn Met Leu Ala Glu Thr Thr Glu Leu Ile Gly Tyr Tyr Pro
580 585 590
Met Gln Pro Phe His Cys Phe Ala Gly Phe Ser Trp Thr Phe
595 600 605

(2) INFORMATION FOR SEQ ID NO:341

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 357 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
50 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
55 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc feature
60 (B) LOCATION 1...357
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341

65 Asn Ser His Ala Thr Val Ser Val Ile Cys Ser Met Met Glu Lys Cys
1 5 10 15
Ile Phe Ala His Tyr Pro His Asn Leu Val Phe Met Ile Arg Lys His
20 25 30
Phe Gly Ile Ile Leu Gly Phe Leu Ser Leu Val Phe Ser Ala Gly Ala
35 40 45
70 Gln Gln Glu Lys Gln Val Phe His Phe Leu Asn Leu Pro Ala Thr Ala
50 55 60
Gln Ala Leu Ala Ala Gly Gly Lys Ala Ile Thr Ile Val Asp Asp Asn
65 70 75 80
75 Pro Gly Leu Ala Phe Glu Asn Pro Ala Leu Leu Gly Tyr Glu Ser Gly
85 90 95

WO 99/29870

PCT/AU98/01023

270/ 490

5 Gly Arg Ala Phe Leu Ser Tyr Leu Tyr Tyr Met Ser Gly Ser His Met
100 105 110
Gly Asn Ala Cys Tyr Ala Ser Ser Val Gly Glu Arg Gly Met Trp Gly
115 120 125
Val Gly Met Arg Phe Leu Asn Tyr Gly Ser Met Gln Gly Tyr Asp Gln
130 135 140
Asn Ala Ile Ala Thr Gly Ser Phe Ser Ala Ser Asp Ile Ala Val Gln
145 150 155 160
Gly Phe Tyr Ser His Glu Leu Ser Asn His Phe Arg Gly Gly Val Ser
10 165 170 175
Leu Lys Ala Leu Tyr Ser Ser Ile Glu Thr Tyr Ser Ser Phe Gly Leu
180 185 190
Gly Val Asp Val Gly Ile Ser Tyr Tyr Asp Asp Lys Gly Tyr Ser
195 200 205
15 Ala Ser Ala Leu Phe Lys Asn Val Gly Ala Gln Leu Lys Gly Tyr Asn
210 215 220
Glu Glu Arg Glu Pro Leu Asp Trp Asp Phe Gln Leu Gly Phe Ser Arg
225 230 235 240
Ser Phe Ile Asn Ala Pro Phe Arg Leu His Ile Thr Leu Phe Asn Leu
20 245 250 255
Asn Pro His Tyr Phe Lys Arg Leu Val Pro Arg Asp Leu Ser Lys Met
260 265 270
Gln Lys Phe Leu Arg His Phe Ser Ile Gly Ala Glu Phe Thr Pro Ser
275 280 285
25 Glu Arg Phe Trp Val Gly Leu Gly Tyr Thr Pro Gln Ile Ala Gln Asp
290 295 300
Phe Glu Val Glu Gly Gly Asn Lys Trp Gly Gly Leu Ser Ala Gly Val
305 310 315 320
Gly Phe Thr Ser Gly Val Val Arg Val Gly Val Ser Ala Ala Thr Tyr
30 325 330 335
His Pro Ala Ala Leu Ser Phe Met Cys Ser Val Gly Ile Arg Leu Asp
340 345 350
Asp Lys Ser Ile Phe
355

35 (2) INFORMATION FOR SEQ ID NO:342
40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 337 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
45 (iii) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
50 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...337

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:342
Pro Gln Pro Val Gly Leu Lys Glu Ile Thr Ile Lys Pro Met Cys Leu
1 5 10 15
Glu Pro Ile Ile Ala Pro Ile Ser Ser Glu Leu Leu Glu Gln Glu Leu
20 25 30
60 Thr Ala Asp Arg Phe Leu Arg Met Thr Asn Lys Ala Gly Asn Glu Ile
35 40 45
Tyr Val Phe Thr Ala Glu Glu Ala Pro His Cys Met Lys Glu Val Gly
50 55 60
65 Arg Leu Arg Glu Glu Ala Phe Arg His Tyr Gly Gly Thr Gly Lys
65 70 75 80
Ala Ile Asp Ile Asp Glu Phe Asp Thr Met Pro Gly Ser Tyr Lys Gln
85 90 95
Leu Ile Val Trp Asp Pro Gln Asn Lys Ala Ile Leu Gly Gly Tyr Arg
100 105 110
70 Phe Ile Tyr Gly Arg Asp Val Ala Phe Asp Thr Asp Gly Lys Pro Leu
115 120 125
Leu Ala Thr Ala Glu Met Phe Arg Phe Ser Asp Ala Phe Leu His Asp
130 135 140
75 Tyr Leu Pro Tyr Thr Val Glu Leu Gly Arg Ser Phe Val Ser Leu Gln
145 150 155 160

WO 99/29870

PCT/AU98/01023

271/ 490

5 Tyr Gln Ser Thr Arg Met Gly Thr Lys Ala Ile Phe Val Leu Asp Asn
165 170 175
Leu Trp Asp Gly Ile Gly Ala Leu Thr Val Val Asn Pro Glu Ala Leu
180 185 190
5 Tyr Phe Tyr Gly Lys Val Thr Met Tyr Lys Asp Tyr Asp Arg Arg Ala
195 200 205
Arg Asn Leu Ile Leu Tyr Phe Leu Arg Lys His Phe Ser Asp Pro Glu
210 215 220
10 Gly Leu Val Lys Pro Ile His Pro Leu Pro Ile Glu Ile Ser Ala Glu
225 230 235 240
Asp Glu Ala Leu Phe Ser Ser Ser Asp Phe Asp Thr Asn Tyr Lys Thr
245 250 255
Leu Asn Ile Glu Val Arg Lys Leu Gly Ile Asn Ile Pro Pro Leu Val
260 265 270
15 Ser Ala Tyr Ile Ala Leu Ser Pro Glu Met Arg Val Phe Gly Thr Ala
275 280 285
Val Asn Glu Ser Phe Gly Glu Val Glu Glu Thr Gly Ile Phe Ile Ala
290 295 300
20 Val Gly Lys Ile Leu Glu Glu Lys Lys Gln Arg His Ile Glu Ser Phe
305 310 315 320
Ile Leu Ser Arg Asn Glu Lys Lys Gly Leu Asp Ser Ser Asn Gly Arg
325 330 335
Ser

25 (2) INFORMATION FOR SEQ ID NO:343
30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 566 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
35 (iii) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
40 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...566
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343

45 Tyr Asp Gly Ala Arg Leu Val Tyr Thr Leu Phe Arg Asn Arg Asn Asp
1 5 10 15
Ile His Pro Met Lys Thr Ile Val Arg Tyr Ser Arg Leu Pro Val Ala
20 25 30
50 Leu Phe Phe Cys Leu Leu Gly Ala Val His Leu Ser Val Glu Ala Gln
35 40 45
Met Leu Asn Thr Pro Phe Glu Leu Ser Asp Gln Ile Val Leu Ser Pro
50 55 60
Thr Glu Arg Gln Tyr Arg Glu Ile Cys Val Gln Thr Lys Glu Lys Arg
65 70 75 80
55 Gly Ala Asp Leu Phe Pro Leu Ser Asp Lys Leu Arg Asp Ser Ala Tyr
85 90 95
Val Arg Phe Gly Ser Ala Tyr Gly Asp Ile Ala Gly Asp Tyr Leu Pro
100 105 110
60 Tyr Asn Gly Asn Asn Tyr Ser Ser Leu Ser Leu Glu Ser Gly Gly Arg
115 120 125
Ile Ser Val Arg Asn Tyr Gly Thr Leu Gln Gly Ser Ala Ser Tyr Ser
130 135 140
65 Arg Gly Met His Lys Arg Ile Gly Trp Asn Ala Leu Arg Asn Ala Glu
145 150 155 160
Ala Tyr Tyr Pro Tyr Leu Val Ser Asp Ser Thr Gly Gly Asp Tyr His
165 170 175
Phe Glu Asp Tyr Arg Leu Ala Gly Tyr Tyr Ser Phe Arg Ala Gly Arg
180 185 190
70 Leu Pro Leu Gly Ile Gly Phe Ser Tyr Arg Gly Glu Val Ala Tyr Arg
195 200 205
Leu Thr Asp Pro Arg Thr Thr Asn Thr Thr Gly Ala Leu Glu Leu Ser
210 215 220
75 Cys Ala Thr Ser Leu Thr Leu Pro Arg Glu Asn Arg Leu Ser Leu Ser
225 230 235 240

272/490

Ala Ala Tyr Leu Tyr His Arg Gln His Leu Thr Gln Tyr Asn Trp Arg
245 250 255
Pro Gly Gln Gln Asp Lys Phe Phe Val Ser Tyr Gly Phe Gly Gln Val
260 265 270
5 Asp Val Ser Asn Ser Pro Ile Trp Phe Gly Ile Ser Arg Met Asn Tyr
275 280 285
Val Asn Gly Trp Lys Leu Ser Ser Arg Leu Asp Thr Arg Arg Gly Asp
290 295 300
10 Ala Ile Gly Leu Asp Tyr Ser Gly Tyr Phe Leu Asp Thr Glu Glu Arg
305 310 315 320
Ser Ser Ile Asn Leu Phe Ala Leu Leu Tyr Asn Arg Leu Arg Leu Tyr
325 330 335
Gly Ser Trp His Leu Ser Asp Phe Asp Phe Ser Phe Ser Ala Asp Tyr
340 345 350
15 Ala Leu Arg Gln Gly Ile Glu Arg Ile Tyr Glu Asp Tyr Lys Pro Asp
355 360 365
Asp Asn Tyr His Ile Tyr Asp Leu Arg Ile Leu Ala Ile Arg Arg Trp
370 375 380
20 Tyr Met Leu Asn Glu Phe Ser Ala Gln Ala Gln Ala Ser Tyr Arg Ile
385 390 395 400
Arg Thr Asp Arg Gly Cys Ala Leu Arg Val Ser Ala Gly Ser Asp Phe
405 410 415
Tyr Gly Tyr Asp Glu Thr Tyr Arg Lys His Gly His His Thr Met Ser
420 425 430
25 Gly Met Leu Arg Pro Phe Ala Gly Ile Ala Tyr Asp His Ala Gly Ser
435 440 445
Lys Leu Asp Phe Gly Leu Ser Leu Ser Ala Ala Tyr Arg Met Val Leu
450 455 460
30 Thr His Ser Tyr Lys Ile Arg Thr Ile Gln Lys Glu Gln Leu Asp Tyr
465 470 475 480
Gln Leu Ala Tyr Leu Pro Tyr Ala Tyr Arg Asn Arg Glu Gly Val Glu
485 490 495
Val Arg Ser Ser Leu Tyr Val Ser Ile Pro Met Gln Asn Thr His Arg
500 505 510
35 Leu Met Thr Glu Leu Arg Leu Tyr Gly Asp Leu Met Lys Arg Lys Asp
515 520 525
Gly Ile Ala Tyr Gly Lys Thr Pro Gly Val Ile Ser His Ile Leu Ser
530 535 540
40 Asp Pro Gln Ala Glu Arg Thr Ser Gly His Thr Ile Gly Ala Ile Cys
545 550 555 560
Asn Ile Ser Tyr Leu Phe
565

(2) INFORMATION FOR SEQ ID NO:344

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 819 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344

Arg Thr Asn Val Phe Leu Ser Leu Ser His Lys Ile Gly Arg Arg Gly
1 5 10 15
Ala Ser Cys Ser Asn Arg Asn Ala Trp Met Ala Glu Asn Lys Pro Ser
20 25 30
Ser Pro Glu Pro Asp Asn Thr Gly Val Gly Asn Ser Pro Ser Asp Tyr
35 40 45
70 Leu His Gly Glu Ala Ile Ile Pro Pro Leu Ser Ser Leu Ser Asn Phe
50 55 60
Asn Asp Lys Arg Phe Met Lys Lys Leu His Met Ile Ala Ala Leu Ala
65 70 75 80
75 Val Leu Pro Phe Cys Leu Thr Ala Gln Ala Pro Val Ser Asn Ser Glu
85 90 95

WO 99/29870

PCT/AU98/01023

273/ 490

	Ile	Asp	Ser	Leu	Ser	Asn	Val	Gln	Leu	Gln	Thr	Val	Gln	Val	Val	Ala
	Thr	Arg	Ala	Thr	Ala	Lys	Thr	Pro	Val	Ala	Tyr	Thr	Asn	Val	Arg	Lys
5	Ala	Glu	Leu	Ser	Lys	Ser	Asn	Tyr	Gly	Arg	Asp	Ile	Pro	Tyr	Leu	Leu
	Met	Leu	Thr	Pro	Ser	Val	Val	Ala	Thr	Ser	Asp	Ala	Gly	Thr	Gly	Ile
10	Gly	Tyr	Ser	Gly	Phe	Arg	Val	Arg	Gly	Thr	Asp	Ala	Asn	Arg	Ile	Asn
	Ile	Thr	Thr	Asn	Gly	Val	Pro	Leu	Asn	Asp	Ser	Glu	Ser	Gln	Ser	Val
	Phe	Trp	Val	Asn	Met	Pro	Asp	Phe	Ala	Ser	Ser	Ile	Glu	Asp	Leu	Gln
15	Val	Gln	Arg	Gly	Val	Gly	Thr	Ser	Thr	Asn	Gly	Ala	Gly	Ala	Phe	Gly
	Ala	Ser	Val	Asn	Met	Arg	Thr	Asp	Asn	Leu	Gly	Leu	Ala	Pro	Tyr	Gly
20	Arg	Val	Asp	Leu	Ser	Gly	Gly	Ser	Phe	Gly	Thr	Phe	Arg	Arg	Ser	Val
	Lys	Leu	Gly	Ser	Gly	Arg	Ile	Gly	Arg	His	Trp	Ala	Val	Asp	Ala	Arg
	Leu	Ser	Lys	Ile	Gly	Ser	Asp	Gly	Tyr	Val	Asp	Arg	Gly	Ser	Val	Asp
25	Leu	Lys	Ser	Tyr	Phe	Ala	Gln	Val	Gly	Tyr	Phe	Gly	Ser	Asn	Thr	Ala
	Leu	Arg	Phe	Ile	Thr	Phe	Gly	Gly	Lys	Glu	Val	Thr	Gly	Ile	Ala	Trp
30	Asn	Gly	Leu	Ser	Lys	Glu	Asp	Glu	Ala	Lys	Tyr	Gly	Arg	Arg	Tyr	Asn
	Ser	Ala	Gly	Leu	Met	Tyr	Val	Asp	Ala	Gln	Gly	Val	Pro	His	Tyr	Tyr
	His	Asn	Thr	Asp	Asn	Tyr	Glu	Gln	Arg	His	Tyr	His	Ala	Ile	Met	Thr
35	His	Ser	Phe	Ser	Pro	Ser	Val	Ile	Leu	Asn	Leu	Thr	Ala	His	Tyr	Thr
	Ala	Gly	Tyr	Gly	Tyr	Thr	Asp	Glu	Tyr	Arg	Thr	Gly	Arg	Lys	Leu	Lys
40	Glu	Tyr	Ala	Leu	Gln	Pro	Tyr	Val	Glu	Asn	Ser	Val	Thr	Val	Lys	Lys
	Thr	Asp	Leu	Ile	Arg	Gln	Lys	Tyr	Leu	Asp	Asn	Asp	Phe	Gly	Gly	Leu
	Ile	Gly	Ser	Leu	Asn	Trp	His	Thr	Gly	Ala	Trp	Asp	Leu	Gln	Phe	Gly
45	Ala	Ser	Gly	Asn	Ile	Tyr	Lys	Gly	Asp	His	Phe	Gly	Arg	Ile	Thr	Tyr
	Ile	Lys	Lys	Tyr	Asn	Gln	Pro	Leu	Ala	Pro	Asp	Phe	Glu	Tyr	Tyr	Arg
50	Asn	Arg	Ala	Asp	Lys	Arg	Glu	Gly	Ala	Ala	Phe	Ala	Lys	Ala	Asn	Trp
	Gln	Ile	Thr	Pro	Glu	Leu	Asn	Met	Tyr	Ala	Asp	Leu	Gln	Tyr	Arg	Thr
	Ile	Gly	Tyr	Thr	Ile	Asn	Gly	Ile	Thr	Asp	Glu	Tyr	Asp	Glu	Val	Gln
55	Gly	Ser	Met	Gln	His	Ile	Asp	Leu	Asp	Lys	Thr	Phe	Arg	Phe	Leu	Asn
	Pro	Lys	Ala	Gly	Leu	Thr	Tyr	Ser	Phe	Asp	Asp	Ala	His	Thr	Ala	Tyr
60	Ala	Ser	Val	Ala	Val	Ala	His	Arg	Glu	Pro	Asn	Arg	Thr	Asn	Tyr	Thr
	Glu	Ala	Gly	Ile	Gly	Gln	Tyr	Pro	Thr	Pro	Glu	Arg	Leu	Ile	Asp	Tyr
	Glu	Leu	Gly	Tyr	Arg	Tyr	Ala	Ser	Pro	Leu	Leu	Ser	Ala	Gly	Val	Gly
65	Leu	Tyr	Tyr	Met	Gln	Tyr	Lys	Asp	Gln	Leu	Val	Leu	Asp	Gly	Arg	Leu
	Ser	Asp	Val	Gly	Gln	Met	Leu	Thr	Ser	Asn	Val	Pro	Asp	Ser	Tyr	Arg
70	Met	Gly	Leu	Glu	Leu	Thr	Leu	Gly	Trp	Gln	Ile	Leu	Pro	Arg	Leu	Leu
	Arg	Trp	Asp	Ala	Ser	Phe	Thr	Met	Ser	Arg	Asn	Lys	Ile	Asp	Arg	Tyr
	Val	Gln	Tyr	Thr	Ser	Val	Tyr	Asp	Ala	Asp	Tyr	Asn	Trp	Leu	Glu	Leu
75	Lys	Glu	Glu	Thr	Leu	Glu	Ser	Thr	Asp	Ile	Ala	Tyr	Ser	Pro	Asn	Val

274/ 490

690 695 700
 Ile Ala Gly Ser Met Leu Thr Leu Ser His Ala Gly Phe Glu Met Ala
 705 710 715 720
 Trp Thr Ser Arg Phe Val Ser Lys Gln Tyr Leu Asp Asn Thr Gln Arg
 5 725 730 735
 Ser Asp Arg Met Leu Ser Ser Tyr Trp Val Asn Asp Leu Arg Leu Gly
 740 745 750
 Tyr Val Leu Pro Val His Phe Val Lys Arg Val Ala Leu Gly Val Gln
 755 760 765
 10 Leu Asn Asn Leu Phe Asn Leu Met Tyr Ala Ser Asn Ala Tyr Ile Tyr
 770 775 780
 Asp Ala Gly Tyr Val Gln Ala Ser Gly Glu Leu Ser Ala Tyr Ala Asp
 785 790 795 800
 15 Leu Arg Tyr Tyr Pro Gln Ala Gly Phe Asn Ala Leu Gly Ser Leu Thr
 805 810 815
 Ile Asp Phe

(2) INFORMATION FOR SEQ ID NO:345

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- (A) NAME/KEY: misc feature
 (B) LOCATION 1...532

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345

Tyr Arg Arg Ser Gly Arg Val Cys Pro Arg Ile Leu Arg Asn Lys Arg
 1 5 10 15
 Ser Tyr Ala Asp Thr Arg Leu Gln Pro Arg Arg Ala Val Arg Leu Arg
 20 25 30
 Ala Gly Thr Arg Thr Lys Met Lys Arg Arg Phe Leu Ser Leu Leu
 35 40 45
 45 Leu Tyr Ile Leu Ser Ser Ile Ser Leu Ser Ala Gln Arg Phe Pro Met
 50 55 60
 Val Gln Gly Ile Glu Leu Asp Thr Asp Ser Leu Phe Ser Leu Pro Lys
 65 70 75 80
 50 Arg Pro Trp Arg Ala Ile Gly Lys Thr Ile Gly Val Asn Leu Ala Val
 85 90 95
 Trp Gly Phe Asp His Phe Ile Met Asn Glu Asp Phe Ala Asp Ile Ser
 100 105 110
 Trp Gln Thr Ile Lys Ser Asn Phe Gln Thr Gly Phe Gly Trp Asp Asn
 115 120 125
 55 Asp Lys Phe Val Thr Asn Leu Phe Ala His Pro Tyr His Gly Ser Leu
 130 135 140
 Tyr Phe Asn Ala Ala Arg Ser Asn Gly Leu Ser Phe Arg His Ser Ala
 145 150 155 160
 60 Pro Phe Ala Phe Phe Gly Ser Leu Met Trp Glu Leu Leu Met Glu Asn
 165 170 175
 Glu Pro Pro Ser Ile Asn Asp Leu Cys Ala Thr Thr Ile Gly Gly Ile
 180 185 190
 Ala Leu Gly Glu Met Gly His Arg Leu Ser Asp Leu Leu Ile Asp Asn
 195 200 205
 65 Arg Thr Thr Gly Trp Glu Arg Met Gly Arg Glu Val Ala Ile Ala Leu
 210 215 220
 Ile Asn Pro Met Arg Phe Leu Asn Arg Leu Thr Ala Gly Glu Val Thr
 225 230 235 240
 Ser Val Gly Ser Arg Ser Gly Gln Ile Phe Gln Ser Val Pro Ile Asn
 245 250 255
 70 Ile Val Val Asp Ala Gly Phe Arg Phe Leu Ala Asp Lys Arg His Ala
 260 265 270
 Arg Thr Gly Ala Thr Ala Leu Thr Leu Asn Leu Arg Phe Asp Tyr Gly
 275 280 285
 75 Asp Pro Phe Arg Ser Glu Thr Phe Ser Pro Tyr Asp Phe Phe Gln Phe

WO 99/29870

PCT/AU98/01023

275 / 490

290 295 300
Lys Ala Gly Leu Ser Phe Ser Glu Ser Gln Pro Leu Leu Ser Gln Ile
305 310 315 320
Asn Leu Ile Gly Ile Leu Ser Gly Cys Gln Leu Leu Ala His Glu Arg
5 325 330 335
Thr Val Leu Val Gly Gly Leu Phe Gln His Phe Asp Tyr Tyr Asn Ser
340 345 350
Glu Lys Arg Ile Ser Lys Asn Ser Glu Glu Val Leu Val Thr Pro Tyr
355 360 365
10 Arg Ile Ser Gln Val Ala Ala Leu Gly Gly Gly Leu Ile Phe Gln His
370 375 380
His Gly Lys Phe Arg Arg Arg Pro Leu Glu Leu Tyr Ala Glu Thr Tyr
385 390 395 400
Leu Asn Val Val Pro Met Gly Ala Ser Leu Ser Asp His Tyr Asn Val
15 405 410 415
Asp Asn Arg Asp Tyr Asn Leu Gly Ser Gly Leu Ser Gly Lys Leu Tyr
420 425 430
Leu Gly Ala Thr Tyr Asn Asp Leu Trp Ser Trp Leu Leu Gly Val Glu
435 440 445
20 Ser Tyr Arg Leu Tyr Thr Trp Ile Gly Tyr Glu Glu Pro His Gln Lys
450 455 460
Asn Thr Asp Val Ser Ser Phe Met Val Gln Gly Asp Glu Ser Lys Ala
465 470 475 480
Arg Leu Leu Val Thr Ser Ser Glu Phe Ala Phe His Pro Gly Pro Trp
25 485 490 495
His Val Ala Ile Val Ala Arg Arg Phe Ile Arg Lys Thr Ala Tyr Gln
500 505 510
Phe Tyr Pro Asn Val Ser Phe Asp Thr Gly Asp Ile Gln Leu Arg Val
515 520 525
30 Gly Phe His Phe
530

(2) INFORMATION FOR SEQ ID NO:346

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 300 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- 40 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
- 45 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
- 50 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...300
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:346

Lys Arg Arg Lys Lys Gln Met Lys Arg Leu Ile Val Phe Leu Ala Met
1 5 10 15
55 Gly Gly Leu Leu Phe Thr Leu Ala Asn Ala Gln Glu Ala Asn Thr Ala
20 25 30
Ser Asp Thr Pro Lys Lys Asp Trp Thr Ile Lys Gly Val Thr Gly Leu
35 40 45
60 Asn Ala Ser Gln Thr Ser Leu Thr Asn Trp Ala Ala Gly Gly Glu Asn
50 55 60
Thr Val Ala Gly Asn Leu Tyr Leu Asn Ile Asp Ala Asn Tyr Leu Lys
65 70 75 80
Asp Lys Trp Ser Trp Asp Asn Gly Leu Arg Thr Asp Phe Gly Leu Thr
85 90 95
65 Tyr Thr Thr Ala Asn Lys Trp Asn Lys Ser Val Asp Lys Ile Glu Leu
100 105 110
Phe Thr Lys Ala Gly Tyr Glu Ile Gly Lys His Trp Tyr Gly Ser Ala
115 120 125
70 Leu Phe Thr Phe Leu Ser Gln Tyr Ala Lys Gly Tyr Glu Lys Pro Ser
130 135 140
Asp His Leu Thr Gly Val Lys His Ile Ser Asn Phe Phe Ala Pro Ala
145 150 155 160
Tyr Leu Thr Leu Gly Ile Gly Ala Asp Tyr Lys Pro Asn Glu Lys Phe
165 170 175
75 Ser Leu Tyr Leu Ser Pro Thr Thr Gly Lys Leu Thr Val Val Ala Asp

276/ 490

180 185 190
 Asp Tyr Leu Ser Ser Leu Gly Ala Phe Gly Val Lys Val Gly Glu Lys
 195 200 205
 Thr Met Phe Glu Leu Gly Ala Leu Val Val Gly Ser Ala Asn Ile Asn
 210 215 220
 5 Leu Met Glu Asn Val Asn Leu Ile Thr Lys Ala Ser Phe Phe Ser Ala
 225 230 235 240
 Tyr Thr His Asp Phe Gly Asn Ile Asp Ile Asn Trp Glu Ala Met Leu
 245 250 255
 10 Ala Met Lys Ile Asn Lys Phe Leu Thr Ala Thr Ile Ala Thr Asn Leu
 260 265 270
 Ile Tyr Asp Asp Asp Val Lys Ile Asn Asp Gly Pro Lys Ile Gln Phe
 275 280 285
 15 Lys Glu Val Val Gly Val Gly Val Ala Tyr Thr Phe
 290 295 300

(2) INFORMATION FOR SEQ ID NO:347

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 221 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein

25 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 30 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...221

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:347

Thr Arg Glu Ser Val Leu His Cys Arg Thr Lys Leu Lys Lys Glu Arg
 1 5 10 15
 40 Lys Met Lys Lys Met Ile Leu Ala Ala Thr Met Leu Leu Ala Thr Ile
 20 25 30
 Gly Phe Ala Asn Ala Gln Ser Arg Pro Ala Leu Arg Leu Asp Ala Asn
 35 40 45
 Phe Val Gly Ser Asn Leu Met Gln Lys Val Ala Asn Thr Ser Val Asn
 50 55 60
 45 Asn Lys Met Ile Val Gly Leu Arg Val Gly Ala Ala Ala Glu Phe Ala
 65 70 75 80
 Leu Ser Asn Asp Gly Phe Tyr Leu Ala Pro Gly Leu Ala Tyr Thr Met
 85 90 95
 Arg Gly Ala Lys Met Glu Ser Leu Ser Glu Thr Thr Thr Arg Leu His
 100 105 110
 50 Tyr Leu Gln Ile Pro Val Asn Ala Gly Met Arg Phe Ser Phe Ala Asp
 115 120 125
 Asn Met Ala Ile Ser Leu Glu Ala Gly Pro Tyr Phe Ala Tyr Gly Val
 130 135 140
 55 Ala Gly Thr Ile Lys Thr Lys Val Ala Gly Val Thr Ala Ser Val Asp
 145 150 155 160
 Ala Phe Gly Asp Asn Gly Tyr Asn Arg Phe Asp Leu Gly Leu Gly Leu
 165 170 175
 60 Ser Ala Ala Leu Ser Tyr Asp Arg Tyr Tyr Val Gln Ile Gly Tyr Glu
 180 185 190
 His Gly Leu Leu Asn Met Leu Lys Asp Ala Pro Asp Lys Thr Ser Leu
 195 200 205
 Arg Asn His Asp Phe Phe Val Gly Leu Gly Val Arg Phe
 210 215 220

65 (2) INFORMATION FOR SEQ ID NO:348

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 248 amino acids
 70 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

75 (iii) HYPOTHETICAL: YES

WO 99/29870

PCT/AU98/01023

277/ 490

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

5 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348

10 Ile Lys Arg Ile Glu Met Lys Arg Ile Phe Thr Val Ala Leu Val Leu
1 5 10 15
Leu Ala Ser Val Thr Met Ala Ile Gly Gln Ser Arg Pro Ala Leu Arg
20 25 30
15 Val Asp Ala Asn Phe Val Gly Ser Asn Gln Ser Met Lys Arg Asp Gly
35 40 45
Tyr Val Trp Asp Thr Lys Met Asn Val Gly Leu Arg Val Gly Ala Ala
50 55 60
20 Ala Glu Phe Met Ile Gly Ser Arg Gly Phe Tyr Leu Ala Pro Gly Leu
65 70 75 80
Asn Tyr Thr Met Lys Gly Ser Lys Thr Glu Trp Asp Ile Pro Glu Met
85 90 95
Val Pro Gly Thr Tyr Ile Thr Met Val Ser Thr Arg Leu His Tyr Leu
100 105 110
25 Gln Leu Pro Ile Asn Ala Gly Met Arg Phe Asp Leu Met Asn Asp Met
115 120 125
Ala Val Ser Ile Glu Ala Gly Pro Phe Leu Ala Tyr Gly Ile Tyr Gly
130 135 140
30 Thr Tyr Arg Gln Lys Leu Glu Gly Trp Lys Pro Asn Asn Tyr Ser Thr
145 150 155 160
Glu Phe Phe Gly Pro Thr Leu Gly Gly Pro Thr Asn Ile Arg Trp Asp
165 170 175
Ile Gly Ala Asn Ile Ile Ala Ala Phe His Tyr Lys Arg Tyr Tyr Ile
180 185 190
35 Gln Ile Gly Tyr Glu His Gly Phe Val Asp Ile Val Ser Gly Gly Gly
195 200 205
Ser Asp Ile Pro Arg Leu Asn Asp Asn Arg Gln Ser Ser Ser Thr Thr
210 215 220
40 Ala Leu Arg Glu Lys Gly Asn Asn Glu Tyr Ala Tyr Asn Arg Asp Phe
225 230 235 240
Phe Val Gly Ile Gly Tyr Arg Phe
245

(2) INFORMATION FOR SEQ ID NO:349

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 211 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

55 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
60 (B) LOCATION: 1...211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349

65 Lys Arg Lys Ser Met Lys Arg Met Leu Leu Leu Val Val Leu Leu
1 5 10 15
Tyr Gly Ile Ala Gly Arg Leu Ala Ala Gln Asp Val Ile Arg Pro Trp
20 25 30
Ser Leu Gln Val Gly Ala Gly Tyr Ser Asp Thr Glu Asn Ile Pro Gly
35 40 45
70 Gly Phe Thr Tyr Gly Phe Tyr Leu Gly Lys Arg Met Gly Ser Phe Leu
50 55 60
Glu Val Gly Leu Ser Met Tyr Asn Ser Thr Arg Gln Thr Ala Asn Asn
65 70 75 80
75 Ala Asp Ser Phe Ala Ser Asn Glu Gly Asp Gly Ser Phe Gln Val Asn
85 90 95

278/490

Met Ser Ser Pro Asn Glu Lys Trp Ser Phe Phe Asp Ala Gly Ser Ala
 100 105 110
 Asn Cys Tyr Met Ile Val Val Gly Val Asn Pro Leu His Leu Phe Trp
 115 120 125
 5 Gln Asn Ser Arg His Asn Leu Phe Leu Ala Val Gln Ala Gly Leu Ser
 130 135 140
 Asn Lys His Asn Ile His Phe Ile Tyr Gly Asp Lys Gly Ala Lys Val
 145 150 155 160
 10 Ser Ile Tyr Thr Asn Ser Asn Thr Tyr Ile Gly Tyr Gly Ala Arg Val
 165 170 175
 Ala Tyr Glu Tyr Gln Ile His Lys Asn Val Gly Ala Gly Ala Ala Val
 180 185 190
 Met Tyr Asp His Gly Asn Lys Met Leu Thr Ala Met Ala Thr Leu Ser
 195 200 205
 15 Thr His Phe
 210

(2) INFORMATION FOR SEQ ID NO:350

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 953 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 25 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 30 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...953
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:350

Ile Arg Met Arg Val Ser Asp Leu Cys Ser Arg Leu Ser Trp Leu Leu
 1 5 10 15
 40 Pro Val Ile Leu Val Gly Leu Leu Cys Ala Thr Leu Val Ala Ala Glu
 20 25 30
 Arg Pro Met Ala Gly Ala Val Gly Leu His His Arg Arg His Ala Ala
 35 40 45
 45 Leu Ser Asp Ser Thr Ala Lys Asp Thr Val Pro Leu Ala Lys Pro Ile
 50 55 60
 Pro Asp Ser Ala Phe Arg Asp Ser Leu Pro Ala Asp Ser Thr Gly Ser
 65 70 75 80
 Met Arg Gln Asp Ser Val Tyr Asp Asp Glu Phe Glu Leu Glu Asp Ile
 85 90 95
 50 Val Glu Tyr Glu Ala Ala Asp Ser Ile Val Leu Leu Gly Gln Asn Arg
 100 105 110
 Ala Tyr Leu Phe Gly Lys Ser Tyr Val Ser Tyr Gln Lys Ser Arg Leu
 115 120 125
 55 Glu Ala Asn Phe Met Tyr Leu Asn Thr Asp Ser Ser Thr Val Tyr Thr
 130 135 140
 Arg Tyr Val Leu Asp Thr Ala Gly Tyr Pro Met Ala Phe Pro Val Phe
 145 150 155 160
 Lys Asp Gly Glu Gln Ser Phe Glu Ala Lys Asn Phe Thr Tyr Asn Phe
 165 170 175
 60 Arg Thr Glu Lys Gly Ile Ile Ser Gly Val Ile Thr Gln Gln Gly Glu
 180 185 190
 Gly Tyr Leu Thr Ala Gly Lys Thr Lys Lys Met Pro Asp Asn Ile Met
 195 200 205
 65 Phe Met Gln Gly Gly Arg Tyr Thr Thr Cys Asp Asn His Asp His Pro
 210 215 220
 His Phe Tyr Ile Asn Leu Ser Lys Ala Lys Val His Pro Glu Lys Asp
 225 230 235 240
 Ile Val Thr Gly Pro Val Asn Leu Val Ile Ala Asp Met Pro Leu Pro
 245 250 255
 70 Ile Gly Leu Pro Phe Gly Tyr Phe Pro Phe Ser Asn Lys Tyr Ser Ser
 260 265 270
 Gly Ile Leu Met Pro Thr Tyr Gly Glu Asp Asn Arg Tyr Gly Phe Tyr
 275 280 285
 75 Leu Arg Asn Gly Gly Tyr Tyr Phe Ala Phe Ser Asp Tyr Ile Asp Leu
 290 295 300

WO 99/29870

PCT/AU98/01023

279/ 490

	Ala	Leu	Arg	Gly	Glu	Ile	Phe	Ser	Lys	Gly	Ser	Trp	Gly	Ile	Ser	Ala
	305					310					315					320
	Gln	Ser	Lys	Tyr	Lys	Lys	Arg	Tyr	Lys	Tyr	Asn	Gly	Ser	Phe	Glu	Ala
					325					330						335
5	Asn	Tyr	Leu	Val	Ser	Lys	Ser	Gly	Asp	Lys	Tyr	Val	Pro	Gly	Asp	Tyr
				340						345					350	
	Ser	Lys	Thr	Thr	Ser	Leu	Asn	Ile	Arg	Trp	Thr	His	Ser	Gln	Asp	Pro
				355					360					365		
10	Lys	Ala	Asn	Pro	Leu	Gln	Thr	Leu	Ser	Ala	Asn	Val	Asn	Phe	Ala	Thr
				370				375					380			
	Gly	Ser	Tyr	Phe	Gln	Asn	Ser	Leu	Asn	Thr	Thr	Tyr	Asp	Val	Asn	Ala
						390						395				400
	Arg	Thr	Ala	Thr	Thr	Arg	Ser	Ser	Ala	Val	Ser	Tyr	Ser	Arg	Lys	Phe
						405					410				415	
15	Pro	Gly	Thr	Pro	Phe	Ser	Ile	Thr	Gly	Ser	Met	Asp	Ile	Ser	Gln	Asn
				420					425						430	
	Met	Arg	Asp	Thr	Thr	Val	Ser	Leu	Thr	Leu	Pro	Asn	Leu	Ser	Ile	Asn
				435					440					445		
20	Met	Ser	Thr	Arg	Tyr	Pro	Phe	Lys	Arg	Lys	Thr	Arg	Val	Gly	Pro	Glu
				450				455					460			
	Arg	Trp	Tyr	Glu	Lys	Leu	Ser	Val	Gly	Tyr	Ser	Gly	Gln	Leu	Arg	Asn
						470					475					480
	Ser	Ile	Leu	Thr	Lys	Glu	Lys	Asp	Leu	Leu	Gln	Ser	Asn	Leu	Val	Arg
					485						490				495	
25	Asp	Trp	Lys	Asn	Gly	Met	Arg	His	Ser	Val	Pro	Ile	Ser	Leu	Thr	Val
				500					505						510	
	Pro	Leu	Leu	Asp	Tyr	Ile	Asn	Leu	Thr	Met	Gly	Val	Asn	Tyr	Asn	Glu
				515					520					525		
30	Trp	Trp	Tyr	Thr	Lys	Gly	Ile	Arg	Lys	Ser	Trp	Asn	Glu	Asp	Lys	Lys
				530				535					540			
	Thr	Phe	Leu	Pro	Ser	Asp	Thr	Thr	Tyr	Lys	Phe	Arg	Arg	Leu	Tyr	Asp
						550					555					560
	Tyr	Ser	Leu	Ser	Ala	Gly	Leu	Ser	Thr	Thr	Leu	Tyr	Gly	Met	Phe	Lys
						565					570				575	
35	Pro	Trp	Lys	Pro	Phe	Ser	Phe	Gly	Gly	Asn	Leu	Ile	Met	Ile	Arg	His
				580					585						590	
	Arg	Phe	Thr	Pro	Thr	Val	Ser	Phe	Ser	Tyr	Met	Pro	Asp	Phe	Thr	Lys
				595					600					605		
40	Arg	Arg	Tyr	Gly	Phe	Trp	Glu	Leu	Leu	Glu	His	Thr	Asp	Gln	Asn	Gly
				610					615				620			
	Lys	Leu	His	Thr	Leu	Leu	Tyr	Ser	Pro	Tyr	Phe	Glu	Gln	Ile	Phe	Gly
						630					635					640
	Ala	Pro	Ser	Met	Gly	Asn	Ala	Gly	Ser	Val	Asn	Phe	Ser	Phe	Asp	Asn
						645					650				655	
45	Asn	Leu	Glu	Ala	Lys	Ile	Lys	Ser	Lys	Ser	Asp	Ser	Thr	Gly	Ile	Lys
				660					665						670	
	Lys	Ile	Ser	Leu	Ile	Asp	Gln	Phe	Thr	Trp	Ser	Thr	Ser	Tyr	Asn	Met
				675					680					685		
50	Phe	Ala	Asp	Ser	Ile	Arg	Trp	Ser	Asn	Ile	Ser	Ala	Ser	Leu	Ala	Lcu
				690					695					700		
	Arg	Leu	Ser	Lys	Ser	Phe	Thr	Leu	Arg	Leu	Ser	Gly	Leu	Phe	Asp	Pro
						710					715					720
	Tyr	Leu	Thr	Lys	Tyr	Tyr	Glu	Gly	Glu	Asp	Gly	Lys	Ile	Ile	Pro	Tyr
						725					730				735	
55	Lys	Ser	Asn	Asp	Leu	Arg	Ile	Phe	Asn	Gly	Lys	Gly	Leu	Ala	Arg	Leu
					740				745						750	
	Ile	Ser	Thr	Gly	Thr	Ser	Phe	Ser	Tyr	Thr	Leu	Asn	Lys	Glu	Ser	Leu
					755				760					765		
60	Ser	Gly	Leu	Ile	Ala	Leu	Phe	Ser	Gly	Lys	Lys	Glu	Arg	Arg	Asp	Glu
							775						780			
	Lys	Lys	Asn	Thr	Gly	Ala	Thr	Pro	His	Glu	Gly	Asp	Asp	Ala	Ala	Asp
						790					795					800
	Ile	Leu	Glu	Gly	Gly	Arg	Pro	Gln	Asn	Glu	Ser	Gly	Gly	Ser	Leu	Leu
						805					810				815	
65	Glu	Arg	Asn	Arg	Gln	Gly	Gly	Ala	Val	Asp	Gln	Asp	Gly	Tyr	Phe	Ala
					820					825					830	
	Tyr	Ser	Ile	Pro	Trp	Ser	Leu	Ser	Phe	Asp	Tyr	Ser	Trp	Asn	Ile	Ala
					835				840					845		
70	Thr	Asp	Tyr	Asn	Arg	Tyr	Asn	Val	Asn	Lys	Met	Glu	His	Tyr	Tyr	Arg
						850						860				
	Val	Thr	Gln	Asn	Leu	Ser	Phe	Arg	Gly	Asn	Ile	Gln	Pro	Thr	Pro	Asn
						870					875					880
	Trp	Ser	Phe	Gly	Phe	Asn	Ala	Asn	Tyr	Asn	Phe	Asp	Leu	Lys	Lys	Ile
					885						890				895	
75	Thr	Ser	Leu	Thr	Cys	Asn	Val	Thr	Arg	Asp	Met	His	Cys	Trp	Ala	Ile

WO 99/29870

PCT/AU98/01023

280/ 490

5 Ser Ala Ser Phe Ile Pro Ile Gly Ala Tyr Lys Ser Tyr Asn Phe Val
900 905 910
915 920 925
Ile Ser Val Lys Ser Ser Leu Leu Gln Asp Leu Lys Tyr Gln Gln Ser
930 935 940
Asn Arg Pro Ile Thr Asn Thr Trp Tyr
945 950

10 (2) INFORMATION FOR SEQ ID NO:351
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1251 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES

20 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1251

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:351

30 Lys Trp Lys Leu Ala Cys Ala Phe Asp Cys Ala Cys Cys Phe Asp Pro
1 5 10 15
Phe Val Val Thr Asn Glu Val Ile Ile Met Met Lys Arg Tyr Thr Ile
20 25 30
Ile Leu Ala Val Phe Leu Leu Phe Cys Thr Val Phe Thr Phe Gln Ile
35 40 45
Lys Ala Arg Pro Tyr Glu Arg Phe Ala Asp Val Glu Lys Pro Trp Ile
50 55 60
Gln Lys His Ser Met Asp Ser Lys Leu Val Pro Ala Asn Lys Gly Asn
65 70 75 80
Leu Ile Gln Ala Glu Ile Val Tyr Gln Ser Val Ser Glu His Ser Asp
40 85 90 95
Leu Val Ile Ser Pro Val Asn Glu Ile Arg Pro Ala Asn Arg Phe Pro
100 105 110
Ser His Arg Lys Ser Phe Phe Ala Glu Asn Leu Arg Ala Ser Pro Pro
115 120 125
45 Val Val Pro Val Ala Val Asp Lys Tyr Ala Val Pro Val Ala Asn Pro
130 135 140
Met Asp Pro Glu Asn Pro Asn Ala Trp Asp Val Thr Leu Lys Ile Thr
145 150 155 160
Thr Lys Ala Val Thr Val Pro Val Asp Val Val Met Val Ile Asp Gln
50 165 170 175
Ser Ser Ser Met Gly Gly Gln Asn Ile Ala Arg Leu Lys Ser Ala Ile
180 185 190
Ala Ser Gly Gln Arg Phe Val Lys Lys Met Leu Pro Lys Gly Thr Ala
195 200 205
55 Thr Glu Gly Val Arg Ile Ala Leu Val Ser Tyr Asp His Glu Pro His
210 215 220
Arg Leu Ser Asp Phe Thr Lys Asp Thr Ala Phe Leu Cys Gln Lys Ile
225 230 235 240
Arg Ala Leu Thr Pro Ile Trp Gly Thr His Thr Gln Gly Gly Leu Lys
60 245 250 255
Met Ala Arg Asn Ile Met Ala Thr Ser Thr Ala Val Asp Lys His Ile
260 265 270
Ile Leu Met Ser Asp Gly Leu Ala Thr Glu Gln Tyr Pro Val Lys Asn
275 280 285
65 Val Thr Thr Ala Asp Phe Ile Gly Lys Thr Gly Asn Ala Asn Asp Pro
290 295 300
Ile Asp Leu Val Ile Gln Gly Ala Ile Asn Phe Pro Thr Asn Tyr Val
305 310 315 320
Ser Asn Asn Pro Ser Thr Pro Leu Thr Pro Asn Tyr Pro Thr His Ser
70 325 330 335
Ser Lys Val Gly Arg Arg Asn Leu Pro Glu Ser Lys Phe Asp Tyr Ser
340 345 350
Asn Leu Ser Ala Arg Ile Thr Phe Asp Gly Val Ala Gly Ala Leu Val
355 360 365
75 Tyr Glu Pro Arg Phe Pro His Pro Tyr Tyr Tyr Tyr Phe Pro Cys Asn

WO 99/29870

PCT/AU98/01023

282/ 490

Lys Asn Thr Ala Gly Gln Asp Asn Leu Pro Asp Arg Ile Pro Ser Met
 980 985 990
 His Ser Phe Leu Val Lys Met Gln Asn Gly Ala Ser Cys Thr Leu Unk
 995 1000 1005
 5 Ile Leu Tyr Asp Lys Leu Leu Lys Asn Thr Thr Val Asn Asn Gly Asn
 1010 1015 1020
 Gly Thr Gln Ile Thr Trp Arg Ser Gly Asn Ser Gly Ser Ala Asn Met
 1025 1030 1035 1040
 10 Pro Ser Leu Val Met Asp Val Leu Gly Asn Glu Ser Ala Asp Arg Leu
 1045 1050 1055
 Trp Ile Phe Thr Asp Gly Gly Leu Ser Phe Gly Phe Asp Asn Gly Trp
 1060 1065 1070
 Asp Gly Arg Lys Leu Thr Glu Lys Gly Leu Ser Gln Leu Tyr, Ala Met
 1075 1080 1085
 15 Ser Asp Ile Gly Asn Asp Lys Phe Gln Val Ala Gly Val Pro Glu Leu
 1090 1095 1100
 Asn Asn Leu Leu Ile Gly Phe Asp Ala Asp Lys Asp Gly Gln Tyr Thr
 1105 1110 1115 1120
 20 Leu Glu Phe Ala Leu Ser Asp His Phe Ala Lys Gly Ala Val Tyr Leu
 1125 1130 1135
 His Asp Leu Gln Ser Gly Ala Lys His Arg Ile Thr Asn Ser Thr Ser
 1140 1145 1150
 Tyr Ser Phe Asp Ala Lys Arg Gly Asp Ser Gly Ala Arg Phe Arg Leu
 1155 1160 1165
 25 Ser Tyr Gly Cys Asp Glu Asn Val Asp Asp Ser His Val Val Ser Thr
 1170 1175 1180
 Asn Gly Arg Glu Ile Ile Ile Leu Asn Gln Asp Ala Leu Asp Cys Thr
 1185 1190 1195 1200
 30 Val Thr Leu Phe Thr Ile Glu Gly Lys Leu Leu Arg Arg Leu Lys Val
 1205 1210 1215
 Leu Ala Gly His Arg Glu Val Met Lys Val Gln Thr Gly Gly Ala Tyr
 1220 1225 1230
 Ile Val His Leu Gln Asn Ala Phe Thr Asn Asp Val His Lys Val Leu
 1235 1240 1245
 35 Val Glu Tyr
 1250

(2) INFORMATION FOR SEQ ID NO:352

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 426 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 45 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 50 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...426
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:352

Thr Met Glu Val Lys Lys Asn Thr Val Val Leu Arg Leu Leu Ile Trp
 1 5 10 15
 60 Phe Val Ala Ile Leu Leu Phe His Ser Ser Arg Leu Trp Gly Gln Glu
 20 25 30
 Gly Glu Gly Ser Ala Arg Tyr Arg Phe Lys Gly Phe Val Asp Thr Tyr
 35 40 45
 65 His Ala Val Arg Ser Ser Ser Pro Phe Asp Phe Met Ser Ser Arg Thr
 50 55 60
 Arg Val Arg Gly Glu Leu Glu Arg Ser Phe Gly Asn Ser Lys Val Ala
 65 70 75 80
 Val Ser Val Asn Ala Thr Tyr Asn Ala Leu Leu Lys Asp Glu Thr Gly
 85 90 95
 70 Leu Arg Leu Arg Glu Ala Phe Phe Glu His Gln Glu Glu His Trp Gly
 100 105 110
 Leu Arg Leu Gly Arg Gln Ile Val Ile Trp Gly Ala Ala Asp Gly Val
 115 120 125
 75 Arg Ile Thr Asp Leu Ile Ser Pro Met Asp Met Thr Glu Phe Leu Ala
 130 135 140

WO 99/29870

PCT/AU98/01023

283/490

5 Gln Asp Tyr Asp Asp Ile Arg Met Pro Val Asn Ala Leu Arg Phe Ser
145 150 155 160
Val Phe Asn Glu Ser Met Lys Val Glu Val Val Leu Pro Val Phe
165 170 175
5 Glu Gly Tyr Arg Leu Pro Val Asp Pro Arg Asn Pro Trp Asn Ile Phe
180 185 190
Ser Leu Ser Pro Ile Ala Gln Gly Met Asn Ile Val Trp Lys Glu Glu
195 200 205
10 Ala Gly Lys Pro Ala Phe Lys Val Ala Asn Ile Glu Tyr Gly Ala Arg
210 215 220
Trp Ser Thr Thr Leu Ser Gly Ile Asp Phe Ala Leu Ala Ala Leu His
225 230 235 240
Thr Trp Asn Lys Met Pro Val Ile Glu Val Gln Gly Ile Val Pro Thr
245 250 255
15 Glu Ile Ile Val Ser Pro Arg Tyr Tyr Arg Met Gly Phe Val Gly Gly
260 265 270
Asp Leu Ser Val Pro Val Gly Gln Phe Val Phe Arg Gly Glu Ala Ala
275 280 285
20 Phe Asn Ile Asp Lys His Phe Thr Tyr Lys Ser His Ala Glu Gln Glu
290 295 300
Gly Phe Gln Thr Ile Asn Trp Leu Ala Gly Ala Asp Trp Tyr Ala Pro
305 310 315 320
Gly Glu Trp Met Ile Ser Gly Gln Phe Ser Met Glu Ser Ile Phe Arg
325 330 335
25 Tyr Arg Asp Phe Ile Ser Gln Arg Gln His Ser Thr Leu Ile Thr Leu
340 345 350
Asn Val Ser Lys Lys Phe Phe Gly Ser Thr Leu Gln Leu Ser Asp Phe
355 360 365
30 Thr Tyr Tyr Asp Leu Thr Gly Lys Gly Trp Phe Ser Arg Phe Ala Ala
370 375 380
Asp Tyr Ala Leu Asn Asp Gln Ile His Leu Met Ala Gly Tyr Asp Trp
385 390 395 400
Phe Ser Ser Lys Gly Ser Gly Ile Phe Asp Arg Tyr Lys Asp Asn Ser
405 410 415
35 Glu Leu Trp Phe Lys Ala Arg Tyr Ser Phe
420 425

(2) INFORMATION FOR SEQ ID NO:353

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 464 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
45 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
50 (A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...464
55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:353

60 Tyr Gly Lys Arg Arg Lys Leu Gly Thr Ser Val Arg Pro Ser Val Leu
1 5 10 15
Thr Gln Ile Arg Phe Ile Leu Asp Leu His Leu Ile Thr Asp Phe Phe
20 25 30
Glu Gly Leu Arg Val Asn Pro Ile Gly Ala Ala Ala Ile Val Ala Phe
35 40 45
65 Ile Ile Asp Leu Leu Leu Leu Cys Cys Ser Ala Phe Met Ser Ser Cys
50 55 60
Glu Val Ala Tyr Phe Ser Leu Lys Pro Ile Asp Leu Gln Asn Ile Arg
65 70 75 80
Glu Arg Asn His Ser Ser Asp Ile Ala Leu Ser Asn Leu Leu Asp Asn
85 90 95
70 Ser Asn Gln Leu Leu Ala Thr Ile Leu Ile Gly Asn Asn Val Ile Asn
100 105 110
Val Ala Ile Val Ile Leu Ser Asn Tyr Ala Ile Glu Gln Thr Phe Val
115 120 125
75 Phe Ser Ser Pro Ile Ile Gly Phe Leu Ile Gln Thr Ile Leu Leu Thr
130 135 140

SUBSTITUTE SHEET (Rule 26) (RO/AU)

284/ 490

Thr Val Leu Leu Leu Phe Gly Glu Ile Leu Pro Lys Val Tyr Ala Arg
 145 150 155 160
 Lys Asn Pro Leu Gln Tyr Ser Arg Phe Ser Ala Ala Met Ser Val
 165 170 175
 5 Ile Tyr Lys Ile Leu Ser Pro Phe Ser Lys Leu Leu Val Lys Ser Thr
 180 185 190
 Gly Ile Val Thr Arg Gly Ile Ser Lys Lys Tyr Asp Met Ser Val
 195 200 205
 10 Asp Glu Leu Ser Lys Ala Val Ala Leu Thr Thr Thr Glu Gly Glu Pro
 210 215 220
 Glu Glu Lys Glu Met Ile Asn Glu Ile Ile Lys Phe Tyr Asn Lys Thr
 225 230 235 240
 Ala Cys Glu Ile Met Val Pro Arg Ile Asp Ile Val Asp Val Asp Leu
 245 250 255
 15 Ser Trp Pro Phe Arg Lys Met Leu Asp Phe Val Val Ser Ser Gly Tyr
 260 265 270
 Ser Arg Leu Pro Val Ser Glu Gly Ser Glu Asp Asn Ile Lys Gly Val
 275 280 285
 20 Ile Tyr Ile Lys Asp Leu Ile Pro His Met Asp Lys Gly Asp Glu Phe
 290 295 300
 Asp Trp His Pro Leu Ile Arg Lys Ala Tyr Phe Val Pro Glu Asn Lys
 305 310 315 320
 Arg Ile Asp Asp Leu Leu Glu Glu Phe Arg Ala Asn Lys Val His Val
 325 330 335
 25 Ser Ile Val Val Asp Glu Phe Gly Gly Thr Cys Gly Leu Ile Thr Met
 340 345 350
 Glu Asp Ile Leu Glu Glu Ile Val Gly Glu Ile Thr Asp Glu Tyr Asp
 355 360 365
 30 Glu Glu Glu Leu Pro Phe Lys Val Leu Gly Asp Gly Ser Tyr Leu Phe
 370 375 380
 Glu Gly Lys Thr Ser Leu Ser Asp Val Arg His Tyr Leu Asp Leu Pro
 385 390 395 400
 Glu Asn Ala Phe Gly Glu Leu Gly Asp Glu Val Asp Thr Leu Ser Gly
 405 410 415
 35 Leu Phe Leu Glu Ile Lys Gln Glu Leu Pro His Val Gly Asp Thr Ala
 420 425 430
 Val Tyr Glu Pro Phe Arg Phe Gln Val Thr Gln Met Asp Lys Arg Arg
 435 440 445
 40 Ile Ile Glu Ile Lys Ile Phe Pro Phe Glu Arg Thr Trp Glu Val Glu
 450 455 460

(2) INFORMATION FOR SEQ ID NO:354

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 266 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 50 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 55 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...266
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:354

Ile Ile Tyr Arg Ser Thr Met Lys Leu Leu Leu Tyr Leu Leu Leu Val
 1 5 10 15
 Leu Ser Thr Leu Ser Pro Met Tyr Ser Gln Met Leu Phe Ser Glu Asn
 20 25 30
 65 Leu Thr Met Asn Ile Asp Ser Thr Thr Ile Gln Gly Thr Ile Leu
 35 40 45
 Pro Val Leu Asp Phe Lys Thr Glu Lys Glu Asn Val Phe Thr Phe Lys
 50 55 60
 70 Asn Thr Ala Asn Leu Asn Leu Ile Lys His Gly Gln Val Ile Asn
 65 70 75 80
 Leu Ile Asn Lys Leu Glu Phe Ser Thr Tyr Gly Asn Lys Val Thr Val
 85 90 95
 75 Ser Gly Gly Tyr Val His Thr Glu Tyr Arg Tyr Leu Leu His His Val
 100 105 110

WO 99/29870

PCT/AU98/01023

285/ 490

5 Phe Glu Val Tyr Pro Tyr Val Glu Ser Gln Trp Ala Glu Ser Arg Gly
115 120 125
Met Lys Tyr Lys Val Ser Thr Gly Leu Gln Ser Arg Tyr Arg Leu Val
130 135 140
Asn Ser Asp Asn Cys Leu Met Phe Ala Thr Leu Gly Val Phe Phe Glu
145 150 155 160
Phe Glu Lys Trp Glu Gln Pro Ala Thr Ser Leu Phe Ala Gly Thr Tyr
165 170 175
Ala Tyr Ser Arg Ser Ile Lys Ser His Leu Ser Ile Ser Phe Arg His
180 185 190
10 Arg Leu Gly Glu His Trp Glu Phe Thr Thr Thr Ala Ile His Gln Gly
195 200 205
Lys Pro Asp Ser Tyr Phe Lys Lys Ala Arg Phe Gly Gly Ala Ile Asp
210 215 220
15 Leu Lys Tyr His Ile Thr Pro Thr Ile Gly Ile Arg Gly Ala Tyr Arg
225 230 235 240
Ile Ile Tyr Asp Thr Ala Pro Ile Val Pro Val Arg Lys Asp Tyr Asn
245 250 255
20 Thr Val Asp Val Gly Ile Asp Ile Ser Phe
260 265

(2) INFORMATION FOR SEQ ID NO:355

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 907 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
35 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...907

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:355

Thr Ile Cys Val Ala Phe Leu Ser Ala Pro Val Ala Ala Leu Arg Glu
1 5 10 15
45 Ser Pro Pro Met Gly Ala Glu Arg Lys Thr Pro Ser Leu Leu Pro Leu
20 25 30
Leu Phe Glu His Ser Asp Lys Gly Lys Gly Phe Asp Tyr Arg Leu Phe
35 40 45
Thr Ser Asn Lys Leu Lys Val Phe Ala Thr Gly Asn Ser Arg Tyr Ile
50 55 60
His Asn Lys Pro Thr Ile Ile Gln Ala Met Lys Arg Ile Val Leu Ser
65 70 75 80
Ser Phe Leu Phe Val Leu Ser Ile Leu Ser Leu Met Ala Gln Asn Asn
85 90 95
55 Thr Leu Asp Val His Ile Ser Gly Thr Ile Lys Asp Ala Ser Ser Gly
100 105 110
Glu Pro Val Pro Tyr Ala Thr Val Ser Ile Arg Leu Thr Gly Ala Asp
115 120 125
Thr Thr Gln Val Phe Arg Gln Val Thr Asp Gly Asn Gly Tyr Phe Val
130 135 140
60 Ile Gly Leu Pro Ala Ala Pro Ser Tyr His Leu Thr Ala Ser Phe Val
145 150 155 160
Gly Met Lys Thr His Thr Met Gln Ile Ser Arg Gly Asn Gly Gln His
165 170 175
Asp Ile Lys Ser Ile Asp Ile Ser Leu Glu Ser Glu Asp Lys Gln Leu
180 185 190
65 Ser Thr Val Thr Val Ser Ala Ala Arg Pro Leu Val Lys Met Glu Ile
195 200 205
Asp Arg Leu Ser Tyr Asn Met Lys Asp Asp Pro Ala Ala Lys Thr Asn
210 215 220
70 Asn Leu Leu Glu Met Leu Arg Asn Val Pro Leu Val Thr Val Asp Gly
225 230 235 240
Gln Gly Asn Ile Gln Val Lys Gly Ser Ser Asn Phe Lys Ile His Leu
245 250 255
75 Asn Gly Arg Pro Ser Thr Met Val Ser Ser Asn Pro Lys Glu Val Phe
260 265 270

WO 99/29870

PCT/AU98/01023

286/490

	Arg	Ser	Ile	Pro	Ala	His	Thr	Ile	Lys	Arg	Val	Glu	Val	Ile	Thr	Asp
	275						280					285				
	Pro	Gly	Val	Lys	Tyr	Asp	Ala	Glu	Gly	Thr	Ser	Ala	Ile	Leu	Asp	Ile
	290					295					300					
5	Val	Thr	Glu	Glu	Gly	Lys	Lys	Leu	Glu	Gly	Tyr	Ser	Gly	Ser	Ile	Thr
	305					310					315					320
	Ala	Ser	Val	Ser	Asn	Asn	Pro	Thr	Ala	Asn	Gly	Ser	Ile	Phe	Leu	Thr
					325					330					335	
10	Ala	Lys	Ser	Gly	Lys	Val	Gly	Leu	Thr	Thr	Asn	Tyr	Asn	Tyr	Tyr	Gly
				340					345					350		
	Gly	Lys	Asn	Lys	Gly	Ser	Arg	Tyr	Phe	Thr	Glu	Arg	Thr	Thr	Ser	Met
			355					360					365			
	Leu	Gln	Thr	Ile	Glu	Glu	Gly	Lys	Gly	Gln	Glu	Thr	Phe	Gly	Gly	His
			370				375					380				
15	Phe	Gly	Asn	Ala	Leu	Leu	Ser	Phe	Glu	Ile	Asp	Ser	Leu	Asn	Leu	Phe
						390					395					400
	Thr	Val	Gly	Gly	Asn	Val	Arg	Leu	Trp	Glu	Met	Thr	Thr	Asp	Arg	Asn
					405					410					415	
20	Ser	Val	Glu	Lys	Ser	Phe	Ala	Gly	Ser	Asn	Leu	Met	Ser	Tyr	Ile	Asp
				420					425					430		
	Arg	Lys	Leu	Lys	Thr	Gln	Met	Asp	Ala	Gly	Ser	Tyr	Glu	Leu	Asn	Ala
				435				440						445		
	Asp	Tyr	Gln	His	Ser	Thr	Arg	Leu	Pro	Gly	Glu	Leu	Leu	Thr	Val	Ser
				450			455					460				
25	Tyr	Arg	Phe	Thr	His	Asn	Pro	Asn	Asn	Ser	Glu	Thr	Phe	Ile	Asp	Gln
						470					475					480
	Trp	Lys	Arg	Asp	Pro	Leu	Asn	Thr	Ala	Asn	Thr	Ile	Gln	Tyr	Ala	Gly
						485					490					495
30	Gln	His	Ser	Lys	Ser	Asp	Ala	Gly	Met	Asp	Glu	His	Thr	Ala	Gln	Val
					500					505				510		
	Asp	Tyr	Thr	Arg	Pro	Leu	Gly	Gln	Ala	His	Ser	Leu	Glu	Ala	Gly	Leu
					515				520					525		
	Lys	Tyr	Ile	Tyr	Arg	His	Ala	Thr	Ser	Asp	Pro	Leu	Tyr	Glu	Ile	Arg
							535					540				
35	Pro	Ser	Glu	Asp	Ala	Pro	Trp	Gln	Pro	Gly	Ser	Leu	Tyr	Ala	Gln	Asn
						550					555					560
	Pro	Ser	Asn	Gly	Lys	Phe	Arg	His	Asp	Gln	Tyr	Ile	Gly	Ala	Ala	Tyr
					565					570					575	
40	Ala	Gly	Tyr	Asn	Tyr	Arg	Lys	Asp	Gln	Tyr	Ser	Leu	Gln	Thr	Gly	Leu
				580					585					590		
	Arg	Val	Glu	Ser	Ser	Arg	Leu	Lys	Ala	Leu	Phe	Pro	Glu	Asn	Ala	Ala
				595				600					605			
	Ala	Asp	Phe	Ser	His	Asn	Ser	Phe	Asp	Trp	Val	Pro	Gln	Leu	Thr	Leu
				610				615				620				
45	Gly	Tyr	Thr	Pro	Ser	Pro	Met	Lys	Gln	Leu	Lys	Leu	Ala	Tyr	Asn	Phe
						630					635					640
	Arg	Ile	Gln	Arg	Pro	Ala	Ile	Gly	Gln	Leu	Asn	Pro	Tyr	Arg	Leu	Gln
						645					650				655	
50	Thr	Asn	Asp	Tyr	Gln	Val	Gln	Tyr	Gly	Asn	Pro	Asp	Leu	Lys	Ser	Glu
				660					665					670		
	Lys	Arg	His	His	Val	Gly	Leu	Ser	Tyr	Asn	Gln	Tyr	Gly	Ala	Lys	Val
							680						685			
	Met	Leu	Thr	Ala	Ser	Leu	Asp	Tyr	Asp	Phe	Cys	Asn	Asn	Ala	Ile	Gln
							695					700				
55	Asn	Tyr	Thr	Phe	Ser	Asp	Pro	Ala	Asn	Pro	Asn	Leu	Phe	His	Gln	Thr
						710					715					720
	Tyr	Gly	Asn	Ile	Gly	Arg	Glu	His	Ser	Phe	Ser	Leu	Asn	Thr	Tyr	Ala
						725					730				735	
60	Met	Tyr	Thr	Pro	Ala	Val	Trp	Val	Arg	Ile	Met	Leu	Asn	Gly	Asn	Ile
				740					745					750		
	Asp	Arg	Thr	Phe	Gln	Lys	Ser	Glu	Ala	Leu	Gly	Ile	Asp	Val	Asn	Ser
								760					765			
	Trp	Ser	Gly	Met	Val	Tyr	Ser	Gly	Leu	Met	Phe	Thr	Leu	Pro	Lys	Asp
								775					780			
65	Trp	Thr	Val	Asn	Leu	Phe	Gly	Gly	Tyr	Tyr	His	Gly	Gly	Arg	Ser	Tyr
						790					795					800
	Gln	Thr	Lys	Tyr	Asp	Gly	Asn	Val	Phe	Asn	Asn	Ile	Gly	Ile	Ala	Lys
						805					810				815	
70	Gln	Leu	Phe	Asp	Lys	Lys	Leu	Arg	Val	Ser	Leu	Ser	Ala	Asn	Asn	Ile
						820				825				830		
	His	Ala	Lys	Tyr	Ser	Thr	Trp	Lys	Ser	Arg	Thr	Ile	Gly	Asn	Gly	Phe
						835					840			845		
	Thr	Ile	Tyr	Ser	Glu	Asn	Ala	Gly	Ile	Gln	Arg	Ser	Val	Ser	Leu	Ser
						850					855			860		
75	Leu	Thr	Tyr	Ser	Phe	Gly	Lys	Met	Asn	Thr	Gln	Val	Arg	Lys	Val	Glu

WO 99/29870

PCT/AU98/01023

287/490

865 870 875 880
Arg Thr Ile Val Asn Asp Asp Leu Lys Gln Thr Ser Ser Gln Gly Gln
885 890 895
Gln Gly Gly Gly Gln Gly Asn Pro Thr Gly Asn
5 900 905

(2) INFORMATION FOR SEQ ID NO:356

(1) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 450 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
20 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356

Trp Cys Gln Ser Asp Pro Ile Pro His Cys His Ala Val Tyr Arg Asn
1 5 10 15
Ala Gln Gly His Gln Gln Gly Arg Ser Asp Gln Asp Arg Leu Pro Pro
20 25 30
Val Arg Gly Tyr Arg Tyr Ala Arg Cys Leu Gly Arg Tyr Glu Gly Phe
35 40 45
Gly Glu Arg Met Arg Leu Ser Ala Ile Leu Ile Ala Leu Ile Val Met
50 55 60
35 Leu Pro Ala Val Leu Ser Gly Gln His Tyr Tyr Ser Met Ala Gly Glu
65 70 75 80
Arg Leu Glu Thr Asp Ser Ile Arg Pro Asn Glu Leu Ser Ala Ser Ile
85 90 95
40 Arg Ser Ala Leu Phe Phe Arg Asn Asn Glu Tyr Asn Ala Arg Ser Val
100 105 110
Lys Gly Tyr Thr Leu Pro Gly Ala Arg Val Ser Ala Phe Ala Ser Tyr
115 120 125
Ser Leu Pro Ala Ala His Gly Val Lys Leu Ser Leu Gly Val Ser Thr
130 135 140
45 Leu Asn Tyr Trp Gly Ala Ser Arg Tyr Pro Ala Gly Ile Ala Tyr Ser
145 150 155 160
Asp Leu Pro Tyr Trp Thr Asp Tyr Asn Asp Tyr Val Arg Leu Arg Ile
165 170 175
50 Leu Pro Tyr Val Gln Ala Met Leu Lys Pro Thr Ala Thr Thr Ala Leu
180 185 190
Met Leu Gly Asn Ile Ala Gly Gly Thr Ala His Gly Leu Ile Glu Pro
195 200 205
Ile Tyr Asn Pro Glu Leu Asp Leu Thr Ala Asp Pro Glu Ala Gly Val
210 215 220
55 Gln Phe Arg Gly Asp Trp Thr Arg Phe Arg Met Arg Val Trp Val Asn
225 230 235 240
Trp Met Ser Met Ile Phe Lys Asn Asp Asn His Gln Glu Ser Phe Val
245 250 255
60 Phe Gly Leu Ser Thr Thr Ser Lys Leu Leu Ser Gly Glu Gly Lys Trp
260 265 270
Arg Leu Glu Leu Pro Leu Gln Ala Ile Ala Thr His Arg Gly Gly Glu
275 280 285
Tyr Asn Trp Ala Gln Gln Asp Thr Val His Thr Trp Val Asn Gly Ala
290 295 300
65 Val Gly Leu Lys Leu Ser Tyr Arg Pro Arg Thr Asp Lys Pro Met Gln
305 310 315 320
Ile Trp Gly Ser Ala Tyr Gly Val Ala Ala Leu Ser Ser Gly Gly Tyr
325 330 335
70 Phe Pro Tyr Glu Arg Gly Trp Gly Gly Tyr Leu Ser Leu Gly Met Asp
340 345 350
Leu Glu His Phe Ala Phe Arg Thr Asp Tyr Trp Tyr Gly Arg His Tyr
355 360 365
Val Ser Pro Phe Ala Ala Pro Phe Ala Asn Ser Leu Thr Tyr Asp Lys
370 375 380
75 Gln Pro Leu Thr Asn Gly Trp Gly Asp Tyr Ile Arg Leu Tyr Ala Asp

WO 99/29870

PCT/AU98/01023

288/490

385 390 395 400
Tyr Ser Trp Arg Met Ala Arg Ser Val Ser Leu Ala Ala Val Ala Arg
405 410 415
Val Trp Phe Gln Pro Ser Asp Arg Phe Ala Met Ser His Ala Leu Glu
420 425 430
Leu Thr Met Arg Ile Asp Pro Lys Phe Pro Ile Ala Phe Leu Lys Glu
435 440 445
Asn His
450

10

(2) INFORMATION FOR SEQ ID NO:357

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: protein

20

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

25

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...447

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357

Pro Phe Ser Pro Pro Trp Val Cys Ala Gly Ala Ala Ser Ser Val Arg
1 5 10 15
Thr Arg Pro Cys Ser Thr Val Ser Ser Thr Ala Ala Ser Ser His Arg
20 25 30
35 Arg Ser Glu His Met Arg Ser Ala Asp Ser Ser Pro Ala Tyr Ser Pro
35 40 45
Ile Gly Ser Leu Ser Ser Ser His Ser Phe Asp Ser Ile Pro Asp Gln
50 55 60
40 Arg Met Asn Lys Ser Leu Leu Ser Leu Ala Cys Leu Ile Leu Cys Gly
65 70 75 80
Met Pro Ala Ile Ala Gln Gln Thr Gly Pro Ala Glu Arg Ser Gly Glu
85 90 95
Pro Ser Leu Ala Glu Arg Val Phe Gly Leu Glu Gln Lys Gln Lys Lys
100 105 110
45 Leu Lys Val Tyr Leu Gly Ile Gln Ser Phe Tyr Asp Gln Pro Leu Val
115 120 125
Asp Asp Glu Ser His Ile Gly His Phe Lys Val Gln Glu Leu Arg Met
130 135 140
50 Ser Ala His Gly Glu Leu Asn Arg His Leu Ser Phe Asp Trp Arg Gln
145 150 155 160
Arg Leu Asn Arg Ala Ala Asp Gly Thr Ser Phe Ala Asp Asn Leu Ser
165 170 175
Asn Ala Ile Asp Ile Ala Gly Val Asp Trp His Pro Asn Asp Lys Val
180 185 190
55 Ser Phe Phe Phe Gly Arg Gln Tyr Ala Arg Phe Gly Gly Ile Glu Tyr
195 200 205
Asp Met Asn Pro Val Glu Ile Tyr Gln Tyr Ser Asp Leu Val Asp Tyr
210 215 220
60 Met Thr Cys Tyr Thr Ser Gly Val Asn Phe Ala Trp Asn Phe His Pro
225 230 235 240
Glu Gln Gln Leu Gln Leu Gln Val Leu Asn Ala Tyr Asn Asn Arg Phe
245 250 255
Ala Asp Arg Tyr His Val Thr Pro Asp Val Ala Thr Ala Thr Ser Tyr
260 265 270
65 Pro Leu Leu Tyr Ser Ala Gln Trp Asn Gly Thr Leu Leu Gly Gly Ala
275 280 285
Leu His Met Arg Tyr Ala Val Ser Met Ala His Gln Ala Gln Glu Arg
290 295 300
70 Asn Met Trp Tyr Phe Thr Ala Gly Asn Leu Phe Asn Pro Gly Lys Arg
305 310 315 320
Ile Asn Gly Tyr Leu Asp Leu Thr Tyr Ser Ile Glu Gly Leu Asp Asp
325 330 335
Lys Gly Ile Met Thr Ala Arg Tyr Gly Lys Gly Lys Thr Leu Thr Asp
340 345 350
75 Val Lys Tyr Tyr Ala Leu Val Ser Lys Trp Asn Phe Arg Ile Phe Asp

WO 99/29870

PCT/AU98/01023

289/490

355 360 365
Gln Val Asn Leu Phe Leu Lys Gly Met Tyr Glu Asn Gly Tyr Ala Pro
370 375 380
5 Ala Gln Tyr Gly Glu Ser Ser His Thr Arg His Ser Tyr Gly Tyr Met
385 390 395 400
Gly Gly Val Glu Tyr Tyr Pro Thr Glu Thr Asn Phe Arg Leu Phe Val
405 410 415
Thr Tyr Ile Gly Arg His Tyr Arg Tyr Ser Ala Thr Glu Thr Glu Ser
420 425 430
10 Thr Asn Ala Leu Arg Ala Gly Leu Ile Tyr Gln Ile Pro Phe Leu
435 440 445

(2) INFORMATION FOR SEQ ID NO:358

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 227 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- 20 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
25 (A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...227
30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:358

Tyr Lys Gln Ala Ile Met Lys His Leu Phe Lys Ser Thr Leu Val Leu
1 5 10 15
35 Leu Cys Ala Leu Ser Phe Ser Gly Thr Tyr Thr Phe Ala Gln Glu Asn
20 25 30
Asn Thr Glu Lys Ser Arg Phe Asp Phe Ser Val Arg Leu Gly Gln Gly
35 40 45
40 Tyr Ile Ala Gly Ser Thr Thr Asn Leu Met Tyr Gly Tyr Thr Ser Ala
50 55 60
Asn Asp Arg Leu Leu Ser Gly Ala Ile Tyr Leu Gly Leu Thr Pro Ser
65 70 75 80
Lys Lys Glu Asn Ala Thr Gly Val Ala Phe Arg Phe Leu Ser Pro Ser
85 90 95
45 Pro Gly Tyr Tyr Val Asp Ile Ser Gly Lys Glu Asn Thr Leu Asn Tyr
100 105 110
Ala Phe Tyr Val Val Gly Ala Tyr Asn Arg Ile Ala Ile Pro Ile Arg
115 120 125
50 Pro Ile Lys Asn Phe Asn Phe Ile Phe Ser Thr Glu Val Gly Met Ala
130 135 140
Trp Met Ser Arg His Glu Gln Ile Tyr Asn Ser Thr Ser Gln Thr Trp
145 150 155 160
Asp Lys Gln Arg Lys Ser Arg Ser Gly Leu Asp Phe Gly Leu Gly Met
165 170 175
55 His Leu Gln Unk His Ile Asn Lys Thr Val Tyr Phe Met Ala Gly Thr
180 185 190
Asp Leu Thr Ser Cys Met Phe Gly Lys Arg Ile Asn Asp Tyr Gln Gln
195 200 205
60 Lys Asp Arg Thr Phe Ile Ala Leu Ile Asp Asn Ser Ile Gly Ile Gly
210 215 220
Leu Asn Leu
225

(2) INFORMATION FOR SEQ ID NO:359

- 65 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 406 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- 70 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
75 (vi) ORIGINAL SOURCE:

290/490

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature
(B) LOCATION 1...406

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359

10 Ile Phe Ile Asp Pro Asp Lys Asn Thr Lys Gln Asn Glu Arg Asn Met
1 5 10 15
Ile Ile Lys Lys Met Leu Lys Asn Lys Leu Ala Pro Leu Ala Ile Leu
20 25 30
Phe Leu Phe Ala Pro Lys Ala Met Lys Ala Gln Glu Gln Leu Asn Val
35 40 45
15 Val His Thr Ser Val Pro Ser Leu Asn Ile Ser Pro Asp Ala Arg Ala
50 55 60
Ala Gly Met Gly Asp Ile Gly Val Ala Thr Thr Pro Asp Ala Tyr Ser
65 70 75 80
20 Gln Tyr Trp Asn Pro Ser Lys Tyr Ala Phe Met Asp Thr Lys Ala Gly
85 90 95
Ile Ser Phe Ser Tyr Thr Pro Trp Leu Ser Lys Leu Val Asn Asp Ile
100 105 110
Ala Leu Met Gln Met Thr Gly Phe Tyr Lys Leu Gly Thr Asp Glu Asn
115 120 125
25 Gln Ala Ile Ser Ala Ser Leu Arg Tyr Phe Thr Leu Gly Lys Leu Glu
130 135 140
Thr Phe Asp Glu Leu Gly Glu Ser Met Gly Glu Ala His Pro Asn Glu
145 150 155 160
Phe Ala Val Asp Leu Gly Tyr Ser Arg Gln Leu Ser Glu Asn Phe Ser
165 170 175
30 Met Ala Val Ala Leu Arg Tyr Ile Arg Ser Asp Gln Ser Thr His Asn
180 185 190
Thr Gly Glu Asn Gln Ala Gly Asn Ala Phe Ala Ala Asp Ile Ala Gly
195 200 205
35 Tyr Leu Gln Lys Tyr Val Leu Leu Gly Asn Ala Glu Ser Leu Trp Ser
210 215 220
Leu Gly Phe Asn Val Lys Asn Ile Gly Thr Lys Ile Ser Tyr Asp Gly
225 230 235 240
40 Gly Val Thr Ser Phe Phe Ile Pro Thr Ser Leu Asn Leu Gly Thr Gly
245 250 255
Leu Leu Tyr Pro Ile Asp Asp Tyr Asn Ser Ile Asn Phe Asn Leu Glu
260 265 270
Leu Ser Lys Leu Leu Val Pro Thr Pro Pro Ile Met Asp Gln Asn Asp
275 280 285
45 Gln Ala Gly Tyr Glu Ala Ala Leu Lys Lys Tyr Gln Glu Thr Ser Ser
290 295 300
Ile Ser Gly Ile Phe Ser Ser Phe Gly Asp Ala Pro Gly Gly Leu Lys
305 310 315 320
50 Glu Glu Phe Arg Glu Ile Thr Trp Gly Leu Gly Ala Glu Tyr Ser Tyr
325 330 335
Asp Asp Lys Phe Phe Val Arg Ala Gly Tyr Ser Tyr Leu His Pro Thr
340 345 350
Lys Gly Asn Leu Gln Tyr Phe Thr Ala Gly Ala Gly Phe Lys Met Asn
355 360 365
55 Ile Phe Arg Ile Asp Ala Ser Tyr Leu Leu Ser Thr Ile Gln Ser Asn
370 375 380
Pro Leu Asp Gln Thr Leu Arg Phe Thr Leu Ala Phe Asp Met Asp Gly
385 390 395 400
60 Leu Arg Asn Leu Phe His
405

(2) INFORMATION FOR SEQ ID NO:360

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 452 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

65

(ii) MOLECULE TYPE: protein

70

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

75

WO 99/29870

PCT/AU98/01023

292/490

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

5 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361

10 Gly Leu Tyr Gly Met Ser Val Val Pro Ile Ile Ile Tyr Leu Cys Gly
1 5 10 15
Ile Ser Asn Tyr Ala Arg Leu Met Ile Ile Arg Cys Leu Ile Arg Arg
20 25 30
15 Pro Arg Thr Val Leu Phe Gly Leu Ile Phe Val Val Gly Leu Phe Ser
35 40 45
Ala Met Ala Gln Glu Lys Lys Asp Ser Leu Ser Thr Val Gln Pro Val
50 55 60
20 Pro Asn Ser Ser Met Val Glu Gln Thr Pro Leu Leu Ser Ile Asp His
65 70 75 80
Pro Val Leu Pro Ala Ser Phe Gln Asn Thr Arg Thr Leu Lys Arg Phe
85 90 95
Arg Asp Lys His Leu Ser Asp Ala Leu Leu Asn Gly Leu Lys Pro His
100 105 110
25 Arg Ser Ser Leu Gln Leu Asn Glu Glu Leu Asn Phe Ala Ala Glu Arg
115 120 125
Arg Asp Phe Val Ser Pro Leu Leu Gln Thr Arg His Ala Ala Gly Val
130 135 140
30 Leu Ser Trp Arg Pro Thr Asp Arg Met His Phe Tyr Thr Ser Gly Asn
145 150 155 160
Ile Gly Leu Gly His Asp Leu Leu Thr Gly Val Arg Lys Asp Phe Gly
165 170 175
Trp Asn Ala Gly Ala Asp Phe Leu Leu Ser Gln Asn Leu Thr Ala His
180 185 190
35 Val Gln Gly Gly Trp Gln Gln Asn Phe Gly Phe Ile Pro Met Thr Ala
195 200 205
Val Asn Gly Gln Leu Arg Trp Gln Ala Thr Glu Arg Leu Ser Phe Thr
210 215 220
Thr Gly Ile Asp Tyr Arg Gln Val Gln Trp Asn Ala Phe Asp Asn Arg
225 230 235 240
40 Thr Phe Ser Leu Lys Gly Ser Ala Arg Tyr Glu Val Met Asp Asn Val
245 250 255
Phe Val Asn Gly Phe Gly Ser Tyr Pro Leu Tyr Ser Ser Thr Arg Ser
260 265 270
45 Gly Leu Asn Met Ala Val Pro Met His Gly Phe Gly Pro Gln Tyr Gly
275 280 285
Gly Ser Leu Glu Leu Lys Val Ser Glu Arg Phe Gly Phe Ala Val Gly
290 295 300
50 Met Glu Arg Glu Tyr Asn Ile Trp Thr Arg Arg Trp Glu Thr His Tyr
305 310 315 320
Phe Ala Tyr Pro Val Phe Tyr Gly Asp Lys Lys
325 330

(2) INFORMATION FOR SEQ ID NO:362

55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 329 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

65 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
70 (B) LOCATION 1...329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362

75 Glu Thr Asn Ser Trp Val Ser Ser Asp Cys Asn Ser Thr Thr Met Lys
1 5 10 15

WO 99/29870

PCT/AU98/01023

294/ 490

5 Ala Ser Ser Ile His Val Ala Val Arg Thr Asp Phe Gly Gln Ala Gly
 115 120 125
 Ile His Cys Pro Met Ala Thr Asp Ala Ser Ala Thr Glu Phe Asp Arg
 130 135 140
 10 Ser Ala Glu Cys Ala Glu Arg Thr Ser Ala Gln Ile Asp Thr Ala Ile
 145 150 155 160
 Arg Ser Gln Ser Gln Ile Ile Arg Thr His Ile Asp Thr Cys Pro Lys
 165 170 175
 15 Ser Ser Gly Thr Ile Gly Gly Ser Thr His Thr Ser Leu His Leu Lys
 180 185 190
 Val Phe Asp Gly Arg Gly Glu Val Gly His Ile His Pro Lys Asp Gly
 195 200 205
 Leu Arg Phe Gly Val Val Glu Gly Tyr Ser Ile Gly Ser Tyr Val Asp
 210 215 220
 20 Ala Ile Gly Ile Gly Ala Thr His Ala Lys Ala Gly Ile Ser Asp Thr
 225 230 235 240
 Arg Thr Gly Ile Ala Gly Gly Tyr His Gly Gly Ser Gln His Gln Gln
 245 250 255
 25 Ile Gly Asp Val Thr Thr Ile Ile Gly Leu Gly Lys Phe Gly Leu Ala
 260 265 270
 Asn Val Gly Val Ser Asp Arg Gly Phe Arg Arg Gly Ala Ser Ser Tyr
 275 280 285
 Asp Leu Tyr Gly Leu Glu Leu His Ile Ala Lys Thr Ile Tyr Leu Ala
 290 295 300
 30 Val Gly Asp Gly Cys Leu Cys Arg Gln Ala Glu Arg Gln Asp Gly
 305 310 315

(2) INFORMATION FOR SEQ ID NO:364

- 30 (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 614 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 35 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 40 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...614
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:364

50 Pro Tyr Asn Val Gln Ser Ile Ser Asn Lys Thr Ile Lys Lys Gln Met
 1 5 10 15
 Glu Asn Leu Lys Asn Ile Gln Pro Arg Glu Asp Phe Asn Trp Glu Glu
 20 25 30
 Phe Glu Ala Gly Gly Val His Ala Ala Val Ser Arg Gln Glu Gln Glu
 35 40 45
 55 Ala Ala Tyr Asp Lys Thr Leu Asn Thr Ile Lys Glu Lys Glu Val Val
 50 55 60
 Met Gly Arg Val Thr Ala Ile Asn Lys Arg Glu Val Val Ile Asn Val
 65 70 75 80
 Gly Tyr Lys Ser Glu Gly Val Val Pro Ala Thr Glu Phe Arg Tyr Asn
 85 90 95
 60 Pro Glu Leu Lys Val Gly Asp Glu Val Glu Val Tyr Ile Glu Asn Gln
 100 105 110
 Glu Asp Lys Lys Gly Gln Leu Val Leu Ser His Arg Lys Gly Arg Ala
 115 120 125
 65 Ala Arg Ser Trp Glu Arg Val Asn Glu Ala Leu Glu Lys Asp Glu Ile
 130 135 140
 Val Lys Gly Tyr Val Lys Cys Arg Thr Lys Gly Met Ile Val Asp
 145 150 155 160
 Val Phe Gly Ile Glu Ala Phe Leu Pro Gly Ser Gln Ile Asp Val Arg
 165 170 175
 70 Pro Ile Arg Asp Tyr Asp Ala Phe Val Glu Lys Thr Met Glu Phe Lys
 180 185 190
 Ile Val Lys Ile Asn Gln Glu Tyr Lys Asn Val Val Val Ser His Lys
 195 200 205
 75 Val Leu Ile Glu Ala Glu Leu Glu Gln Gln Lys Lys Glu Ile Ile Gly
 210 215 220

WO 99/29870

PCT/AU98/01023

296/ 490

His Ser Ile Tyr Asp Glu Leu Asp Gly Arg Pro Lys Leu Thr Thr Thr
35 40 45
Val Glu Asn Phe Thr Pro Asp Lys Trp Gly Ser Thr Phe Phe Phe Ile
50 55 60
5 Asp Met Asp Tyr Thr Gly Lys Gly Ile Gln Ser Ala Tyr Trp Glu Ile
65 70 75 80
Ser Arg Glu Leu Lys Phe Trp Gln Ala Pro Val Ser Ile His Leu Glu
85 90 95
Tyr Asn Gly Gly Leu Ser Thr Ser Phe Thr Phe Gly His Asp Ala Leu
100 105 110
10 Ile Gly Ala Thr Tyr Thr Tyr Asn Asn Pro Ser Phe Thr Arg Gly Phe
115 120 125
Thr Ile Thr Pro Met Tyr Lys His Leu Gly Ala His Asp Phe His Thr
130 135 140
15 Tyr Gln Ile Thr Gly Thr Trp Tyr Met His Phe Leu Asp Gly Leu Leu
145 150 155 160
Thr Phe Asn Gly Phe Leu Asp Leu Trp Gly Phe Pro Gln Glu Asn Pro
165 170 175
20 Ile Gly Gly Pro Val Leu Lys Glu Gly Asp Lys Phe Val Phe Leu Ser
180 185 190
Glu Pro Gln Phe Trp Ile Asn Leu Asn Arg Ile Lys Gly Ile Asp Lys
195 200 205
Asp Phe Asn Leu Ser Ile Gly Thr Glu Met Glu Ile Ser Arg Asn Phe
210 215 220
25 Ala Arg Met Asp Lys Phe Ser Cys Ile Pro Thr Leu Ala Val Lys Trp
225 230 235 240
Thr Phe Asn

- 30 (2) INFORMATION FOR SEQ ID NO:366
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 235 amino acids
(B) TYPE: amino acid
35 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 40 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
- 45 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...235
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:366

50 Met Lys Thr Ile Ser Lys Asn His Ala Ala Arg Ile Cys Ala Ala Ile
1 5 10 15
Ala Leu Phe Ala Val Cys Asn Gly Arg Ile Ala Ala Gln Asp Phe Leu
20 25 30
55 Tyr Glu Ile Gly Gly Phe Gly Ala Ala Gln Tyr Phe Gly Asp Ala
35 40 45
Asn Arg Gly Leu Phe Gly Ser Ser Gly Val Gly Leu Glu Leu Val Gly
50 55 60
Arg Tyr Asn Tyr Asn Phe Arg Trp Ala Phe Ser Thr Met Leu Asp Trp
65 70 75 80
60 Arg Thr Leu Arg Gly Asp Thr Asp Lys Ser Gly Asn Val Phe Pro Asp
85 90 95
Phe Ala Gln Ala Asp Phe Lys Val Gly Leu Thr Gln Leu His Val Arg
100 105 110
65 Ser Glu Phe Asn Phe Leu Pro Tyr Ser Asp Gly Tyr Lys Tyr Leu Gly
115 120 125
Thr Ala Arg Leu Ser Pro Tyr Val Ala Ala Gly Leu Ser Leu Gly Phe
130 135 140
Ala Ser Gly Ala Lys Gly Ser Ala Phe Ala Pro Gly Ile Thr Ala Gly
145 150 155 160
70 Met Gly Val Lys Tyr Lys Leu Lys Pro Arg Ile Asn Val Gly Ile Glu
165 170 175
Tyr Ser Phe Thr Gly Leu Leu Thr Asp Ala Leu Asp Ala Leu Thr Asp
180 185 190
75 Lys Ser Val Trp Leu Glu Asp Pro Tyr Lys Ile Asn Asp Ser Trp Val
195 200 205

297/490

Lys Asn Lys Asp Ala Thr Gly Ala Leu Val Leu Arg Ile Thr Tyr Asp
 210 215 220
 Phe Gly Leu Arg Lys Thr Phe Cys Asn Lys Gln
 225 230 235

5 (2) INFORMATION FOR SEQ ID NO:367
 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 436 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 15 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 20 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...436
 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:367
 Asn Ile Met Tyr Lys Asp Tyr Lys Gly Leu Tyr Ala Ser Leu Arg Trp
 1 5 10 15
 Tyr Ala Leu Ile Ile Gly Leu Leu Phe Ala Ala Asp Gly Ile Gln Ala
 20 25 30
 30 Gln Asn Asn Asn Phe Thr Glu Ser Pro Tyr Thr Arg Phe Gly Leu Gly
 35 40 45
 Arg Leu Gly Glu Arg Thr Thr Ile Ser Gly His Ser Met Gly Gly Leu
 50 55 60
 35 Gly Val Gly Leu Arg Gln Gly Thr Tyr Val Asn Ala Val Asn Pro Ala
 65 70 75 80
 Ser Tyr Ser Ala Val Asp Ser Met Thr Phe Ile Phe Asp Phe Gly Ala
 85 90 95
 Ser Thr Gly Ile Thr Trp Tyr Ala Glu Asn Gly Lys Lys Asp Asn Arg
 100 105 110
 40 Lys Met Gly Asn Ile Glu Tyr Phe Ala Met Leu Phe Pro Ile Ser Lys
 115 120 125
 Ser Ile Ala Met Ser Ala Gly Val Leu Pro Tyr Ser Ala Ser Gly Tyr
 130 135 140
 45 Gln Phe Gly Ser Val Asp Gln Val Glu Gly Gly Ser Val Gln Tyr Thr
 145 150 155 160
 Arg Lys Tyr Leu Gly Thr Gly Asn Leu Asn Asp Leu Tyr Val Gly Ile
 165 170 175
 Gly Ala Thr Pro Phe Lys Asn Phe Ser Ile Gly Ala Asn Ala Ser Ser
 180 185 190
 50 Leu Phe Gly Arg Phe Thr His Ser Arg Gln Val Ile Phe Ser Thr Glu
 195 200 205
 Ala Pro Tyr Asn Pro Val His Leu Ser Thr Leu Tyr Leu Lys Ala Ala
 210 215 220
 55 Lys Phe Asp Phe Gly Met Gln Tyr His Leu Leu Lys Ser Asp Arg
 225 230 235 240
 Ser Leu Val Ile Gly Ala Val Tyr Ser Pro Arg Val Lys Met His Ser
 245 250 255
 Glu Leu Thr Gln Ile Lys Asn Gln Val Gln Asn Gly Val Val Val Glu
 260 265 270
 60 Ser Glu Thr Gln Glu Tyr Ile Lys Gly Met Asp Tyr Tyr Thr Leu Pro
 275 280 285
 His Thr Leu Gly Ile Gly Phe Ser Tyr Glu Lys Lys Asp Lys Leu Leu
 290 295 300
 65 Leu Gly Ala Asp Val Gln Tyr Ser Lys Trp Lys Gly Glu Lys Phe Tyr
 305 310 315 320
 Lys Ser Asp Cys Lys Phe Gln Asp Arg Ile Arg Val Ser Leu Gly Gly
 325 330 335
 Glu Ile Ile Pro Asp Ile Asn Ala Val Gly Met Trp Pro Lys Val Arg
 340 345 350
 70 Tyr Arg Phe Gly Leu His Gly Glu Asn Ser Tyr Leu Lys Val Pro Thr
 355 360 365
 Lys Gly Gly Val Tyr Gln Gly Tyr His Ile Val Gly Ala Val Phe Gly
 370 375 380
 75 Ile Gly Ile Pro Leu Asn Asp Arg Arg Ser Phe Val Asn Val Ser Leu
 385 390 395 400

WO 99/29870

PCT/AU98/01023

298/ 490

5 Glu Tyr Asp Arg Leu Ile Pro Lys Glu Gly Met Ile Lys Glu Asn Ala
405 410 415
Leu Lys Leu Thr Phe Gly Leu Thr Phe Asn Glu Ser Trp Phe Lys Lys
420 425 430
Leu Lys Leu Asn
435

(2) INFORMATION FOR SEQ ID NO:368

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 945 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- 15 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
- 20 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...945
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:368

30 Asn Thr Ile Ser Glu Asn Gly Asn Asp Ser Thr Tyr Phe Ser Phe Gln
1 5 10 15
Thr Phe Leu Met Arg Ser Ile Tyr Gln Leu Leu Ser Ile Leu Leu
20 25 30
Ala Ser Leu Gly Phe Val Gly Leu Glu Ala Gln Gln Ala Gly Val Ala
35 40 45
Gly Arg Val Leu Asp Glu Glu Gly Asn Pro Met Ile Gln Ala Asn Val
50 55 60
Gln Leu Val Gln Ser Thr Gly Gln Val Ala Val Ala Ala Gly Ala Thr
65 70 75 80
Asn Glu Lys Gly Leu Phe Ser Leu Lys Thr Ser Gln Glu Gly Asp Tyr
85 90 95
40 Ile Leu Arg Val Ser Tyr Val Gly Tyr Thr Thr His Asp Glu Lys Ile
100 105 110
Ser Leu Arg Asn Gly Gln Thr Ile Thr Leu Lys Asp Ile Ser Met Asn
115 120 125
Glu Asp Ala Arg Leu Leu Gln Ser Val Thr Val Gln Ala Lys Ala Ala
45 130 135 140
Glu Val Val Val Arg Asn Asp Thr Leu Glu Phe Asn Ala Gly Ser Tyr
145 150 155 160
Thr Val Ala Gln Gly Ala Ser Ile Glu Glu Leu Ile Lys Lys Leu Pro
165 170 175
50 Gly Ala Glu Ile Gly Ser Asp Gly Lys Ile Thr Ile Asn Gly Lys Asp
180 185 190
Ile Ser Lys Ile Leu Val Asp Gly Lys Glu Phe Phe Ser Lys Asp Pro
195 200 205
Gln Val Ala Ile Lys Asn Leu Pro Ala Asp Met Val Asn Lys Val Gln
55 210 215 220
Val Leu Asn Lys Leu Ser Glu Leu Ser Arg Met Ser Gly Phe Asp Asp
225 230 235 240
Gly Glu Glu Glu Thr Val Ile Asn Leu Thr Val Lys Pro Glu Lys Lys
245 250 255
60 Lys Gly Leu Phe Gly Thr Leu Gln Ala Gly Tyr Gly Thr Asp Gln Arg
260 265 270
Tyr Met Ala Gly Gly Asn Val Asn Arg Phe Asp Gly Asn Lys Gln Trp
275 280 285
Thr Leu Ile Gly Ser Ala Asn Asn Thr Asn Asn Met Gly Phe Ser Glu
65 290 295 300
Met Asp Ser Glu Met Gly Ser Met Thr Phe Phe Ser Pro Gln Gly Gly
305 310 315 320
Gly Arg Arg Gly Phe Gly Asn Ser Gly Gly Val Thr Ser Ser Ser Met
325 330 335
70 Leu Gly Gly Asn Phe Ser Val Glu Phe Ser Ser Ala Leu Asn Thr Gly
340 345 350
Gly Asp Ala Arg Tyr Gly Tyr Asn Asp Lys Ala Ile Glu Thr Thr Lys
355 360 365
75 Arg Val Glu Asn Ile Leu Ala Glu Gly Asn Thr Tyr Met Asp Glu Asn
370 375 380

WO 99/29870

PCT/AU98/01023

299/ 490

Ile Leu Glu Arg Ser Phe Ser His Asn Gly Gln Ala Arg Phe Arg Met
 385 390 395 400
 Gln Trp Lys Pro Ser Glu Arg Thr Glu Val Val Phe Glu Pro Asp Leu
 405 410 415
 5 Ser Ile Ser Lys Ile Asp Gly Phe Phe Asn Asp Thr Tyr Glu Thr Lys
 420 425 430
 Asp Ala Thr Gly Ile Ser Ile Asn Lys Gly Ser Ile His Gln Thr Thr
 435 440 445
 10 Gln Gly Asn Asn Phe Arg Leu Asn Gly Glu Leu Asp Ile Ser His Lys
 450 455 460
 Leu Asn Asp Glu Gly Arg Thr Ile Ser Ala Ser Val Ser Gly Gly Leu
 465 470 475 480
 Thr Asp Glu Asp Gly Asp Gly Ile Tyr Gln Ala Val Leu Gln Ser Val
 485 490 495
 15 Glu Thr Asn Gln Lys Gln Phe Asn Asp Asn Ser Asn Leu Gln Tyr Arg
 500 505 510
 Leu Arg Leu Ser Tyr Val Glu Pro Leu Gly Lys Asn Tyr Phe Ala Gln
 515 520 525
 20 Ala Ile Leu Asn Arg Arg Phe Ser Arg Arg Asn Ser Asp Arg Glu Val
 530 535 540
 Tyr Arg Leu Gly Asp Asp Gly Gln Tyr Ser Ile Leu Asp Ser Gln Tyr
 545 550 555 560
 Gly Leu Ser Tyr Ser Asn Glu Phe Thr Gln Tyr Arg Ile Gly Leu Asn
 565 570 575
 25 Leu Lys Lys Ile Ala Lys Thr Trp Asp Tyr Thr Val Gly Phe Asn Val
 580 585 590
 Asp Pro Asn Arg Thr Val Ser Tyr Arg Ser Val Ala Gly Val Glu Gln
 595 600 605
 30 Asp Lys Leu Ala Phe Asn Arg Val Asn Leu Ser Pro Met Leu Arg Ile
 610 615 620
 Asn Tyr Lys Pro Ser Arg Thr Thr Asn Leu Arg Val Asp Tyr Arg Gly
 625 630 635 640
 Arg Thr Thr Gln Pro Ser Ile Asn Gln Ile Ala Pro Val Gln Asp Ile
 645 650 655
 35 Thr Asn Pro Leu Phe Val Thr Glu Gly Asn Pro Gly Leu Lys Pro Ser
 660 665 670
 Tyr Ser Asn Asn Val Met Ala Met Phe Ser Asp Phe Asp Ala Lys Ser
 675 680 685
 40 Gln Arg Ala Phe Asn Ile Val Phe Phe Gly Asn Tyr Thr Phe Asp Asp
 690 695 700
 Ile Val Pro Asn Thr His Tyr Asp Pro Ser Thr Gly Ile Arg Thr Thr
 705 710 715 720
 Arg Tyr Glu Asn Ala Ser Gly Thr Trp Gln Ala Asn Leu His Gly Thr
 725 730 735
 45 Leu Ser Leu Pro Leu Lys Asn Arg Ala Phe Ser Phe Arg Met Ser Leu
 740 745 750
 Phe Asn Arg Leu Ala Glu Gly Gln Ser Phe Ile Asn Asp Asp Lys Asn
 755 760 765
 50 Lys Ala Leu Ser Phe Arg Thr Arg Glu Arg Leu Thr Leu Thr Tyr Arg
 770 775 780
 Asn Asn Trp Ile Asp Thr Ser Ile Gly Gly Asn Ile Gly Phe Tyr Met
 785 790 795 800
 Ala Asn Asn Ser Leu Ser Gly Gln Lys Asp Ser Arg Thr Tyr Asp Phe
 805 810 815
 55 Gly Gly Asn Tyr Gln Val Ala Leu Thr Leu Pro Tyr Gly Phe Arg Ile
 820 825 830
 Asp Ser Asp Val Glu Tyr Asn Thr Asn Ser Gly Tyr Ser Gly Gly Phe
 835 840 845
 60 Ser Leu Asp Glu Trp Leu Trp Asn Ala Ser Leu Ser Tyr Ser Phe Leu
 850 855 860
 Arg Asp Lys Ala Gly Thr Leu Arg Val Asn Gly Tyr Asp Ile Leu Gly
 865 870 875 880
 Gln Arg Ser Ser Ile Ser Arg Ser Ala Ser Ala Ile Asn Ile Glu Glu
 885 890 895
 65 Ser Met Ser Asn Thr Ile Gly Arg Tyr Val Met Val Asp Phe Ile Tyr
 900 905 910
 Arg Phe Asn Ala Phe Ser Gly Gly Gly Ser Arg Ser Asp His Gln Arg
 915 920 925
 70 Gly Asn Met Asn Arg Pro Gly Pro Pro Phe Gly Gly Gly Arg Arg Pro
 930 935 940
 Ser
 945

(2) INFORMATION FOR SEQ ID NO:369

75

WO 99/29870

PCT/AU98/01023

300/ 490

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 412 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION: 1...412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369

Gly Glu Tyr Pro Ala Asn Ser Asn Asp Lys Lys Glu Met Val Met Lys
 1 5 10 15
 Leu Ile Lys Arg Ser Leu Leu Leu Gly Ala Val Leu Leu Ile Thr
 20 25 30
 Leu Pro Ala Tyr Ser Gln Asn Asp Asp Ile Phe Glu Asp Asp Ile Tyr
 35 40 45
 Thr Ser Arg Lys Glu Ile Arg Lys Gln Asn Gln Val Lys Asp Trp Gln
 50 55 60
 Asn Gln Glu Asp Gly Tyr Gly Asp Asp Thr Glu Tyr Thr Val Ala Ser
 65 70 75 80
 Asp Arg Asp Ile Asp Ala Tyr Asn Arg Arg Asp Gly Gln Ser Tyr Asp
 85 90 95
 Gly Lys Lys Leu Ser Lys Asp Lys Lys Arg Asp Ser Thr Arg Ser Ser
 100 105 110
 Val Pro Gly Arg Tyr Ser Arg Arg Leu Ala Arg Phe Tyr Lys Pro Asn
 115 120 125
 Thr Ile Val Ile Ser Gly Ala Asp Asn Val Tyr Val Thr Asp Asp Gly
 130 135 140
 Glu Tyr Phe Val Tyr Gly Asp Glu Tyr Tyr Asp Asp Ala Ser Ser Val
 145 150 155 160
 Asn Ile Tyr Ile Asn Ser Pro Trp Cys Asp Pro Phe Pro Tyr Thr Ser
 165 170 175
 Trp Tyr Pro Ser Phe Ser Gly Trp Tyr Asn Tyr Thr Trp Asn Tyr Pro
 180 185 190
 Trp Phe Tyr Tyr Gly Ser His Ile Gly Trp Gly Gly Tyr Tyr Pro Gly
 195 200 205
 Tyr Asn Trp Tyr Trp Ser Tyr Tyr Tyr Asp Pro Phe Tyr Asn Pro Tyr
 210 215 220
 Gly Ile Gly Met Gly Trp Gly Tyr Pro Tyr Gly Trp Gly Ser Tyr Tyr
 225 230 235 240
 Gly Trp Gly Gly Tyr Pro Gly Val Ile His His Tyr His His Tyr Pro
 245 250 255
 Lys Lys Thr Tyr Ser Asn Gly Gln His Ser Gly Ala Tyr Tyr Ser Tyr
 260 265 270
 Gly Arg Pro Asn Arg Ile Lys Gly Gly Thr Ser Gly Ala Lys Leu Gly
 275 280 285
 Thr Gly Arg Tyr Asp Arg Ile Gln Asn Ser Ser Ser Gln Lys Asn Lys
 290 295 300
 Phe Gly Leu Gln Ser Asn Lys Pro Asn Asn Asn Leu Gln Asn Val Lys
 305 310 315 320
 Ser Gly Arg Thr Gly Arg Ala Asn Arg Asp Arg Asn Ile Glu Thr Val
 325 330 335
 Thr Pro Asn Asn Gly Gln Lys Gln Asn Arg Pro Val Phe Gln Gln Asn
 340 345 350
 Gln Ser Gly Asn Asp Arg Pro Thr Gly Arg Asn Ile Arg Ser Glu Arg
 355 360 365
 Gln Gly Glu Asn Asn Asp Arg Thr Phe Ser Thr Pro Ser Arg Ser Asn
 370 375 380
 Ser Asn Gly Gly Phe Ser Thr Pro Ser Arg Ser Ser Ser Gly Ser Met
 385 390 395 400
 Ser Gly Gly Gly Gly Arg Ser Gly Arg Gly Arg Asn
 405 410

(2) INFORMATION FOR SEQ ID NO:370

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 601 amino acids

301/490

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370

Ser Asn Ser Ser Ser His Lys Trp Leu Ile Tyr Tyr His Ile Glu Lys
1 5 10 15
Thr Lys Ser Ile Met Ile Arg Lys Leu Ile Leu Leu Ala Leu Met
20 25 30
Pro Val Ala Ser Val Ala Phe Ala Val Pro Thr Asp Ser Thr Glu Ser
35 40 45
Lys Asp Asn Arg Ile Leu Thr Ser Met Gln Ser Ser Leu Asn Arg
50 55 60
Asp Asp Ala Pro Asp Lys Trp Gln Pro Met His Ala Asn Phe Ser Ile
65 70 75 80
Gln Ser Asp Met Leu Leu Ser Thr Ala Gln Lys Ser Lys Asn Thr Trp
85 90 95
Phe Gly Asn Ser Tyr Ile Met Gly Ile Ile Lys Asn Asn Tyr Leu Glu
100 105 110
Phe Gly Ala Arg Phe Glu Asp Leu Tyr Lys Pro Leu Pro Gly His Glu
115 120 125
Pro Glu Met Gly Arg Gly Val Pro His Met Tyr Val Lys Gly Ser Tyr
130 135 140
His Trp Ala Glu Leu Thr Met Gly Asp Phe Tyr Asp Gln Phe Gly Ser
145 150 155 160
Gly Met Val Phe Arg Thr Tyr Glu Glu Arg Asn Leu Gly Ile Asp Asn
165 170 175
Ala Val Arg Gly Gly Arg Ile Val Leu Thr Pro Phe Asp Gly Val Arg
180 185 190
Val Lys Gly Ile Ala Gly Gln Gln Arg Asn Tyr Phe Asp Arg Thr Gly
195 200 205
Lys Val Phe Asn Ser Gly Arg Gly Tyr Leu Leu Gly Ser Asp Leu Glu
210 215 220
Leu Asn Val Glu Arg Trp Ser Ser Ala Met Arg Asp Asn Asp Tyr His
225 230 235 240
Leu Ala Ile Gly Gly Ser Phe Val Ser Lys His Glu Ala Asp Glu Asp
245 250 255
Ile Phe Val Gly Val Gly Glu Asp Arg Lys Arg Leu Asn Leu Pro Leu
260 265 270
Asn Val Pro Ile Met Gly Leu Arg Thr Asn Phe Gln Lys Gly Gly Leu
275 280 285
Ala Leu Tyr Ala Glu Tyr Gly Tyr Lys Tyr Asn Asp Pro Ser Ala Asp
290 295 300
Asn Asp Tyr Ile Tyr His Asp Gly Gln Ala Ala Leu Leu Ser Ala Ser
305 310 315 320
Tyr Ser Lys Lys Gly Met Ser Ile Leu Leu Gln Ala Lys Arg Cys Glu
325 330 335
Asn Phe Ala Phe Arg Ser Lys Arg Ser Ala Gln Leu Thr Pro Leu Met
340 345 350
Ile Asn Tyr Met Pro Ala Phe Thr Gln Ala His Thr Tyr Thr Leu Ala
355 360 365
Ala Ile Tyr Pro Tyr Ala Thr Gln Pro Gln Gly Glu Trp Ala Phe Gln
370 375 380
Gly Glu Leu Arg Tyr Asn Phe Ala Arg Arg Thr Ala Leu Gly Gly Arg
385 390 395 400
Tyr Gly Thr Gly Leu Arg Ile Asn Val Ser His Val Arg Gly Leu Asp
405 410 415
Lys Lys Met Leu Lys Glu Asn Pro Asp Glu Leu Ile Gly Thr Asp Gly
420 425 430
Tyr Thr Val Ser Phe Phe Gly Met Gly Asp Leu Tyr Tyr Ser Asp Ile
435 440 445
Asp Val Glu Ile Thr Lys Lys Val Ser Pro Gly Phe Asn Phe Thr Leu
450 455 460
Thr Tyr Leu Asn Gln Ile Tyr Asn Asn Lys Val Leu His Gly Ala Ala

303/ 490

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372

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Leu Leu Phe Ser Ser Pro Leu Pro Arg Met Asp Arg Pro Lys Pro Ser
1      5      10      15
Tyr Ile Val Arg Ile Ala Ala Ile Leu Cys Leu Phe Val Gly Arg Pro
20     25     30
Leu Phe Ala Gln Ser Tyr Val Asp Tyr Val Asp Pro Leu Ile Gly Thr
35     40     45
Leu Ser Ser Phe Glu Leu Ser Ala Gly Asn Thr Tyr Pro Val Ile Gly
50     55     60
Leu Pro Trp Gly Met Asn Ser Trp Thr Pro Met Thr Gly Val Pro Gly
65     70     75     80
Asp Gly Trp Gln Tyr Thr Tyr Ser Ala His Lys Ile Arg Gly Phe Lys
85     90     95
Gln Thr His Gln Pro Ser Pro Trp Ile Asn Asp Tyr Gly Gln Phe Ser
100    105    110
Leu Leu Pro Leu Thr Ala Pro Gln Lys Pro Ser Ser Asn Asp Ser Ile
115    120    125
Ala Leu Thr Lys Trp Cys Lys Gln Leu Phe Ser Asp Glu Gln Thr Ser
130    135    140
Trp Phe Ser His Lys Ala Glu Thr Ala Thr Pro Tyr Tyr Tyr Ser Val
145    150    155    160
Tyr Leu Ala Asp Tyr Asp Thr Arg Val Glu Met Ala Pro Thr Glu Arg
165    170    175
Ala Ala Ile Phe Arg Ile Arg Tyr Ser Gly Asn Thr Glu Ser Gly Ser
180    185    190
Gly Arg Trp Leu Arg Leu Asp Ala Phe Thr Gly Gly Ser Glu Ile Ser
195    200    205
Ile Val Asp Pro His Thr Val Val Gly Ile Ser Arg Lys Asn Ser Gly
210    215    220
Gly Val Pro Ala Asn Phe Ala Cys Tyr Phe Ile Leu Gln Ser Asp Thr
225    230    235    240
Pro Met Ala Asp Val Leu Leu Glu Thr Asp Thr Gly Lys Ser Asp Glu
245    250    255
Gly Thr Arg Ala Trp Ala Ala Cys Arg Phe Asp Ser Gln Glu Val Thr
260    265    270
Val Arg Val Ala Ser Ser Phe Ile Ser Val Glu Gln Ala Glu Arg Asn
275    280    285
Leu Ala Glu Val Lys Gly Gln Ser Phe Asp Arg Ile Arg Leu Ala Gly
290    295    300
Arg Glu Ala Trp Asn Lys Val Leu Gly Arg Ile His Val Glu Gly Gly
305    310    315    320
Thr Lys Asp Glu Arg Thr Thr Phe Tyr Ser Ala Leu Tyr Arg Cys Leu
325    330    335
Leu Phe Pro Arg Arg Phe Tyr Glu Glu Asp Ala Ser Gly Asn Phe Val
340    345    350
His Tyr Ser Pro Tyr Asn Gly Glu Val Leu Pro Gly Tyr Leu Tyr Thr
355    360    365
Asp Thr Gly Phe Trp Asp Thr Phe Arg Ala Leu Phe Pro Leu Leu Asn
370    375    380
Leu Leu Tyr Pro Asp Glu Asn Ile Lys Ile Gln Glu Gly Leu Leu Asn
385    390    395    400
Val Tyr Arg Glu Ser Gly Phe Phe Pro Glu Trp Ala Ser Pro Gly His
405    410    415
Arg Asp Cys Met Ile Gly Asn Asn Ser Ala Ser Val Leu Ala Asp Ala
420    425    430
Tyr Leu Lys Gly Val Arg Val Glu Asp Thr Arg Thr Leu Met Asn Gly
435    440    445
Leu Leu His Ala Thr Lys Ala Val His Pro Lys Ile Ser Ser Thr Gly
450    455    460
Arg Lys Gly Trp Glu Trp Tyr Asn Ser Leu Gly Tyr Val Pro Ala Asp
75

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WO 99/29870

PCT/AU98/01023

304/ 490

465 470 475 480
Ala Gly Ile Asp Glu Ser Ala Ala Arg Thr Leu Glu Tyr Ala Tyr Asn
485 490 495
5 Asp Trp Cys Ile Leu Arg Leu Gly Arg Thr Leu Gly Trp Asp Arg Ala
500 505 510
Ala Leu Asp Thr Leu Ala His Arg Ser Met Asn Tyr Arg His Leu Phe
515 520 525
10 Asp Pro Glu Thr Lys Leu Met Arg Gly Arg Asn Gln Asp Gly Ser Phe
530 535 540
Arg Thr Pro Phe Ser Pro Phe Lys Trp Gly Asp Val Phe Thr Glu Gly
545 550 555 560
Asn Ala Trp His Tyr Thr Trp Ser Val Phe His Asp Val Gln Gly Leu
565 570 575
15 Ile Asp Leu Met Gly Gly Asp Arg Pro Phe Val Ser Met Leu Asp Ser
580 585 590
Val Phe Asn Thr Pro Pro Met Phe Asp Glu Ser Tyr Tyr Gly Phe Val
595 600 605
Ile His Glu Ile Arg Glu Met Gln Ile Ala Asp Met Gly Asn Tyr Ala
610 615 620
20 His Gly Asn Gln Pro Ile Gln His Met Ile Tyr Leu Tyr Asn His Ala
625 630 635 640
Gly His Pro Trp Lys Ala Gln Glu Arg Leu Arg Glu Val Met Gly Arg
645 650 655
25 Leu Tyr Arg Pro Thr Pro Asp Gly Tyr Cys Gly Asp Glu Asp Asn Gly
660 665 670
Gln Thr Ser Ala Trp Tyr Val Phe Ser Ala Leu Gly Phe Tyr Pro Val
675 680 685
Thr Pro Ala Thr Asp Gln Tyr Val Leu Gly Ser Pro Ile Phe Ser Lys
690 695 700
30 Val Ile Leu Ser Phe Pro Asp Gly His Lys Thr Val Leu His Ala Pro
705 710 715 720
Ala Asn Ser Ala Asp Thr Pro Tyr Ile Arg Ser Ile Ser Val Glu Gly
725 730 735
35 Lys Glu Trp Ser Cys Asn Tyr Leu Thr His Glu Gln Leu Arg Ser Ser
740 745 750
Ala Ser Ile Gln Trp Met Met Asp Thr Lys Pro Asn Tyr Asn Arg Gly
755 760 765
Met Lys Glu Ser Asp Arg Pro Tyr Ser Phe Ser Thr Glu Gln Gln Arg
770 775 780
40 Arg Ala Asn His Ser Asn
785 790

(2) INFORMATION FOR SEQ ID NO:373

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 286 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
50 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
55 (A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc_feature
60 (B) LOCATION 1...286
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373

Ile Cys Gly Ser Lys Met Asn Leu Ser Gly Leu Gln Ser Phe Thr Met
1 5 10 15
65 Met Lys Ser Met Arg Ser Val Leu Leu Leu Leu Phe Pro Leu Ser Leu
20 25 30
Ile Thr Ala Leu Gly Cys Ser Asn Asn Lys Ala Ala Glu Ser Lys Ser
35 40 45
70 Val Ser Phe Asp Ser Ala Tyr Leu Glu Arg Tyr Ile Pro Leu Arg Ala
50 55 60
Asp Ile Asp Thr Pro Ser Leu His Val Met Ile Ser Tyr Val Tyr Pro
65 70 75 80
Ser Gly Asp Asp Met Leu Thr Glu Ile Phe Asn Gly Leu Leu Phe Gly
85 90 95
75 Asp Ser Leu Met Asp Ser Ser Ser Pro Glu Asn Ala Met Glu Gly Tyr

WO 99/29870

PCT/AU98/01023

305/ 490

100 105 110
Ala Gln Met Leu Gly Glu Asp Tyr Arg Ser Asn Asn Ala Glu Ala Asn
115 120 125
5 Leu Gln Gly Leu Pro Ser Asp Leu Leu Asp Tyr Ile Tyr Lys Gln Glu
130 135 140
Asn Thr Ile Ala Tyr Cys Asp Thr Gly Leu Ile Ser Thr Arg Ile Asn
145 150 155 160
Thr Tyr Thr Tyr Glu Gly Gly Ala His Thr Glu Asn Thr Val Arg Phe
165 170 175
10 Ala Asn Ile Leu Arg Thr Thr Gly Lys Val Leu Glu Glu Arg Asp Ile
180 185 190
Phe Lys Ile Asp Tyr Ala Glu Arg Leu Ser Ala Leu Ile Ile Gly Gln
195 200 205
15 Leu Val His Asp Phe Gly Lys Thr Thr Pro Ala Glu Leu Asp Ala Ile
210 215 220
Gly Phe Phe Asn Ala Glu Glu Ile Gln Pro Asn Gly Asn Phe Met Ile
225 230 235 240
Asp Asp Lys Gly Leu Thr Tyr Cys Phe Asn Glu Tyr Gln Ile Ala Ala
245 250 255
20 Tyr Ala Arg Gly Ala Val Tyr Val Arg Leu Gly Tyr Asp Val Leu Ala
260 265 270
Pro Leu Leu Arg Asp Asp Ser Pro Leu Lys Arg Tyr Leu Pro
275 280 285

25 (2) INFORMATION FOR SEQ ID NO:374
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 378 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
30 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
35 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...378
40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:374
45 Gly Ile Ile Ser Val Leu Ser His Val Val Asp Arg Pro Gln Trp Gly
1 5 10 15
Ala Ser Pro Glu Ala Ala Gly Thr His Ser Val Tyr Ser Ile Leu His
20 25 30
50 Pro Ser Ala Gly Ile Ile Arg Ile Arg Ser Met Gly Ile Ile Ser Ala
35 40 45
Cys Arg Ile Ala Ile Leu Ala Gly Lys His Pro Arg Ser Gly Leu Ser
50 55 60
Arg Ala Asn Val Gly Ile Leu Ser Tyr Asn Pro Glu Asn Thr Pro Glu
65 70 75 80
55 Lys Lys Arg Lys Leu Gln Glu Lys Asn Val Phe Leu Gln Ile Arg Leu
85 90 95
Arg Gln Ser Phe Asn Asn Leu Ile Pro Ser Leu Pro Phe Arg Ile Asp
100 105 110
60 Asn Thr Lys Lys Ile Thr Glu Met Lys Lys Thr Thr Leu Thr Gly Ser
115 120 125
Ile Cys Ala Leu Leu Leu Phe Leu Gly Leu Ser Ala Asn Ala Gln Ser
130 135 140
Lys Leu Lys Ile Lys Ser Ile Glu Ala Ala Thr Thr Phe Ser Ser Ala
145 150 155 160
65 Thr Ala Gly Asn Gly Phe Gly Gly Asn Ile Phe Gly Met Asp Met Ser
165 170 175
Ile Arg Met Arg Val His His Ser Ile Leu Pro Glu Gly Leu Asp Phe
180 185 190
70 Ser Val Gly Ile His Glu Arg Arg Ala His Trp Glu Glu Ala Gly Ser
195 200 205
Pro Lys Leu Met Tyr Thr Asn Val Pro Ser Ile Ile Gly Ile Val Glu
210 215 220
Lys Val Ile Val Phe Glu Asp Ala Glu Asp Phe Phe Asp Lys Lys Ala
225 230 235 240
75 Leu Gly Arg Phe Leu Ile Ser Leu Gly Ile Ser Tyr Thr Lys His Leu

WO 99/29870

PCT/AU98/01023

306/490

5 Gly Ala Tyr Trp 245 Gly Trp Thr Asn Asp 250 Ala His Ile Leu Phe Ser Pro 255
 Ile Pro Lys Ser 260 Lys Val His Tyr Asp 265 Thr Tyr Thr Arg Ala Gly Ser 270
 Asp Leu Val Leu Gln Ser Glu Asp Val Ala Thr Val Ser Asn Gly Phe 285
 Ser Pro Gly Ile Gly Leu Lys Ser Ser Ile Trp Trp Lys Met Pro Ile 300
 10 Lys Ser Lys Tyr Asp Phe Arg Leu Gly Phe Ser Leu Gly Tyr Glu Tyr 315
 Leu Asn Leu Leu Tyr Pro Tyr Arg Asn Phe Lys Leu Asp Gly Asn Lys 330
 Pro Leu Ser Ala Leu Ser Pro Arg Met Asn His Ile Gly His Val Gly 345
 15 Phe Asn Phe Thr Val Gly Leu Trp Thr Asn 360
 370 375

20 (2) INFORMATION FOR SEQ ID NO:375
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1269 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 25 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 30 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 35 (B) LOCATION 1...1269
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:375

40 Val Lys Cys Met Gly Lys Tyr Lys Arg Ala Lys Tyr Arg Tyr Trp Leu 5
 Phe Pro Phe Cys Ser Asp Tyr Tyr Thr Phe Glu Gly Val Thr Phe Leu 10
 Cys Ala Ser Asp Asp Met Thr Thr Lys Lys Pro Gln Ala Ile Leu Asp 15
 45 Leu Glu Lys Ala Tyr Asn Ile Glu Ile Pro Asp Leu Ser Ser Gln Glu 20
 Gly Ile Ser Trp Ser Val Asn Arg Tyr Phe Lys Gln Asp Ser Ser Gly 25
 50 Ala Val Val Glu Leu Cys Leu Arg Glu Cys Gln Ile Glu Ser Met Thr 30
 Trp Leu Ile Asp Phe Pro Ala Leu Lys Lys Leu Asp Leu Ser Tyr Asn 35
 Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys 40
 55 Leu Arg Leu Arg Ser Asn Gln Ile Arg Lys Leu Glu Gly Leu Asp Ser 45
 Leu Thr Ser Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys 50
 60 Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu 55
 Asp Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu 60
 Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu Gly Leu 65
 Glu Arg Leu Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile 70
 Arg Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys Leu Arg 75
 70 Leu Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr 80
 Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu 85
 Gly Leu Glu Arg Leu Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn 90
 75 Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Ser Ser Leu Thr Lys 95

WO 99/29870

PCT/AU98/01023

308/ 490

Leu Lys Phe Glu Arg Phe Ile Pro Phe Gly Leu Ile Asn Gln Ile Ile
 900 905 910
 Ala Tyr Tyr Gly Arg Glu Glu Gly Ala Leu Lys Arg Tyr Trp Arg Asp
 915 920 925
 5 Gln Val Ile Phe Thr Ala Gly Arg Glu Met Asp Arg Gln Thr Leu Glu
 930 935 940
 Gln Glu Glu Glu Lys Glu Gly Leu Pro Lys Thr Asn Ala Glu Asp Tyr
 945 950 955 960
 10 Gln Ile Trp Ile Lys Leu Asp Phe Thr Asp Leu Ala Ile Ser Val Phe
 965 970 975
 Ile Lys Glu Gln Arg Lys Thr Ser Ala Lys Asp Met Gln Arg Lys Glu
 980 985 990
 Ala Thr Ile Leu Ser Asp Met Leu Asp Met Tyr Trp Asn Asn Ile Pro
 995 1000 1005
 15 Pro Arg Glu Gln Ile Gly Asp Lys Asp Thr Glu Gln Thr Arg Ser Thr
 1010 1015 1020
 Ile Arg Glu Thr Asn Arg Lys Lys Arg Pro Ile Gln Asp Leu Tyr Leu
 1025 1030 1035 1040
 20 Ser Cys Ala Gln Ala Asp Lys Asp Leu Thr Glu Ser His Tyr Ile His
 1045 1050 1055
 Leu Gly Thr Leu Asp Asp Glu Ser Lys Thr Thr Ala Arg Ile Ala Ala
 1060 1065 1070
 Tyr Pro Leu Lys Asn Gly Val Ile Asp Lys Glu Arg Val Arg Glu Val
 1075 1080 1085
 25 Ser Thr Arg Pro Tyr Lys His Leu Ser Val Asn Lys Asn Leu Ala Thr
 1090 1095 1100
 Ala Lys Gln Ile Phe Ile Ser Tyr Ser Lys Glu Asp Gln Thr Glu Leu
 1105 1110 1115 1120
 30 Glu Thr Cys Leu Gln Phe Phe Lys Pro Leu Glu Lys Asn Gly Gln Ile
 1125 1130 1135
 Glu Ile Tyr Tyr Asp Lys Leu Thr Lys Phe Glu Thr Pro Ile His Pro
 1140 1145 1150
 Glu Ile Arg Lys Arg Ile Val Glu Ala Asp Cys Ile Ile Ala Leu Ile
 1155 1160 1165
 35 Ser Gln Arg Tyr Leu Ala Thr Asp Tyr Ile Leu Asp His Glu Leu Pro
 1170 1175 1180
 Val Phe Arg Glu Tyr Asn Lys Thr Ile Val Pro Ile Leu Ile Lys Pro
 1185 1190 1195 1200
 40 Cys Thr Phe Glu Asp Asp Glu Phe Leu Arg Glu Lys Tyr Phe Ala Gln
 1205 1210 1215
 Lys Ala Gln Ile Ile Asn Leu Gly Lys Glu Gly Lys Thr Ile Lys Ala
 1220 1225 1230
 Tyr Asp Ser Ile Thr Ala Ser Ala His Arg Asp Glu Asn Trp Val Ala
 1235 1240 1245
 45 Val Val Arg Glu Phe Lys Glu Lys Ile Leu Arg Ile Thr Lys Gln Glu
 1250 1255 1260
 Val Asn Thr Asp Glu
 1265

50 (2) INFORMATION FOR SEQ ID NO:376

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376

70 Lys Phe Met Met Lys Lys Ala Phe Val Phe Val Leu Leu Val Cys Leu
 1 5 10 15
 Phe Ser Ser Phe Ser Ser Ser Ala Gln Thr Thr Thr Asn Ser Ser Arg
 20 25 30
 75 Ser Tyr Phe Thr Gly Arg Ile Glu Lys Val Ser Leu Asn Leu Gly Val
 35 40 45

WO 99/29870

PCT/AU98/01023

310/ 490

5 Glu Lys Lys Ile Asp Lys Val Asp Leu Ser Leu Gly Ser Thr Ser Glu
245 250 255
Ser Met Gly His Asn Ala Trp Pro Leu Met Gly Val Val Phe Glu Met
260 265 270
Asn Lys Gln Gly Gly Lys Ser Asp Ile Gly Phe Leu Ser Asn Phe Val
275 280 285
Asp Asn Asp Pro Glu Phe Gln Trp Ser Gly Pro Ile Lys Val Ser Glu
290 295 300
10 Ser Asp Met Ser Phe Ser Pro Lys Ile Gln Met Leu Leu Asp Glu Asp
305 310 315 320
Asn Asn Thr Ile Asn Gly Glu Ser Cys His Asn Phe Met Ile Thr Tyr
325 330 335
Ser Asp Tyr Asp Ser Glu Tyr Ser Asp Trp Asp Ile Arg Tyr Val Tyr
340 345 350
15 Pro Lys Lys Ser Phe Lys Tyr Glu Lys Gly Lys Thr Pro Thr Met Asp
355 360 365
Asp Leu Val Glu Ala Phe Leu Thr Ala Ser Tyr Gln Ser Glu Thr Asn
370 375 380
20 Ser Gly Leu Gly Tyr Asp Lys Asn Ala Asn His Tyr Leu Ile Thr Tyr
385 390 395 400
Ala Lys Lys Glu Glu Asn Gly Thr Asn Thr Leu Lys Tyr Arg Trp Ala
405 410 415
Asn Tyr Asp Lys Ile His Asn Lys Asp Leu Trp Ser Asp Thr Phe Thr
420 425 430
25 Tyr Thr Ser Ala Asn Ala Leu Tyr Thr Pro Gln Val Asp Ile Asn
435 440 445
Pro Thr Lys Gly Leu Val Cys Trp Ser Trp Val Glu Tyr Leu Pro Gly
450 455 460
30 Lys Arg Ile Val Trp Ser Asp Thr Gln Trp Thr His Ala Asn Gly Val
465 470 475 480
Glu Asp Ile Val Met Gln Glu Gly Ser Met Lys Leu Tyr Pro Asn Pro
485 490 495
Ala Gln Glu Tyr Ala Val Ile Ser Leu Pro Thr Ala Ala Asn Cys Lys
500 505 510
35 Ala Val Val Tyr Asp Met Gln Gly Arg Val Val Ala Glu Ala Ser Phe
515 520 525
Ser Gly Asn Glu Tyr Arg Leu Asn Val Gln His Leu Ala Lys Gly Thr
530 535 540
40 Tyr Ile Leu Lys Val Val Ser Asp Thr Glu Arg Phe Val Glu Lys Leu
545 550 555 560
Ile Val Glu

(2) INFORMATION FOR SEQ ID NO:378

45

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 786 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

55

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

60

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378

65 Ile Val Tyr Leu Cys His Cys Met Asn His Arg Arg Ser Lys Thr Met
1 5 10 15
Leu Thr Ile Arg Asn Phe Leu Leu Phe Cys Cys Leu Ser Leu Ile Ala
20 25 30
Phe Ala Ala Asp Ala Gln Ser Ser Val Ser Ser Gly Arg Arg Leu Thr
35 40 45
70 Glu Tyr Val Asn Pro Phe Ile Gly Thr Ala Asn Tyr Gly Thr Thr Asn
50 55 60
Pro Gly Ala Val Leu Pro Asn Gly Leu Met Ser Val Thr Pro Phe Asn
65 70 75 80
75 Val Ser Gly Ser Thr Glu Asn Arg Phe Asp Lys Asp Ser Arg Trp Trp
85 90 95

WO 99/29870

PCT/AU98/01023

311/490

Ser Ala Pro Tyr Ser Ala Asp Asn Ser Tyr Cys Ile Gly Phe Ser His
 100 105 110
 Val Asn Leu Ser Gly Val Gly Cys Pro Glu Leu Ser Gly Ile Leu Leu
 115 120 125
 5 Met Ala Thr Ser Gly Thr Phe Asp Pro Asp Tyr Cys Tyr Gly Ser
 130 135 140
 Ser Leu Ser Arg Glu Tyr Ala Arg Pro Gly Glu Tyr Lys Ala Val Leu
 145 150 155 160
 10 Asp Lys Tyr Gly Ile Asp Ala Ala Val Thr Val Thr Glu Arg Thr Ala
 165 170 175
 Leu Thr Glu Phe Ala Phe Pro Glu Gly Glu Gly His Ile Leu Leu Asn
 180 185 190
 Leu Gly Gln Ala Leu Ser Asn Glu Ser Gly Ala Ser Val Arg Phe Leu
 195 200 205
 15 Asn Asp Ser Thr Val Val Gly Ser Arg Leu Met Gly Thr Phe Cys Tyr
 210 215 220
 Asn Pro Gln Ala Val Phe Arg Gln Tyr Phe Val Leu Gln Val Ser Arg
 225 230 235 240
 20 Arg Pro Ile Ser Ala Gly Tyr Trp Lys Lys Gln Pro Pro Met Thr Val
 245 250 255
 Glu Ala Gln Trp Asp Ser Thr Ala Gly Lys Tyr Lys Gln Tyr Asp Gly
 260 265 270
 Tyr Lys Arg Glu Met Ser Gly Asp Asp Ile Gly Val Arg Phe Ser Phe
 275 280 285
 25 Asn Cys Asp Gln Gly Glu Lys Ile Tyr Val Arg Ser Ala Val Ser Phe
 290 295 300
 Val Ser Glu Ala Asn Ala Leu Tyr Asn Leu Glu Ala Glu Gln Glu Glu
 305 310 315 320
 30 Val Phe Lys Ser Val Gly Gly Asn Pro Ala Lys Ala Phe Ser Ala Ile
 325 330 335
 Arg Ser Arg Ala Ile Glu Arg Trp Glu Glu Ala Leu Gly Thr Val Glu
 340 345 350
 Val Glu Gly Gly Thr Pro Asp Glu Lys Thr Ile Phe Tyr Thr Ala Leu
 355 360 365
 35 Tyr His Leu Leu Ile His Pro Asn Ile Leu Gln Asp Ala Asn Gly Glu
 370 375 380
 Tyr Pro Met Met Gly Ser Gly Lys Thr Gly Asn Thr Ala His Asp Arg
 385 390 395 400
 40 Tyr Thr Val Phe Ser Leu Trp Asp Thr Tyr Arg Asn Val His Pro Leu
 405 410 415
 Leu Cys Leu Leu Tyr Pro Glu Lys Gln Leu Asp Met Val Arg Thr Leu
 420 425 430
 Ile Asp Met Tyr Arg Glu Ser Gly Trp Leu Pro Arg Trp Glu Leu Tyr
 435 440 445
 45 Gly Gln Glu Thr Leu Thr Met Glu Gly Asp Pro Ser Leu Ile Val Ile
 450 455 460
 Asn Asp Thr Trp Gln Arg Gly Leu Arg Ala Phe Asp Thr Ala Thr Ala
 465 470 475 480
 50 Tyr Glu Ala Met Lys Lys Asn Ala Ser Ser Ala Gly Ala Thr His Pro
 485 490 495
 Ile Arg Pro Asp Asn Asp Asp Tyr Leu Thr Leu Gly Phe Val Pro Leu
 500 505 510
 Arg Glu Gln Tyr Asp Asn Ser Val Ser His Ala Leu Glu Tyr Tyr Leu
 515 520 525
 55 Ala Asp Trp Asn Leu Ser Arg Phe Ala His Ala Leu Gly His Lys Glu
 530 535 540
 Asp Ala Ala Leu Phe Gly Lys Arg Ser Leu Gly Tyr Arg His Tyr Tyr
 545 550 555 560
 60 Asn Lys Glu Tyr Gly Met Leu Cys Pro Leu Leu Pro Asp Gly Ser Phe
 565 570 575
 Leu Thr Pro Phe Asp Pro Lys Gln Gly Glu Asn Phe Glu Pro Asn Pro
 580 585 590
 Gly Phe His Glu Gly Ser Ala Tyr Asn Tyr Ala Phe Phe Val Pro His
 595 600 605
 65 Asp Ile Gln Gly Leu Ala Arg Leu Met Gly Gly Ala Lys Val Phe Ser
 610 615 620
 Glu Arg Leu Gln Lys Val Phe Asp Glu Gly Tyr Tyr Asp Pro Thr Asn
 625 630 635 640
 70 Glu Pro Asp Ile Ala Tyr Pro Tyr Leu Phe Ser Tyr Phe Pro Lys Glu
 645 650 655
 Ala Trp Arg Thr Gln Lys Leu Thr Arg Glu Leu Ile Asp Lys His Phe
 660 665 670
 Cys Asn Ala Pro Asn Gly Leu Pro Gly Asn Asp Asp Ala Gly Thr Met
 675 680 685
 75 Ser Ala Trp Leu Val Tyr Ser Met Leu Gly Phe Tyr Pro Asp Cys Pro

WO 99/29870

PCT/AU98/01023

313/490

5
325
Ala Tyr Ile Ala Leu Gly Glu Glu Gly Leu Ala Ser Leu Leu Leu Ala
340
Glu Gly Ser Thr Ala Glu Ala Met Pro Val Ala Phe Asp Gly Pro Gly
355
Asp Asn Asp Phe Tyr Glu Met Arg Phe Ser His Gly Arg Leu Tyr Ala
370
Ala Ser Gly Leu Trp Gly Thr Asn Leu Met Gly His Ala Gly Met Val
385
10 Lys Leu Tyr Asp Gly Asn Arg Trp Thr Asn Phe Asp Lys Lys Thr Val
405
Gln Glu Gln Leu Gly Gly Gly Phe Ser Phe Asn Asp Ala Ile Asp Ile
420
15 Ala Val Ser Asn Gly Asp Pro Asp His Phe Phe Val Gly Thr Trp Gly
435
Asn Gly Leu Phe Glu Phe Lys Asp Gly Lys Ala Ile Ala Arg Tyr Ser
450
Gly Asn Glu Thr Ala Ile Ala Glu Cys Asn Pro Gly Asp Ala Arg Val
465
20 Lys Ala Ile Ala Phe Asp Asn Lys Gly Asn Leu Trp Gly Thr Leu Gly
485
Ala Val Gly Lys Asn Ile Phe Met Tyr Asp Pro Gln Ser Ser Thr Trp
500
His Ser Phe Ser Tyr Pro Asp Val Ala Asn Leu Ala Ser Phe Gly Asn
515
25 Met Ile Ile Leu Pro Asn Gly Asp Lys Trp Val Asn Ile Leu His Arg
530
Ser Gly Gly Ser Thr Arg Lys Gly Val Leu Ile Phe Asn Asp Arg Gly
545
30 Thr Pro Glu Thr Thr Ser Asp Asp Ser His Leu Tyr Val Glu Gln Phe
565
Val Asn Arg Leu Gly Ala Ala Ile Gly His Lys Thr Ile Tyr Ala Met
580
35 Ala Val Asp His Asn Gly Ser Val Trp Met Gly Ser Asp Ile Gly Ile
595
Phe Gly Val Tyr Asn Ala Ala Gly Val Leu Ser Ser Thr Ser Thr Pro
610
Ile Ala Val Arg Pro Val Gly Gly Glu Glu Pro Asn Leu Tyr Tyr Val
625
40 Leu Asp Lys Val Thr Val Thr Asp Ile Val Val Asp Lys Leu Asn His
645
Lys Trp Val Ala Thr Gln Gly Thr Gly Leu Tyr Leu Leu Ser Glu Asp
660
45 Cys Ser Lys Ile Leu Ala Gln Phe Thr Val Glu Asn Ser Pro Leu Leu
675
Ser Asn Asn Ile Leu Ser Leu Ala Leu Asn Asp Asp Asn Gly Leu Leu
690
Tyr Ile Gly Thr Ala Asp Gly Leu Met Thr Phe Gln Thr Gly Thr Gly
705
50 Ser Gly Ser Ala Ser Glu Leu Asp Gly Val Tyr Val Tyr Pro Asn Pro
725
Leu Arg Pro Glu Tyr Pro Asp Gly Val Thr Ile Ala Gly Leu Gln Ala
740
Gly Cys Ser Val Lys Ile Thr Asp Thr Thr Gly Arg Leu Leu Tyr Gln
755
55 Thr Glu Ser Val Thr Thr Glu Val Lys Trp Asn Ala Arg Gly Ala Asp
770
Gly Asn Arg Val Ala Ser Gly Val Tyr Ala Val Ala Val Tyr Asp Pro
785
60 Val Ser Lys Lys Ser Lys Leu Ile Arg Phe Ala Val Ile Arg
805
810

(2) INFORMATION FOR SEQ ID NO:380

- 65 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1162 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- 70 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 75 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

WO 99/29870

PCT/AU98/01023

314/ 490

(ix) FEATURE:

(A) NAME/KEY: misc feature
(B) LOCATION 1...1162

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380

	Ala	Ile	Ser	Gln	Met	Lys	Arg	Ile	Leu	Pro	Ile	Val	Ala	Phe	Leu	Ser
	1				5					10				15		
10	Leu	Phe	Leu	Ala	Leu	Ala	Leu	Pro	Ala	Lys	Ala	Gln	Arg	Ala	Met	Gly
			20						25					30		
	Lys	Thr	Ala	Asp	Arg	Ser	Leu	Met	Ala	Ser	Gly	His	Trp	Val	Lys	Ile
			35					40					45			
15	Arg	Val	Asp	Ala	Ser	Gly	Val	Tyr	Arg	Leu	Thr	Asp	Glu	Gln	Leu	Arg
		50				55						60				
	Ala	Asn	Gly	Phe	Ser	Asp	Pro	Ser	Lys	Val	Gly	Val	Phe	Gly	Tyr	Gly
	65					70				75					80	
	Gly	Gly	Val	Leu	Pro	Glu	Asp	Leu	Ser	Arg	Ile	Thr	Thr	Asp	Asp	Leu
					85					90				95		
20	Pro	Pro	Val	Pro	Val	Leu	Arg	Gln	Gly	Asn	Ala	Leu	Tyr	Phe	Tyr	Ala
				100					105					110		
	Val	Gly	Pro	Val	Thr	Trp	Phe	Tyr	Asn	Pro	Ala	Lys	Thr	Thr	Met	Glu
		115					120						125			
25	His	Thr	Val	Asn	Thr	Tyr	Ser	Thr	His	Gly	Tyr	Tyr	Phe	Leu	Ser	Asp
		130				135						140				
	Ala	Ala	Gly	Ala	Pro	Leu	Gln	Met	Ser	Gln	Tyr	Thr	Gly	Gly	Gly	Ala
	145					150					155				160	
	Ser	Ala	Glu	Ala	Leu	Ile	Asp	Tyr	Tyr	Asp	Glu	Leu	Met	Leu	His	Glu
				165					170					175		
30	Gln	Glu	Leu	Tyr	Ser	Pro	Lys	Glu	Ser	Gly	Arg	Asp	Leu	Tyr	Gly	Glu
				180					185					190		
	Ser	Phe	Ser	Ala	Val	Asn	Thr	Arg	Thr	Val	Lys	Phe	Pro	Leu	Arg	Gly
		195						200					205			
35	Asn	Thr	Arg	Ser	Ser	Gly	Glu	Leu	Gly	Thr	Val	Phe	Ser	Tyr	Ile	Ala
		210				215						220				
	Lys	Ala	Arg	Ser	Ala	Gly	Gly	Gly	Arg	Glu	Met	Ser	Leu	Ser	Ala	Asn
	225					230					235				240	
	Gly	Ile	Leu	Ile	Phe	Ser	Asp	Pro	Phe	Ser	Met	Thr	Ser	Asn	Glu	Val
					245					250				255		
40	Ser	Asn	Ser	Tyr	Leu	Ala	Gly	Lys	Lys	Arg	Arg	Leu	Tyr	His	Ser	Thr
				260					265					270		
	Pro	Met	Asn	Ser	Leu	Val	Asn	Glu	Leu	Arg	Leu	Asp	Ala	Asn	Tyr	Ser
			275				280						285			
45	Met	Thr	Gly	Asp	Ala	Val	Asn	Leu	Asp	Phe	Ile	Glu	Val	Ala	Thr	Gln
		290				295						300				
	Asn	Asp	Leu	Arg	Tyr	Asp	Gly	Ala	Pro	Met	His	Ile	Arg	Arg	Phe	Ser
		305				310					315				320	
	Asn	Leu	Pro	Val	Leu	Gly	Gly	Glu	Ser	Cys	Arg	Phe	Val	Ile	Ser	Glu
				325					330					335		
50	Val	Pro	Glu	Ser	Leu	Val	Val	Leu	Gln	Ala	Asn	Ser	Ser	Leu	Thr	Ala
				340					345					350		
	Ser	Leu	Val	Pro	Val	Lys	Thr	Val	Gly	Asp	Lys	Thr	Ile	Glu	Phe	Val
				355					360				365			
55	Ala	Pro	Pro	Lys	Gly	Gln	Asp	Arg	Arg	Thr	Ile	Asn	Thr	Phe	Tyr	Ala
		370				375						380				
	Val	Asp	Leu	Ser	Gln	Ala	Ser	Ala	Pro	Glu	Ile	Leu	Gly	Ala	Val	Pro
					390					395					400	
	Asn	Gln	Asn	Leu	His	Gly	Glu	Glu	Ile	Pro	Asp	Leu	Ile	Ile	Val	Ser
				405					410					415		
60	Thr	Gln	Ala	Leu	Leu	Glu	Ala	Asp	Arg	Leu	Ala	Thr	Tyr	Arg	Arg	
				420					425				430			
	Glu	Lys	Asn	Gly	Leu	Lys	Val	Leu	Val	Val	Leu	Gln	Glu	Gln	Val	Phe
			435					440					445			
65	Asn	Glu	Phe	Ser	Gly	Gly	Thr	Pro	Asp	Ala	Thr	Ala	Tyr	Arg	Leu	Phe
		450				455						460				
	Ala	Lys	Met	Phe	Tyr	Asp	Arg	Trp	Lys	Ala	Asn	Ala	Pro	Val	Gly	Glu
		465				470					475				480	
	Thr	Phe	Pro	Met	Gln	Met	Leu	Leu	Phe	Gly	Asp	Gly	Ala	His	Asp	Asn
				485						490				495		
70	Arg	Lys	Val	Ser	Val	Ala	Trp	Gln	Lys	Pro	Tyr	Leu	Gln	Gln	Thr	Glu
				500					505					510		
	Phe	Leu	Leu	Thr	Phe	Gln	Ala	Val	Asn	Ser	Thr	Asn	Val	Asn	Ser	Tyr
				515				520					525			
75	Val	Thr	Asp	Asp	Tyr	Phe	Gly	Leu	Leu	Asp	Asp	Gln	Pro	Ala	Ser	Val
		530				535						540				

WO 99/29870

PCT/AU98/01023

315/ 490

	Asn	Ile	Gly	Trp	Arg	Asn	Tyr	Asn	Met	Ala	Val	Gly	Arg	Phe	Pro	Val
	545					550					555					560
	Arg	Thr	Pro	Ala	Glu	Ala	Arg	Ile	Ala	Val	Asp	Lys	Thr	Ile	Arg	Tyr
				565						570					575	
5	Glu	Glu	Asp	Arg	Glu	Ser	Gly	Ala	Trp	Arg	Ile	Arg	Ala	Cys	Phe	Ala
			580					585						590		
	Ala	Asp	Asn	Gly	Asp	Lys	His	Ala	Thr	Glu	Thr	Ser	Arg	Leu	Ile	Asp
		595					600						605			
10	Thr	Val	Lys	Arg	Tyr	Ala	Pro	Ala	Ile	Met	Pro	Val	Arg	Ala	Phe	Gln
		610				615						620				
	Asp	Val	Tyr	Pro	His	Val	Ile	Glu	Asn	Gly	Leu	His	Ser	Ile	Pro	Gly
	625					630					635					640
	Ala	Lys	Lys	Lys	Met	Leu	Glu	Thr	Leu	Gln	Ser	Gly	Ile	Ile	Leu	Leu
				645						650					655	
15	Asn	Tyr	Ala	Gly	His	Gly	Gly	Pro	Ala	Gly	Trp	Ser	Asp	Glu	His	Leu
			660						665					670		
	Leu	Thr	Leu	Asn	Asp	Ile	His	Lys	Phe	Asn	Tyr	Lys	His	Met	Pro	Ile
		675						680					685			
20	Trp	Ile	Thr	Ala	Thr	Cys	Asp	Phe	Ala	Asn	Tyr	Asp	Ser	Gln	Thr	Thr
		690				695						700				
	Ser	Ala	Gly	Glu	Glu	Val	Phe	Leu	His	Glu	Lys	Ser	Gly	Thr	Pro	Ile
		705				710					715					720
	Met	Phe	Ser	Thr	Thr	Arg	Val	Val	Tyr	Asn	Thr	Gln	Asn	Glu	Lys	Ile
				725						730					735	
25	Asn	Gly	Phe	Met	Leu	Arg	Arg	Met	Phe	Glu	Lys	Ala	Lys	Asp	Gly	Arg
			740						745					750		
	Tyr	Arg	Thr	Met	Gly	Glu	Ile	Ile	Arg	Ser	Ala	Lys	Gln	Gly	Met	Leu
		755						760					765			
30	Ser	Thr	Val	Phe	Pro	Asp	Ser	Ile	Asn	Gln	Leu	Ser	Phe	Phe	Leu	Met
		770				775						780				
	Gly	Asp	Pro	Ser	Val	Arg	Met	Asn	Leu	Pro	Thr	His	Lys	Val	Gln	Leu
		785				790					795					800
	Thr	Ala	Ile	Asn	Gly	Gln	Asp	Pro	Glu	Gly	Gln	Tyr	Gly	Thr	Ile	Met
				805						810					815	
35	Leu	Lys	Ser	Leu	Glu	Arg	Val	Ala	Leu	Lys	Gly	Lys	Val	Thr	Asp	Glu
			820						825					830		
	Lys	Gly	Thr	Phe	Asp	Glu	Thr	Phe	Ser	Gly	Lys	Val	Phe	Leu	Thr	Val
		835						840					845			
40	Phe	Asp	Gly	Arg	Lys	Lys	Met	Thr	Ala	Leu	Glu	Glu	Gly	Asn	Asp	
		850					855					860				
	Leu	Ser	Leu	Val	Tyr	Tyr	Asp	Tyr	Pro	Asn	Val	Met	Tyr	Ala	Gly	Ile
		865				870					875					880
	Ala	Glu	Val	Lys	Asp	Gly	Leu	Phe	Glu	Thr	Ser	Phe	Ile	Val	Pro	Lys
				885						890					895	
45	Asp	Val	Asn	Tyr	Ser	Glu	His	Glu	Gly	Arg	Ile	Asn	Leu	Tyr	Ala	Tyr
			900						905					910		
	Asn	Glu	Ser	Thr	Lys	Ala	Glu	Ala	Met	Gly	Val	Asp	Phe	Ser	Ile	Arg
			915						920					925		
50	Val	Gln	Pro	Gly	Ile	Pro	Asp	Glu	Val	Thr	Glu	Asp	Asn	Thr	Pro	Pro
			930				935					940				
	Glu	Ile	Ile	Ser	Cys	Phe	Leu	Asn	Asp	Ser	Thr	Phe	Arg	Ser	Gly	Asp
			945			950					955					960
	Glu	Val	Asn	Pro	Thr	Pro	Leu	Phe	Met	Ala	Glu	Val	Phe	Asp	Leu	Asn
				965						970					975	
55	Gly	Ile	Asn	Ile	Thr	Gly	Ser	Gly	Val	Gly	His	Asp	Ile	Thr	Leu	Cys
			980						985					990		
	Ile	Asp	Gly	Arg	Ala	Asp	Leu	Thr	Tyr	Asn	Leu	Asn	Ala	Tyr	Phe	Thr
			995						1000					1005		
60	Ser	Ser	Ala	Thr	Asp	Ala	Gly	Val	Gly	Thr	Ile	Leu	Phe	Met	Ile	Pro
			1010					1015						1020		
	Ala	Leu	Ala	Glu	Gly	Asp	His	Thr	Ala	Arg	Leu	Thr	Val	Trp	Asp	Ile
			1025				1030					1035				1040
	Phe	Asn	Asn	Ala	Val	His	His	Asp	Phe	Ser	Phe	Arg	Val	Val	Asp	Gly
				1045						1050					1055	
65	Ile	Ala	Pro	Asp	Val	Ala	Asp	Val	Ile	Leu	Phe	Pro	Asn	Pro	Val	Arg
			1060							1065					1070	
	Glu	Ser	Ala	Thr	Phe	Arg	Ile	Phe	His	Asn	Arg	Pro	Gly	Ser	Asp	Leu
			1075						1080					1085		
70	Asn	Val	Ala	Val	Glu	Ile	Tyr	Asp	Phe	Thr	Gly	Arg	Leu	Val	Asn	Ser
			1090				1095						1100			
	Leu	Pro	Val	Lys	Thr	Tyr	Ser	Ser	Ser	Tyr	Gly	Glu	Pro	Ile	Glu	Ile
			1105				1110					1115				1120
	Lys	Trp	Asp	Leu	Thr	Ser	Lys	Tyr	Gly	Val	Lys	Ile	Gly	Asn	Gly	Phe
				1125						1130					1135	
75	Tyr	Leu	Tyr	Arg	Cys	Val	Val	Asn	Ser	Pro	Gly	Gly	Gln	Thr	Ala	Ser

316/ 490

1140 1145 1150
Met Ala Lys Lys Met Ile Val Val Gly Gln
1155 1160

5 (2) INFORMATION FOR SEQ ID NO:381

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 973 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES

15 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

20 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...973

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:381

25 Phe Tyr Thr Gly Ile Asp Leu His Ile Glu Ser Gln Met Lys Lys Leu
1 5 10 15
Phe Pro Leu Leu Leu Ile Leu Ser Ile Leu Val Gly Cys Gly Lys
20 25 30
30 Lys Glu Lys His Ser Val Thr Glu Ile Ala Arg Glu Lys Lys Arg Ile
35 40 45
Thr Ala Leu Leu Tyr Glu Lys Glu Leu Pro Thr Asp Ser Val Lys Gln
50 55 60
Leu Tyr Glu Asn Ser Val Gln Asn Lys Asn Leu Val Gly Gln Met Leu
65 70 75 80
35 Phe Ala Ile Glu Val Gly Lys Arg Met Arg Asn Met Ser Gln Tyr Thr
85 90 95
Asp Ala Met Leu Tyr His Gln Lys Gly Leu Asn Ala Ala Leu Asn Leu
100 105 110
40 Arg Asp Thr Ile Val Ala Ala Gln Ala Trp Asn His Leu Gly Thr Asp
115 120 125
Ser Arg Arg Ile Gly Ala Leu Ala Glu Ala Ser Asp Tyr His Tyr Lys
130 135 140
45 Ala Leu Ser Leu Ile Glu Ser Phe Ser Gly Asn Gln Asn Arg Pro Ala
145 150 155 160
Ile Lys Ala Arg Ser Ala Ala Leu Asn Gly Ile Gly Asn Ile Asn Leu
165 170 175
Glu Leu Gly Tyr His Asp Glu Ala Glu Lys Asn Phe Leu Lys Ala Leu
180 185 190
50 Gln Gly Glu Lys Glu Leu Asp Ser Pro Leu Gly Gln Ala Ile Asn Tyr
195 200 205
Ala Asn Leu Gly Arg Ile Tyr Arg Gln Arg Lys Glu Tyr Asp Lys Ala
210 215 220
Arg Thr Tyr Phe Leu Leu Ser Leu Glu Gln Asn Met Ala Glu Asn
225 230 235 240
55 Leu Met Gly Ile Gly Leu Cys Ser Ile Asn Leu Gly Glu Val Asp Glu
245 250 255
Glu Lys Gly Asp Tyr Gln Lys Ala Leu Gln Glu Tyr Ala Thr Ala Tyr
260 265 270
60 Lys Leu Met Glu Gln Leu Ser Asp Arg Trp His Trp Leu Asn Ser Cys
275 280 285
Ile Pro Met Ala Arg Ile Asn Leu Lys Gln Gly Asn Glu Arg Leu Tyr
290 295 300
Gln His Phe Ile Ser Leu Ala Glu Gly Thr Ala Lys Glu Ile Asn Ser
305 310 315 320
65 Thr Ser His Leu Ile Glu Ile Tyr Asn Leu Gln Tyr Glu Asn Leu Glu
325 330 335
Arg Lys Lys Glu Tyr Lys Gln Ala Leu Glu Ala Phe Cys Leu Ser Lys
340 345 350
70 Thr Leu Ser Asp Ser Met Ser Ile Ala His Lys Val Ser Ser Ile Gln
355 360 365
Glu Thr Arg Phe Asn Tyr Glu Arg Asn Lys Ser Gln Lys Glu Leu Glu
370 375 380
Glu Ile Gln Gln Val Ser Lys Ala Lys Gln Glu Lys Ser Lys Phe Ile
385 390 395 400
75 Leu Leu Ser Thr Leu Phe Ala Leu Phe Ile Ser Ile Leu Leu Ile Ser

WO 99/29870

PCT/AU98/01023

318/490

(A) LENGTH: 563 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
10 (A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...563

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:382

	His	His	Lys	Thr	Tyr	Gln	Thr	Met	Lys	Lys	Leu	Leu	Gln	Ala	Lys	Ala
	1			5					10					15		
20	Leu	Ile	Leu	Ala	Leu	Gly	Leu	Phe	Gln	Leu	Pro	Ala	Ile	Ala	Gln	Thr
				20					25					30		
	Gln	Met	Gln	Ala	Asp	Arg	Thr	Asn	Gly	Gln	Phe	Ala	Thr	Glu	Glu	Met
				35				40					45			
25	Gln	Arg	Ala	Phe	Gln	Glu	Thr	Asn	Pro	Pro	Ala	Gly	Pro	Val	Arg	Ala
				50				55				60				
	Ile	Ala	Glu	Tyr	Glu	Arg	Ser	Ala	Ala	Val	Leu	Val	Arg	Tyr	Pro	Phe
	65				70						75			80		
	Gly	Ile	Pro	Met	Glu	Leu	Ile	Lys	Glu	Leu	Ala	Lys	Asn	Asp	Lys	Val
					85						90			95		
30	Ile	Thr	Ile	Val	Ala	Ser	Glu	Ser	Gln	Lys	Asn	Thr	Val	Ile	Thr	Gln
				100					105				110			
	Tyr	Thr	Gln	Ser	Gly	Val	Asn	Leu	Ser	Asn	Cys	Asp	Phe	Ile	Ile	Ala
				115				120				125				
	Lys	Thr	Asp	Ser	Tyr	Trp	Thr	Arg	Asp	Tyr	Thr	Gly	Trp	Phe	Ala	Met
35				130				135				140				
	Tyr	Asp	Thr	Asn	Lys	Val	Gly	Leu	Val	Asp	Phe	Ile	Tyr	Asn	Arg	Pro
				145				150			155			160		
	Arg	Pro	Asn	Asp	Asp	Glu	Phe	Pro	Lys	Tyr	Glu	Ala	Gln	Tyr	Leu	Gly
				165					170				175			
40	Ile	Glu	Met	Phe	Gly	Met	Lys	Leu	Lys	Gln	Thr	Gly	Gly	Asn	Tyr	Met
				180				185					190			
	Thr	Asp	Gly	Tyr	Gly	Ser	Ala	Val	Gln	Ser	His	Ile	Ala	Tyr	Thr	Glu
				195				200					205			
45	Asn	Ser	Ser	Leu	Ser	Gln	Ala	Gln	Val	Asn	Gln	Lys	Met	Lys	Asp	Tyr
				210				215				220				
	Leu	Gly	Ile	Thr	His	His	Asp	Val	Val	Gln	Asp	Pro	Asn	Gly	Glu	Tyr
				225				230			235			240		
	Ile	Asn	His	Val	Asp	Cys	Trp	Gly	Lys	Tyr	Leu	Ala	Pro	Asn	Lys	Ile
				245					250				255			
50	Leu	Ile	Arg	Lys	Val	Pro	Asp	Asn	His	Pro	Gln	His	Gln	Ala	Leu	Glu
				260				265					270			
	Asp	Met	Ala	Ala	Tyr	Phe	Ala	Ala	Gln	Thr	Cys	Ala	Trp	Gly	Thr	Lys
				275				280				285				
55	Tyr	Glu	Val	Tyr	Arg	Ala	Leu	Ala	Thr	Asn	Glu	Gln	Pro	Tyr	Thr	Asn
				290				295				300				
	Ser	Leu	Ile	Leu	Asn	Asn	Arg	Val	Phe	Val	Pro	Val	Asn	Gly	Pro	Ala
				305				310			315			320		
	Ser	Val	Asp	Asn	Asp	Ala	Leu	Asn	Val	Tyr	Lys	Thr	Ala	Met	Pro	Gly
				325				330					335			
60	Tyr	Glu	Ile	Ile	Gly	Val	Lys	Gly	Ala	Ser	Gly	Thr	Pro	Trp	Leu	Gly
				340				345					350			
	Thr	Asp	Ala	Leu	His	Cys	Arg	Thr	His	Glu	Val	Ala	Asp	Lys	Gly	Tyr
				355				360				365				
65	Leu	Tyr	Ile	Lys	His	Tyr	Pro	Ile	Leu	Gly	Glu	Gln	Ala	Gly	Pro	Asp
				370				375				380				
	Tyr	Lys	Ile	Glu	Ala	Asp	Val	Val	Ser	Cys	Ala	Asn	Ala	Thr	Ile	Ser
				385				390			395			400		
	Pro	Val	Gln	Cys	Tyr	Tyr	Arg	Ile	Asn	Gly	Ser	Gly	Ser	Phe	Lys	Ala
				405				410					415			
70	Ala	Asp	Met	Thr	Met	Glu	Ser	Thr	Gly	His	Tyr	Thr	Tyr	Ser	Phe	Thr
				420				425				430				
	Gly	Leu	Asn	Lys	Asn	Asp	Lys	Val	Glu	Tyr	Tyr	Ile	Ser	Ala	Ala	Asp
				435				440				445				
75	Asn	Ser	Gly	Arg	Lys	Glu	Thr	Tyr	Pro	Phe	Ile	Gly	Glu	Pro	Asp	Pro
				450			455					460				

WO 99/29870

PCT/AU98/01023

320/ 490

Lys Asn Ile Cys Thr Val Lys Asp Val Glu Lys Ala Lys Ser Lys Asn
 325 330 335
 Trp Arg Val Phe Asp Phe Asn Gly Asp Ser Asp Asn Met Leu Pro Tyr
 340 345 350
 5 Glu Gly Ser Pro Thr Ser Asn Leu Ala Val Asp Ala Pro Thr Val Arg
 355 360 365
 Ile Tyr Pro Asn Pro Val Gly Arg Tyr Ala Leu Val Glu Ile Pro Glu
 370 375 380
 10 Ser Leu Leu Gly Gln Glu Ala Ala Leu Tyr Asp Met Asn Gly Val Lys
 385 390 395 400
 Val Tyr Ser Phe Ala Val Glu Ser Leu Arg Gln Asn Ile Asp Leu Thr
 405 410 415
 His Leu Pro Asp Gly Thr Tyr Phe Phe Arg Leu Asp Asn Tyr Thr Thr
 420 425 430
 15 Lys Leu Ile Lys Gln
 435

(2) INFORMATION FOR SEQ ID NO:384

20 (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 318 amino acids
 (R) TYPE: amino acid
 (D) TOPOLOGY: linear
 25 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 30 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...318
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:384

Asn His Leu Lys Thr Asn Ile Lys Met Arg Lys Thr Ile Ile Phe Cys
 1 5 10 15
 40 Leu Leu Leu Ala Leu Phe Gly Cys Ser Trp Ala Gln Glu Arg Val Asp
 20 25 30
 Glu Lys Val Phe Ser Ala Gly Thr Ser Ile Phe Arg Gly Ile Leu Glu
 35 40 45
 45 Lys Val Lys Ala Pro Leu Met Tyr Gly Asp Arg Glu Val Trp Gly Met
 50 55 60
 Ala Arg Ala Ser Glu Asp Phe Phe Phe Ile Leu Pro Val Thr Asp Asp
 65 70 75 80
 Leu Thr Pro Val Leu Phe Tyr Asn Arg Leu Thr Asn Glu Pro Cys Phe
 85 90 95
 50 Val Ser Asp Gln Gly Ile Thr Glu Tyr Phe Lys Phe Ala Gln Glu Gly
 100 105 110
 Asp Tyr Ile Glu Val Glu Gly Ser Ser Val Phe Met Ala Asn Leu Leu
 115 120 125
 55 Tyr Tyr Arg Phe Phe Pro Thr Arg Ile Thr Ser Tyr Asn Ala Pro Ile
 130 135 140
 Glu Gly Val Val Ser Lys Thr Gly Asn Pro Ala Phe Thr Ile Pro Met
 145 150 155 160
 Leu Pro Gly Val Ser Asp Cys Ile Glu Ile Ser Asn Asn Arg Lys Val
 165 170 175
 60 Phe Leu Thr Asn Gln Leu Gly Val Val Asn Ile Thr Asp Gly Met Glu
 180 185 190
 Pro Pro Ile Ile Ala Gly Val Ser Ala Ser Tyr Gly Ser Ser Val Arg
 195 200 205
 65 Val Tyr Gly His Val Ser Gln Arg Trp Asp Ile Ile Gly His Cys Tyr
 210 215 220
 Leu Asp Ile Tyr Pro Thr Asn Cys Tyr Pro Leu Ser Thr Lys Pro Val
 225 230 235 240
 Ala Gly Asp Asp Glu Val Phe Val Lys Gln Gln Gly Arg Gln Ile Glu
 245 250 255
 70 Ile Asp Ser Asn Ser Pro Ile Val Gln Val Val Val Tyr Asp Leu Glu
 260 265 270
 Gly Lys Ser Val Phe Arg Lys Arg Met Thr Glu Asn Ala Tyr Thr Leu
 275 280 285
 75 Ser Phe Arg Ala Pro Met Leu Gly Phe Met Thr Ile Met Ile Glu Thr
 290 295 300

WO 99/29870

PCT/AU98/01023

321/ 490

Gln Asn Ser Ile Ile Asn Lys Lys Leu Asn Val Thr Gln Leu
305 310 315

(2) INFORMATION FOR SEQ ID NO:385

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 461 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385

Arg Arg Ala Val Lys Ile Arg Ser Pro Pro His Ile His Ser Leu Phe
1 5 10 15
Val Arg Lys Cys Leu Phe Ser Asp Phe Lys Tyr Leu Tyr Leu Ser Arg
20 25 30
Lys Ile Thr Gln Glu Arg Leu Gly Arg Leu Ser Ile Arg Leu Lys Ser
35 40 45
Tyr Asn Pro Ile Ile Ile Ile Glu Met Lys Lys Thr Thr Ile Ile Ser
50 55 60
Leu Ile Val Phe Gly Ala Phe Phe Ala Val Gly Gln Thr Lys Asp
65 70 75 80
Asn Ser Ser Tyr Lys Pro Phe Ser Lys Glu Asp Ile Ala Gly Gly Val
85 90 95
Tyr Ser Leu Pro Thr Gln Asn Arg Ala Gln Lys Asp Asn Ala Glu Trp
100 105 110
Leu Leu Thr Ala Thr Val Ser Thr Asn Gln Ser Ala Asp Thr His Phe
115 120 125
Ile Phe Asp Glu Asn Asn Arg Tyr Ile Ala Arg Asp Ile Lys Ala Asn
130 135 140
Gly Val Arg Lys Ser Thr Asp Ser Ile Tyr Tyr Asp Ala Asn Gly Arg
145 150 155 160
Ile Ser His Val Asp Leu Tyr Ile Ser Phe Ser Gly Gly Glu Pro Ala
165 170 175
Leu Asp Thr Arg Phe Lys Tyr Thr Tyr Asp Asp Glu Gly Lys Met Thr
180 185 190
Val Arg Glu Val Phe Met Leu Val Met Asp Pro Asn Thr Pro Ile Ser
195 200 205
Arg Leu Glu Tyr His Tyr Asp Ala Gln Gly Arg Leu Thr His Trp Ile
210 215 220
Ser Phe Ala Phe Gly Ala Glu Ser Gln Lys Asn Thr Tyr His Tyr Asn
225 230 235 240
Glu Lys Gly Leu Leu Val Ser Glu Val Leu Ser Asn Ala Met Gly Thr
245 250 255
Thr Tyr Ser Asp Thr Gly Lys Thr Glu Tyr Ser Tyr Asp Asp Ala Asp
260 265 270
Asn Met Val Lys Ala Glu Tyr Phe Val Val Gln Gln Gly Lys Ala Trp
275 280 285
Gln Val Leu Lys Arg Glu Glu Tyr Thr Tyr Glu Asp Asn Ile Cys Ile
290 295 300
Gln Tyr Leu Ala Ile Asn Gly Thr Asp Thr Lys Val Tyr Lys Arg Asp
305 310 315 320
Ile Glu Ser Asp Lys Ser Ile Ser Ala Asn Val Ile Asp Ile Pro Ser
325 330 335
Met Pro Glu Gln Thr Trp Pro Asn Met Tyr Gly Phe Asn Ala Lys Arg
340 345 350
Leu Lys Glu Thr Tyr Ser Ser Tyr Glu Gly Asp Val Ala Thr Pro Ile
355 360 365
Phe Asp Tyr Ile Tyr Thr Tyr Lys Ala Leu Thr Ser Met Ala Thr Pro
370 375 380
Ser Thr Glu Ala Gln Val Ala Val Tyr Leu Asn Pro Ser Thr Asp Arg
385 390 395 400
Leu Val Ile Leu Ala Asn Gly Ile Thr His Leu Ser Met Tyr Asp Leu
405 410 415

WO 99/29870

PCT/AU98/01023

322/490

Gln Gly Lys Leu Ile Arg Asp Cys Ala Leu Ser Gly Asp Lys Val Glu
420 425 430
Met Gly Val Gly Ser Leu Thr Lys Gly Thr Tyr Leu Leu Lys Val Asn
435 440 445
5 Thr Asp Gln Gly Ala Phe Val Arg Lys Val Val Ile Arg
450 455 460

(2) INFORMATION FOR SEQ ID NO:386

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 451 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- 15 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
- 20 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...451
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:386

Met Ala Lys Val Ile Lys Thr Lys Lys Gly Leu Ala Leu Asn Leu Lys
1 5 10 15
30 Gly Lys Pro Leu Pro Glu Met Leu Ala Glu Pro Ala Gln Ser Pro Thr
20 25 30
Tyr Ala Val Val Pro Asp Asp Phe Glu Gly Val Ile Pro Lys Val Thr
35 40 45
Ala Arg Pro Gly Asp Lys Val Arg Ala Gly Ser Ala Leu Met His His
50 55 60
Lys Ala Tyr Pro Glu Met Lys Phe Thr Ser Pro Val Ser Gly Glu Val
65 70 75 80
Ile Ala Val Asn Arg Gly Ala Lys Arg Lys Val Leu Ser Ile Glu Val
85 90 95
40 Lys Pro Asp Gly Leu Asn Glu Tyr Glu Ser Phe Pro Val Gly Asp Pro
100 105 110
Ser Ala Leu Ser Ala Glu Gln Ile Lys Glu Leu Leu Ser Ser Gly
115 120 125
45 Met Trp Gly Phe Ile Lys Gln Arg Pro Tyr Asp Ile Val Ala Thr Pro
130 135 140
Asp Ile Ala Pro Arg Asp Ile Tyr Ile Thr Ala Asn Phe Thr Ala Pro
145 150 155 160
Leu Ala Pro Asp Phe Asp Phe Ile Val Arg Gly Glu Glu Arg Ala Leu
165 170 175
50 Gln Thr Ala Ile Asp Ala Leu Ala Lys Leu Thr Thr Gly Lys Val Tyr
180 185 190
Val Gly Leu Lys Pro Gly Ser Ser Leu Gly Leu His Asn Ala Glu Ile
195 200 205
55 Val Glu Val His Gly Pro His Pro Ala Gly Asn Val Gly Val Leu Ile
210 215 220
Asn His Thr Lys Pro Ile Asn Arg Gly Glu Thr Val Trp Thr Leu Lys
225 230 235 240
Ala Thr Asp Leu Ile Val Ile Gly Arg Phe Leu Leu Thr Gly Lys Ala
245 250 255
60 Asp Phe Thr Arg Met Ile Ala Met Thr Gly Ser Asp Ala Ala Ala His
260 265 270
Gly Tyr Val Arg Ile Met Pro Gly Cys Asn Val Phe Ala Ser Phe Pro
275 280 285
Gly Arg Leu Thr Ile Lys Glu Ser His Glu Arg Val Ile Asp Gly Asn
290 295 300
65 Val Leu Thr Gly Lys Lys Leu Cys Glu Lys Glu Pro Phe Leu Ser Ala
305 310 315 320
Arg Cys Asp Gln Ile Thr Val Ile Pro Glu Gly Asp Asp Val Asp Glu
325 330 335
70 Leu Phe Gly Trp Ala Ala Pro Arg Leu Asp Gln Tyr Ser Met Ser Arg
340 345 350
Ala Tyr Phe Ser Trp Leu Gln Gly Lys Asn Lys Glu Tyr Val Leu Asp
355 360 365
75 Ala Arg Ile Lys Gly Gly Glu Arg Ala Met Ile Met Ser Asn Glu Tyr
370 375 380

WO 99/29870

PCT/AU98/01023

324/ 490

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:388

5 Met Lys Lys Ala Leu Leu Ile Gly Ala Ala Leu Leu Gly Ala Val Ser
1 5 10 15
Phe Ala Ser Ala Gln Ser Leu Ser Thr Ile Lys Val Gln Asn Asn Ser
20 25 30
Val Gln Gln Pro Arg Glu Glu Ala Thr Ile Gln Val Cys Gly Glu Leu
35 40 45
10 Ala Glu Gln Val Asp Cys Ile Gly Thr Gly Asn Ser Ala Ile Ile Ala
50 55 60
Ala Ala Ala Lys Phe Glu Ser Asp Asp Leu Glu Ser Tyr Val Gly Trp
65 70 75 80
15 Glu Ile Met Ser Val Asp Phe Phe Pro Gly Tyr Lys Ala Cys Lys Tyr
85 90 95
Thr Ser Ala Val Trp Ala Asp Asp Met Thr Ile Leu Gly Gln Ser Glu
100 105 110
Asp Ser Asp Pro Glu Met Gln Thr Ile Asn Asn Leu Ala Leu Lys Thr
115 120 125
20 Ser Val Lys Ile Glu Ala Gly Lys Asn Tyr Ile Val Gly Tyr Ile Ala
130 135 140
Asn Thr Ala Gly Gly His Pro Ile Gly Cys Asp Gln Gly Pro Ala Val
145 150 155 160
25 Asp Gly Tyr Gly Asp Leu Val Ser Ile Ser Glu Asp Gly Gly Ala Thr
165 170 175
Phe Pro Pro Phe Glu Ser Leu His Gln Ala Val Pro Thr Leu Asn Tyr
180 185 190
Asn Ile Tyr Val Val Val His Leu Lys Lys Gly Glu Gly Val Glu Ala
195 200 205
30 Val Leu Thr Asn Asp Lys Ala Asn Ala Tyr Val Gln Asn Gly Val Ile
210 215 220
Tyr Val Ala Gly Ala Asn Gly Arg Gln Val Ser Leu Phe Asp Met Asn
225 230 235 240
35 Gly Lys Val Val Tyr Thr Gly Val Ser Glu Thr Ile Ala Ala Pro Gln
245 250 255
Lys Gly Met Tyr Ile Leu Arg Val Gly Ala Lys Ser Ile Lys Leu Ala
260 265 270
Ile

(2) INFORMATION FOR SEQ ID NO:389

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...554

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:389

60 Met Pro Arg Ile Met Lys Leu Lys Ile Ala Leu Arg Leu Leu Leu Ala
1 5 10 15
Thr Phe Ala Ile Val Leu Phe Ser Pro Leu Ala Lys Ala Gln Met Asp
20 25 30
65 Ile Gly Gly Asp Asp Val Leu Ile Glu Thr Met Ser Thr Leu Ser Gly
35 40 45
Tyr Ser Glu Asp Phe Tyr Tyr Lys Met Ala Val Ala Asp Asn Gly Trp
50 55 60
70 Ile Tyr Val Met Leu Asp Phe Ser Arg Ile Tyr Phe Asp Asp Val Arg
65 70 75 80
Leu Tyr Arg Ser Lys Asp Gly Gly Ala Thr Tyr Gln Lys Leu Gly Ser
85 90 95
Leu Gly Ser Leu Val Pro Tyr Asp Phe Asp Val Ser His Cys Asp Phe
100 105 110
75 Ile Val Thr Gly Lys Asp Glu Asp Asp Ile Asn Val Trp Thr Val Met

WO 99/29870

PCT/AU98/01023

325/ 490

115 120 125
Thr Ala Phe Glu Tyr Val Gly Gly Thr Ile Gly Asn Gly Val Leu Leu
130 135 140
Met His Arg His Asp Ala Asp Ile Asn Asn Thr Glu Cys Val Tyr Lys
145 150 155 160
Lys Asp Phe Pro Asn Asn Arg Leu Met Gly Val Ala Ile Ala Ser Asn
165 170 175
Tyr Arg Ala Pro Ser Pro Tyr Gly Leu Gly Gly Asp Pro Phe Ala Leu
180 185 190
Ala Val Ala Val Ser Gly Ser Gly Ser Asp His Ser Phe Leu Asp Tyr
195 200 205
Ile Phe Ser Leu Asp Gly Gly Val His Phe Glu Gln Lys Arg Ile Tyr
210 215 220
Thr Arg Pro Gln Lys Leu Thr Ile Asn Arg Val Asp Leu Ser Leu Gly
225 230 235 240
Ser Thr Ser Pro Ser Leu Gly Phe Asn Thr Trp Pro Leu Met Gly Val
245 250 255
Val Phe Glu Met Asn Lys Asn Leu Asp Gly Phe Asp Ile Gly Phe Ile
260 265 270
Ser Asn Phe Val Asp Tyr Asp Pro Arg Tyr Ala Trp Ser Glu Pro Ile
275 280 285
Ile Ile Glu Glu Asp Cys Gly Trp Thr Asp Phe Asn Pro Leu Gly Ala
290 295 300
Leu Ser Ile Glu Ile Gln Met Met Leu Asp Asp Asn Ser Asp Asn Thr
305 310 315 320
Val Gly Gly Glu Arg Ser His Asn Phe Leu Ile Thr Tyr Pro Gly His
325 330 335
Tyr Val Tyr Pro Lys Gln Ser Phe Asn Tyr Ser Pro Gly His Thr Pro
340 345 350
Thr Lys Lys Asp Leu Val Phe Lys His Cys Ile Gly Ile Pro Ala Leu
355 360 365
Ala Tyr Asp Lys Glu Gly Asp Arg Tyr Leu Thr Thr Phe Gln Asp His
370 375 380
Asn Leu Met Arg Tyr Arg Trp Ile Lys Tyr Asp Asp Ile Asn Ser Phe
385 390 395 400
Tyr Gly Trp Ser Trp Pro Tyr Val Tyr Ala Lys Glu Ala Lys Asp Lys
405 410 415
Lys Arg Arg Arg Pro Gln Val Ala Leu Asn Pro Thr Asn Gly Lys Ala
420 425 430
Cys Trp Val Trp His Thr Arg Lys Ser Pro Tyr Asp Glu Thr Lys Pro
435 440 445
His Pro Thr Pro Val Ile Ile Lys His Phe Leu Trp Ser Asp Thr Glu
450 455 460
Trp Val His Ala Leu Asp Val Gly Asp Val Leu Gln Lys Glu Gly Ser
465 470 475 480
Met Lys Leu Tyr Pro Asn Pro Ala Lys Glu Tyr Val Leu Ile Asn Leu
485 490 495
Pro Lys Glu Gly His Glu Ala Val Tyr Asp Met Gln Gly Arg
500 505 510
Ile Val Glu Lys Val Ser Phe Ser Gly Lys Glu Tyr Lys Leu Asn Val
515 520 525
Gln Tyr Leu Ser Lys Gly Thr Tyr Met Leu Lys Val Val Ala Asp Thr
530 535 540
Glu Tyr Phe Val Glu Lys Ile Ile Val Glu
545 550

(2) INFORMATION FOR SEQ ID NO:390

- 60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 550 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- 65 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
- 70 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...550
- 75 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:390

WO 99/29870

PCT/AU98/01023

326/ 490

Met Lys Leu Lys Ile Ala Leu Arg Leu Leu Leu Ala Thr Phe Ala Ile
1 5 10 15
5 Val Leu Phe Ser Pro Leu Ala Lys Ala Gln Met Asp Ile Gly Gly Asp
20 25 30
Asp Val Leu Ile Glu Thr Met Ser Thr Leu Ser Gly Tyr Ser Glu Asp
35 40 45
Phe Tyr Tyr Lys Met Ala Val Ala Asp Asn Gly Trp Ile Tyr Val Met
50 55 60
10 Leu Asp Phe Ser Arg Ile Tyr Phe Asp Asp Val Arg Leu Tyr Arg Ser
65 70 75 80
Lys Asp Gly Gly Ala Thr Tyr Gln Lys Leu Gly Ser Leu Gly Ser Leu
85 90 95
15 Val Pro Tyr Asp Phe Asp Val Ser His Cys Asp Phe Ile Val Thr Gly
100 105 110
Lys Asp Glu Asp Asp Ile Asn Val Trp Thr Val Met Thr Ala Phe Glu
115 120 125
Tyr Val Gly Gly Thr Ile Gly Asn Gly Val Leu Leu Met His Arg His
130 135 140
20 Asp Ala Asp Ile Asn Asn Thr Glu Cys Val Tyr Lys Lys Asp Phe Pro
145 150 155 160
Asn Asn Arg Leu Met Gly Val Ala Ile Ala Ser Asn Tyr Arg Ala Pro
165 170 175
25 Ser Pro Tyr Gly Leu Gly Gly Asp Pro Phe Ala Leu Ala Val Ala Val
180 185 190
Ser Gly Ser Gly Ser Asp His Ser Phe Leu Asp Tyr Ile Phe Ser Leu
195 200 205
Asp Gly Gly Val His Phe Glu Gln Lys Arg Ile Tyr Thr Arg Pro Gln
210 215 220
30 Lys Leu Thr Ile Asn Arg Val Asp Leu Ser Leu Gly Ser Thr Ser Pro
225 230 235 240
Ser Leu Gly Phe Asn Thr Trp Pro Leu Met Gly Val Val Phe Glu Met
245 250 255
35 Asn Lys Asn Leu Asp Gly Phe Asp Ile Gly Phe Ile Ser Asn Phe Val
260 265 270
Asp Tyr Asp Pro Arg Tyr Ala Trp Ser Glu Pro Ile Ile Ile Glu Glu
275 280 285
Asp Cys Gly Trp Thr Asp Phe Asn Pro Leu Gly Ala Leu Ser Ile Glu
290 295 300
40 Ile Gln Met Met Leu Asp Asp Asn Ser Asp Asn Thr Val Gly Gly Glu
305 310 315 320
Arg Ser His Asn Phe Leu Ile Thr Tyr Pro Gly His Tyr Val Tyr Pro
325 330 335
45 Lys Gln Ser Phe Asn Tyr Ser Pro Gly His Thr Pro Thr Lys Lys Asp
340 345 350
Leu Val Phe Lys His Cys Ile Gly Ile Pro Ala Leu Ala Tyr Asp Lys
355 360 365
Glu Gly Asp Arg Tyr Leu Thr Thr Phe Gln Asp His Asn Leu Met Arg
370 375 380
50 Tyr Arg Trp Ile Lys Tyr Asp Asp Ile Asn Ser Phe Tyr Gly Trp Ser
385 390 395 400
Trp Pro Tyr Val Tyr Ala Lys Glu Ala Lys Asp Lys Lys Arg Arg Arg
405 410 415
55 Pro Gln Val Ala Leu Asn Pro Thr Asn Gly Lys Ala Cys Trp Val Trp
420 425 430
His Thr Arg Lys Ser Pro Tyr Asp Glu Thr Lys Pro His Pro Thr Pro
435 440 445
Val Ile Ile Lys His Phe Leu Trp Ser Asp Thr Glu Trp Val His Ala
450 455 460
60 Leu Asp Val Gly Asp Val Leu Gln Lys Glu Gly Ser Met Lys Leu Tyr
465 470 475 480
Pro Asn Pro Ala Lys Glu Tyr Val Leu Ile Asn Leu Pro Lys Glu Gly
485 490 495
65 Gly His Glu Ala Val Val Tyr Asp Met Gln Gly Arg Ile Val Glu Lys
500 505 510
Val Ser Phe Ser Gly Lys Glu Tyr Lys Leu Asn Val Gln Tyr Leu Ser
515 520 525
Lys Gly Thr Tyr Met Leu Lys Val Val Ala Asp Thr Glu Tyr Phe Val
530 535 540
70 Glu Lys Ile Ile Val Glu
545 550

(2) INFORMATION FOR SEQ ID NO:391

75

WO 99/29870

PCT/AU98/01023

327/490

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 390 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION: 1...390
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:391
- Met Lys Arg Leu Leu Pro Phe Leu Leu Leu Ala Gly Leu Val Ala Val
 1 5 10 15
 Gly Asn Val Ser Ala Gln Ser Pro Arg Ile Pro Gln Val Asp Val His
 20 25 30
 Thr Arg Ile Ala Arg Asn Ala Arg Tyr Arg Leu Asp Lys Ile Ser Val
 35 40 45
 Pro Asp Ser Arg Gln Ile Phe Asp Tyr Phe Tyr Lys Glu Glu Thr Ile
 50 55 60
 Pro Thr Lys Ile Gln Thr Thr Thr Gly Gly Ala Ile Thr Ser Ile Asp
 65 70 75 80
 Ser Leu Phe Tyr Glu Asp Asp Arg Leu Val Gln Val Arg Tyr Phe Asp
 85 90 95
 Asn Asn Leu Glu Leu Lys Gln Ala Glu Lys Tyr Val Tyr Asp Gly Ser
 100 105 110
 Lys Leu Val Leu Arg Glu Ile Arg Lys Ser Pro Thr Asp Glu Thr Pro
 115 120 125
 Ile Lys Lys Val Ser Tyr His Tyr Leu Cys Gly Ser Asp Met Pro Phe
 130 135 140
 Glu Ile Thr Thr Glu Met Ser Asp Gly Tyr Phe Glu Ser His Thr Leu
 145 150 155 160
 Asn Tyr Leu Asn Gly Lys Ile Ala Arg Ile Asp Ile Met Thr Gln Gln
 165 170 175
 Asn Pro Ser Ala Glu Leu Ile Glu Thr Gly Arg Met Val Tyr Glu Phe
 180 185 190
 Asp Ala Asn Asn Asp Ala Val Leu Leu Arg Asp Ser Val Phe Leu Pro
 195 200 205
 Leu Gln Asn Lys Trp Val Glu Met Phe Thr His Arg Tyr Thr Tyr Asp
 210 215 220
 Asn Lys His Asn Cys Ile Arg Trp Glu Gln Asp Glu Phe Gly Thr Leu
 225 230 235 240
 Thr Leu Ala Asn Asn Phe Glu Tyr Asp Thr Thr Ile Pro Leu Ser Ser
 245 250 255
 Val Leu Phe Pro Thr His Glu Glu Phe Phe Arg Pro Leu Leu Pro Asn
 260 265 270
 Phe Met Lys His Met Arg Thr Lys Gln Thr Tyr Phe Asn Asn Ser Gly
 275 280 285
 Glu Gly Leu Ser Glu Val Cys Asp Tyr Asn Tyr Phe Tyr Thr Asp Met
 290 295 300
 Gln Gly Asn Ala Leu Thr Asp Val Ala Val Asn Glu Ser Ile Lys Ile
 305 310 315 320
 Tyr Pro Arg Pro Ala Thr Asp Phe Leu Arg Ile Glu Gly Ser Gln Leu
 325 330 335
 Leu Arg Leu Ser Leu Phe Asp Met Asn Gly Lys Leu Ile Arg Ala Thr
 340 345 350
 Glu Leu Thr Gly Asp Leu Ala Ile Ile Gly Val Ala Ser Leu Pro Arg
 355 360 365
 Gly Thr Tyr Ile Ala Glu Ile Thr Ala Ala Asn Ser Lys Thr Ile Arg
 370 375 380
 Ala Lys Val Ser Leu Arg
 385 390
- (2) INFORMATION FOR SEQ ID NO:392
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 411 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

328/490

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
(A) NAME/KLY: misc_feature
(B) LOCATION 1...411
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:392
- Met Arg Gln His Leu Ser Leu Phe Pro Phe Ile Leu Phe Leu Leu Leu
1 5 10 15
Ala Phe Ser Tyr Val Gly Cys Arg Thr Val Arg Gln Thr Pro Lys Gln
20 25 30
Ser Glu Arg Tyr Val Val Val Leu Ser Leu Asp Gly Phe Arg Pro Asp
35 40 45
Tyr Thr Asp Arg Ala Arg Thr Pro Ala Leu Asp Arg Met Ala Gln Glu
50 55 60
Gly Leu Ser Gly Ser Leu Gln Pro Cys Phe Pro Ser Leu Thr Phe Pro
65 70 75
Asn His Tyr Ser Met Ala Thr Gly Leu Tyr Pro Asp His His Gly Ile
80 85 90
Val Ala Asn Glu Phe Val Asp Ser Leu Leu Gly Ile Phe Arg Ile Ser
100 105 110
Asp Arg Lys Ala Val Glu Thr Pro Gly Phe Trp Gly Gly Glu Pro Val
115 120 125
Trp Asn Thr Ala Ala Arg Gln Gly Ile Arg Thr Gly Val Tyr Phe Trp
130 135 140
Val Gly Ser Glu Thr Ala Val Asn Gly Asn Arg Pro Trp Arg Trp Lys
145 150 155
Lys Phe Ser Ser Thr Val Pro Phe Arg Asp Arg Ala Asp Ser Val Ile
160 165 170
Ala Trp Leu Gly Leu Pro Glu Lys Glu Arg Pro Arg Leu Leu Met Trp
180 185 190
Tyr Ile Glu Glu Pro Asp Met Ile Gly His Ser Gln Thr Pro Glu Ser
195 200 205
Pro Leu Thr Leu Ala Met Val Glu Arg Leu Asp Ser Val Val Gly Tyr
210 215 220
Phe Arg Lys Arg Leu Asp Ser Leu Pro Ile Ala Ala Gln Thr Asp Phe
225 230 235
Ile Ile Val Ser Asp His Gly Met Ala Thr Tyr Glu Asn Glu Lys Cys
240 245 250
Val Asn Leu Ser His Tyr Leu Pro Ala Asp Ser Phe Leu Tyr Met Ala
255 260 265
Thr Gly Ala Phe Thr His Leu Tyr Pro Lys Pro Ser Tyr Thr Glu Arg
270 275 280
Ala Tyr Glu Ile Leu Arg Ala Ile Pro His Ile Ser Val Tyr Arg Lys
285 290 295
Gly Glu Val Pro Lys Arg Leu Arg Cys Gly Thr Asn Pro Arg Leu Gly
300 305 310
Glu Leu Val Val Ile Pro Asp Ile Gly Ser Thr Val Phe Phe Ala Ile
315 320 325
Asn Glu Asp Val Arg Pro Gly Ala Ala His Gly Tyr Asp Asn Gln Ala
330 335 340
Pro Glu Met Arg Ala Leu Leu Arg Ala Val Gly Pro Asp Phe Arg Pro
345 350 355
Gly Ser Arg Val Glu Asn Leu Pro Asn Ile Thr Ile Tyr Pro Leu Ile
360 365 370
Cys Arg Leu Leu Gly Ile Glu Pro Ala Pro Asn Asp Ala Asp Glu Thr
375 380 385
Leu Leu Asn Gly Leu Ile Arg Asp Lys Arg Pro
390 395 400
405 410
- (2) INFORMATION FOR SEQ ID NO:393
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 246 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

WO 99/29870

PCT/AU98/01023

329/ 490

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393

Met	Lys	Val	Gly	Leu	Phe	Ile	Pro	Cys	Tyr	Val	Asn	Ala	Val	Tyr	Pro
1				5					10					15	
Glu	Val	Gly	Ile	Ala	Thr	Tyr	Lys	Leu	Lys	Ser	Leu	Asp	Ile	Asp	
			20					25				30			
Val	Asp	Tyr	Pro	Met	Asp	Gln	Thr	Cys	Cys	Gly	Gln	Pro	Met	Ala	Asn
			35				40					45			
Ala	Gly	Phe	Glu	Gln	Lys	Ala	Gln	Lys	Leu	Ala	Leu	Arg	Phe	Glu	Glu
			50				55				60				
Leu	Phe	Glu	Ser	Tyr	Asp	Val	Val	Val	Gly	Pro	Ser	Ala	Ser	Cys	Val
			65			70				75				80	
Ala	Phe	Val	Lys	Glu	Asn	Tyr	Asp	His	Ile	Leu	Arg	Pro	Thr	Gly	His
			85					90					95		
Val	Cys	Lys	Ser	Ala	Ala	Lys	Val	Arg	Asp	Ile	Cys	Glu	Phe	Leu	His
			100					105				110			
Asp	Asp	Leu	Lys	Ile	Thr	Ser	Leu	Pro	Ser	Arg	Phe	Ala	His	Lys	Val
			115				120					125			
Ser	Leu	His	Asn	Ser	Cys	His	Gly	Val	Arg	Glu	Leu	His	Leu	Ser	Thr
			130				135					140			
Pro	Ser	Glu	Val	His	Arg	Pro	Tyr	His	Asn	Lys	Val	Arg	Arg	Leu	Leu
			145				150				155			160	
Glu	Met	Val	Gln	Gly	Ile	Glu	Val	Phe	Glu	Pro	Lys	Arg	Ile	Asp	Glu
			165					170					175		
Cys	Cys	Gly	Phe	Gly	Gly	Met	Tyr	Ser	Val	Glu	Glu	Pro	Glu	Val	Ser
			180					185					190		
Thr	Cys	Met	Gly	His	Asp	Lys	Val	Leu	Asp	His	Ile	Ser	Thr	Gly	Ala
			195				200					205			
Glu	Tyr	Ile	Thr	Gly	Pro	Asp	Ser	Ser	Cys	Leu	Met	His	Met	Gln	Gly
			210				215				220				
Val	Ile	Asp	Arg	Glu	Lys	Leu	Pro	Ile	Lys	Thr	Ile	His	Ala	Val	Glu
			225			230				235				240	
Ile	Leu	Ala	Ala	Asn	Leu										
				245											

(2) INFORMATION FOR SEQ ID NO:394

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 246 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394

Met	Asp	Ile	Val	Ser	Met	Ala	Asp	Lys	Ala	Leu	Val	Val	Glu	Met	Arg
1				5					10					15	
Asp	Val	Thr	Leu	Cys	Gln	Glu	Glu	Asn	Val	Ile	Phe	Gln	Asn	Leu	Asn
			20					25					30		
Leu	Thr	Leu	Ser	Ala	Gly	Asp	Phe	Val	Tyr	Leu	Ile	Gly	Ser	Val	Gly
			35				40					45			
Ser	Gly	Lys	Ser	Thr	Leu	Leu	Lys	Ala	Leu	Tyr	Ala	Glu	Val	Pro	Ile
			50				55				60				
Ser	Ala	Gly	Tyr	Ala	Arg	Val	Ile	Asp	Tyr	Asp	Leu	Ala	Lys	Leu	Lys
			65			70				75				80	

WO 99/29870

PCT/AU98/01023

330/490

Arg Lys Gln Leu Pro Tyr Leu Arg Arg Asn Leu Gly Ile Val Phe Gln
85 90 95
Asp Phe Gln Leu Leu Asn Gly Arg Thr Val Ala Glu Asn Leu Asp Phe
100 105 110
5 Val Leu Arg Ala Thr Asp Trp Lys Asn Arg Ala Asp Arg Glu Gln Arg
115 120 125
Ile Glu Glu Val Leu Thr Arg Val Gly Met Ser Arg Lys Ala Tyr Lys
130 135 140
Arg Pro His Glu Leu Ser Gly Gly Glu Gln Gln Arg Val Gly Ile Ala
145 150 155 160
10 Arg Ala Leu Leu Ala Lys Pro Ala Leu Ile Leu Ala Asp Glu Pro Thr
165 170 175
Gly Asn Leu Asp Ser Val Thr Gly Leu Gln Ile Ala Ser Leu Leu Tyr
180 185 190
15 Glu Ile Ser Lys Gln Gly Thr Ala Val Leu Met Ser Thr His Asn Ser
195 200 205
Ser Leu Leu Ser His Leu Pro Ala Arg Thr Leu Ala Val Arg Lys Asn
210 215 220
20 Gly Asp Ala Ser Ser Leu Val Glu Leu Ser Ala Asp Ala Val Ser Arg
225 230 235 240
Lys Asn Thr Glu Ile Asp

(2) INFORMATION FOR SEQ ID NO:395

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 241 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395

Met Ala Asp Lys Ala Leu Val Val Glu Met Arg Asp Val Thr Leu Cys
1 5 10 15
Gln Glu Glu Asn Val Ile Phe Gln Asn Leu Asn Leu Thr Leu Ser Ala
20 25 30
Gly Asp Phe Val Tyr Leu Ile Gly Ser Val Gly Ser Gly Lys Ser Thr
35 40 45
50 Leu Leu Lys Ala Leu Tyr Ala Glu Val Pro Ile Ser Ala Gly Tyr Ala
50 55 60
Arg Val Ile Asp Tyr Asp Leu Ala Lys Leu Lys Arg Lys Gln Leu Pro
65 70 75 80
55 Tyr Leu Arg Arg Asn Leu Gly Ile Val Phe Gln Asp Phe Gln Leu Leu
85 90 95
Asn Gly Arg Thr Val Ala Glu Asn Leu Asp Phe Val Leu Arg Ala Thr
100 105 110
Asp Trp Lys Asn Arg Ala Asp Arg Glu Gln Arg Ile Glu Glu Val Leu
115 120 125
60 Thr Arg Val Gly Met Ser Arg Lys Ala Tyr Lys Arg Pro His Glu Leu
130 135 140
Ser Gly Gly Glu Gln Gln Arg Val Gly Ile Ala Arg Ala Leu Leu Ala
145 150 155 160
Lys Pro Ala Leu Ile Leu Ala Asp Glu Pro Thr Gly Asn Leu Asp Ser
165 170 175
65 Val Thr Gly Leu Gln Ile Ala Ser Leu Leu Tyr Glu Ile Ser Lys Gln
180 185 190
Gly Thr Ala Val Leu Met Ser Thr His Asn Ser Ser Leu Leu Ser His
195 200 205
70 Leu Pro Ala Arg Thr Leu Ala Val Arg Lys Asn Gly Asp Ala Ser Ser
210 215 220
Leu Val Glu Leu Ser Ala Asp Ala Val Ser Arg Lys Asn Thr Glu Ile
225 230 235
Asp

WO 99/29870

PCT/AU98/01023

331/ 490

(2) INFORMATION FOR SEQ ID NO:396

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 232 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

15 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...232

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:396

Met Arg Asp Val Thr Leu Cys Gln Glu Glu Asn Val Ile Phe Gln Asn
 1 5 10 15
 Leu Asn Leu Thr Leu Ser Ala Gly Asp Phe Val Tyr Leu Ile Gly Ser
 20 25 30
 Val Gly Ser Gly Lys Ser Thr Leu Leu Lys Ala Leu Tyr Ala Glu Val
 35 40 45
 Pro Ile Ser Ala Gly Tyr Ala Arg Val Ile Asp Tyr Asp Leu Ala Lys
 50 55 60
 Leu Lys Arg Lys Gln Leu Pro Tyr Leu Arg Arg Asn Leu Gly Ile Val
 65 70 75 80
 Phe Gln Asp Phe Gln Leu Leu Asn Gly Arg Thr Val Ala Glu Asn Leu
 85 90 95
 Asp Phe Val Leu Arg Ala Thr Asp Trp Lys Asn Arg Ala Asp Arg Glu
 100 105 110
 Gln Arg Ile Glu Glu Val Leu Thr Arg Val Gly Met Ser Arg Lys Ala
 115 120 125
 Tyr Lys Arg Pro His Glu Leu Ser Gly Gly Glu Gln Gln Arg Val Gly
 130 135 140
 Ile Ala Arg Ala Leu Leu Ala Lys Pro Ala Leu Ile Leu Ala Asp Glu
 145 150 155 160
 Pro Thr Gly Asn Leu Asp Ser Val Thr Gly Leu Gln Ile Ala Ser Leu
 165 170 175
 Leu Tyr Glu Ile Ser Lys Gln Gly Thr Ala Val Leu Met Ser Thr His
 180 185 190
 Asn Ser Ser Leu Leu Ser His Leu Pro Ala Arg Thr Leu Ala Val Arg
 195 200 205
 Lys Asn Gly Asp Ala Ser Ser Leu Val Glu Leu Ser Ala Asp Ala Val
 210 215 220
 Ser Arg Lys Asn Thr Glu Ile Asp
 225 230

(2) INFORMATION FOR SEQ ID NO:397

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 219 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

65 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...219

70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:397

Met Ile Glu Ile Ser Asn Leu Thr Lys Val Phe Arg Thr Glu Glu Ile
 1 5 10 15
 Glu Thr Val Ala Leu Asp Gly Val Ser Leu Lys Val Asp Lys Gly Glu

332/ 490

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      20      25      30
Phe Ile Ala Ile Met Gly Pro Ser Gly Cys Gly Lys Ser Thr Leu Leu
  35      40      45
5  Asn Ile Leu Gly Leu Leu Asp Asn Pro Thr Ser Gly Ile Tyr Lys Leu
  50      55      60
   Asp Gly Ala Glu Val Gly Asn Leu Arg Glu Lys Asp Arg Thr Ala Val
  65      70      75      80
   Arg Lys Gly Acn Ile Gly Phe Val Phe Gln Ser Phe Asn Leu Ile Glu
      85      90      95
10  Glu Met Thr Val Ser Glu Asn Val Glu Leu Pro Leu Val Tyr Leu Gly
  100      105      110
   Val Lys Ala Ser Glu Arg Lys Glu Arg Val Glu Glu Ala Leu Arg Lys
  115      120      125
15  Met Ser Ile Ser His Arg Ala Gly His Phe Pro Asn Gln Leu Ser Gly
  130      135      140
   Gly Gln Gln Gln Arg Val Ala Ile Ala Arg Ala Val Val Ala Asn Pro
  145      150      155      160
   Lys Leu Ile Leu Ala Asp Glu Pro Thr Gly Asn Leu Asp Ser Lys Asn
  165      170      175
20  Gly Ala Asp Val Met Glu Leu Leu Arg Gly Leu Asn Arg Glu Gly Ala
  180      185      190
   Thr Ile Val Met Val Thr His Ser Glu His Asp Ala Arg Ser Ala Gly
  195      200      205
25  Arg Ile Ile Asn Leu Phe Asp Gly Lys Ile Arg
  210      215

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(2) INFORMATION FOR SEQ ID NO:398

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30  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 595 amino acids
      (B) TYPE: amino acid
      (D) TOPOLOGY: linear

35  (ii) MOLECULE TYPE: protein

      (iii) HYPOTHETICAL: YES

      (vi) ORIGINAL SOURCE:
40  (A) ORGANISM: Porphyromonas gingivalis

      (ix) FEATURE:
      (A) NAME/KEY: misc feature
      (B) LOCATION 1...595

45  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:398

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```

Met Lys Glu Phe Phe Lys Met Phe Phe Ala Ser Ile Leu Gly Val Ile
  1      5      10      15
50  Thr Ala Gly Ile Ile Leu Phe Cys Ile Phe Leu Phe Ile Phe Phe Gly
  20      25      30
   Ile Val Ala Gly Ile Ala Ser Lys Ala Thr Gly Gly Thr Ile Pro Lys
  35      40      45
   Ile Glu Ala Asn Ser Ile Leu His Ile Unk Asn Ser Ser Phe Pro Glu
  50      55      60
55  Ile Val Ser Ala Asn Pro Trp Ser Met Leu Thr Gly Lys Asp Glu Ser
  65      70      75      80
   Val Ser Leu Ser Gln Ala Val Glu Ala Ile Gly Gln Ala Lys Asn Asn
  85      90      95
60  Pro Asn Ile Thr Gly Ile Phe Leu Asp Leu Asp Asn Leu Ser Val Gly
  100      105      110
   Met Ala Ser Ala Glu Glu Leu Arg Arg Ala Leu Gln Asp Phe Lys Met
  115      120      125
   Ser Gly Lys Phe Val Val Ser Tyr Ala Asp Arg Tyr Thr Gln Lys Gly
  130      135      140
65  Tyr Tyr Leu Ser Ser Ile Ala Asp Lys Leu Tyr Leu Asn Pro Lys Gly
  145      150      155      160
   Met Leu Gly Leu Ile Gly Ile Ala Thr Gln Thr Met Phe Tyr Lys Asp
  165      170      175
70  Ala Leu Asp Lys Phe Gly Val Lys Met Glu Ile Phe Lys Val Gly Thr
  180      185      190
   Tyr Lys Ala Ala Val Glu Pro Phe Met Leu Asn Arg Met Ser Asp Ala
  195      200      205
   Asn Arg Glu Gln Ile Thr Thr Tyr Ile Asn Gly Leu Trp Asp Lys Ile
  210      215      220
75  Thr Ser Asp Ile Ala Glu Ser Arg Lys Thr Ala Met Asp Ser Val Lys

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WO 99/29870

PCT/AU98/01023

333/490

225 230 235 240
Met Phe Ala Asp Lys Gly Glu Met Phe Gly Leu Ala Glu Lys Ala Val
245 250 255
5 Glu Met Lys Leu Val Asp Glu Leu Ala Tyr Arg Thr Asp Val Glu Lys
260 265 270
Glu Leu Lys Lys Met Ser Gln Arg Gly Glu Lys Asp Glu Leu Arg Phe
275 280 285
Val Ser Leu Ser Gln Val Leu Ala Asn Gly Pro Met Asn Lys Thr Lys
290 295 300
10 Gly Ser Arg Ile Ala Val Leu Phe Ala Glu Gly Glu Ile Thr Glu Glu
305 310 315 320
Ile Ile Lys Lys Pro Phe Asp Thr Asp Gly Ser Ser Ile Thr Gln Glu
325 330 335
15 Leu Ala Lys Glu Ile Lys Ala Ala Ala Asp Asp Asp Ile Lys Ala
340 345 350
Val Val Leu Arg Val Asn Ser Pro Gly Gly Ser Ala Phe Thr Ser Glu
355 360 365
Gln Ile Trp Lys Gln Val Ala Asp Leu Lys Ala Lys Lys Pro Ile Val
370 375 380
20 Val Ser Met Gly Asp Val Ala Ala Ser Gly Gly Tyr Tyr Ile Ala Cys
385 390 395 400
Ala Ala Asn Ser Ile Val Ala Glu His Thr Thr Leu Thr Gly Ser Ile
405 410 415
25 Gly Ile Phe Gly Met Phe Pro Asn Phe Ala Gly Val Ala Lys Lys Ile
420 425 430
Gly Val Asn Met Asp Val Val Gln Thr Ser Lys Tyr Ala Asp Leu Gly
435 440 445
Asn Thr Phe Ala Pro Met Thr Val Glu Asp Arg Ala Leu Ile Gln Arg
450 455 460
30 Tyr Ile Glu Gln Gly Tyr Asp Leu Phe Leu Thr Arg Val Ser Glu Gly
465 470 475 480
Arg Asn Arg Thr Lys Ala Gln Ile Asp Ser Ile Ala Gln Gly Arg Val
485 490 495
35 Trp Leu Gly Asp Lys Ala Leu Ala Leu Gly Leu Val Asp Glu Leu Gly
500 505 510
Gly Leu Asp Thr Ala Ile Lys Arg Ala Ala Lys Leu Ala Gln Leu Gly
515 520 525
Gly Asn Tyr Ser Ile Glu Tyr Gly Lys Thr Lys Arg Asn Phe Phe Glu
530 535 540
40 Glu Leu Leu Ser Ser Ser Ala Ala Asp Met Lys Ser Ala Ile Leu Ser
545 550 555 560
Thr Ile Leu Ser Asp Pro Glu Ile Glu Val Leu Arg Glu Leu Arg Ser
565 570 575
45 Met Pro Pro Arg Pro Ser Gly Ile Gln Ala Arg Leu Pro Tyr Tyr Phe
580 585 590
Met Pro Tyr
595

(2) INFORMATION FOR SEQ ID NO:399

50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 589 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

55

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

60

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION: 1...589

65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399

70 Met Phe Phe Ala Ser Ile Leu Gly Val Ile Thr Ala Gly Ile Ile Leu
1 5 10 15
Phe Cys Ile Phe Leu Phe Ile Phe Phe Gly Ile Val Ala Gly Ile Ala
20 25 30
Ser Lys Ala Thr Gly Gly Thr Ile Pro Lys Ile Glu Ala Asn Ser Ile
35 40 45
75 Leu His Ile Unk Asn Ser Ser Phe Pro Glu Ile Val Ser Ala Asn Pro

WO 99/29870

PCT/AU98/01023

334/ 490

	50		55		60											
	Trp	Ser	Met	Leu	Thr	Gly	Lys	Asp	Glu	Ser	Val	Ser	Leu	Ser	Gln	Ala
	65					70					75					80
5	Val	Glu	Ala	Ile	Gly	Gln	Ala	Lys	Asn	Asn	Pro	Asn	Ile	Thr	Gly	Ile
					85						90				95	
	Phe	Leu	Asp	Leu	Asp	Asn	Leu	Ser	Val	Gly	Met	Ala	Ser	Ala	Glu	Glu
					100					105				110		
	Leu	Arg	Arg	Ala	Leu	Gln	Asp	Phe	Lys	Met	Ser	Gly	Lys	Phe	Val	Val
					115				120					125		
10	Ser	Tyr	Ala	Asp	Arg	Tyr	Thr	Gln	Lys	Gly	Tyr	Tyr	Leu	Ser	Ser	Ile
					130				135				140			
	Ala	Asp	Lys	Leu	Tyr	Leu	Asn	Pro	Lys	Gly	Met	Leu	Gly	Leu	Ile	Gly
					145					150			155			160
15	Ile	Ala	Thr	Gln	Thr	Met	Phe	Tyr	Lys	Asp	Ala	Leu	Asp	Lys	Phe	Gly
					165					170				175		
	Val	Lys	Met	Glu	Ile	Phe	Lys	Val	Gly	Thr	Tyr	Lys	Ala	Ala	Val	Glu
					180					185				190		
	Pro	Phe	Met	Leu	Asn	Arg	Met	Ser	Asp	Ala	Asn	Arg	Glu	Gln	Ile	Thr
					195					200				205		
20	Thr	Tyr	Ile	Asn	Gly	Leu	Trp	Asp	Lys	Ile	Thr	Ser	Asp	Ile	Ala	Glu
					210				215				220			
	Ser	Arg	Lys	Thr	Ala	Met	Asp	Ser	Val	Lys	Met	Phe	Ala	Asp	Lys	Gly
					225					230			235			240
	Glu	Met	Phe	Gly	Leu	Ala	Glu	Lys	Ala	Val	Glu	Met	Lys	Leu	Val	Asp
25					245					250				255		
	Glu	Leu	Ala	Tyr	Arg	Thr	Asp	Val	Glu	Lys	Glu	Leu	Lys	Lys	Met	Ser
					260				265					270		
	Gln	Arg	Gly	Glu	Lys	Asp	Glu	Leu	Arg	Phe	Val	Ser	Leu	Ser	Gln	Val
					275				280				285			
30	Leu	Ala	Asn	Gly	Pro	Met	Asn	Lys	Thr	Lys	Gly	Ser	Arg	Ile	Ala	Val
					290				295				300			
	Leu	Phe	Ala	Glu	Gly	Glu	Ile	Thr	Glu	Glu	Ile	Ile	Lys	Lys	Pro	Phe
					305					310				315		320
35	Asp	Thr	Asp	Gly	Ser	Ser	Ile	Thr	Gln	Glu	Leu	Ala	Lys	Glu	Ile	Lys
					325					330				335		
	Ala	Ala	Ala	Asp	Asp	Asp	Asp	Ile	Lys	Ala	Val	Val	Leu	Arg	Val	Asn
					340				345					350		
	Ser	Pro	Gly	Gly	Ser	Ala	Phe	Thr	Ser	Glu	Gln	Ile	Trp	Lys	Gln	Val
					355				360				365			
40	Ala	Asp	Leu	Lys	Ala	Lys	Lys	Pro	Ile	Val	Val	Ser	Met	Gly	Asp	Val
					370				375				380			
	Ala	Ala	Ser	Gly	Gly	Tyr	Tyr	Ile	Ala	Cys	Ala	Ala	Asn	Ser	Ile	Val
					385				390				395			400
45	Ala	Glu	His	Thr	Thr	Leu	Thr	Gly	Ser	Ile	Gly	Ile	Phe	Gly	Met	Phe
					405					410				415		
	Pro	Asn	Phe	Ala	Gly	Val	Ala	Lys	Lys	Ile	Gly	Val	Asn	Met	Asp	Val
					420				425					430		
	Val	Gln	Thr	Ser	Lys	Tyr	Ala	Asp	Leu	Gly	Asn	Thr	Phe	Ala	Pro	Met
					435				440				445			
50	Thr	Val	Glu	Asp	Arg	Ala	Leu	Ile	Gln	Arg	Tyr	Ile	Glu	Gln	Gly	Tyr
					450				455				460			
	Asp	Leu	Phe	Leu	Thr	Arg	Val	Ser	Glu	Gly	Arg	Asn	Arg	Thr	Lys	Ala
					465				470				475			480
	Gln	Ile	Asp	Ser	Ile	Ala	Gln	Gly	Arg	Val	Trp	Leu	Gly	Asp	Lys	Ala
55					485					490				495		
	Leu	Ala	Leu	Gly	Leu	Val	Asp	Glu	Leu	Gly	Gly	Leu	Asp	Thr	Ala	Ile
					500				505				510			
	Lys	Arg	Ala	Ala	Lys	Leu	Ala	Gln	Leu	Gly	Gly	Asn	Tyr	Ser	Ile	Glu
					515				520				525			
60	Tyr	Gly	Lys	Thr	Lys	Arg	Asn	Phe	Phe	Glu	Glu	Leu	Leu	Ser	Ser	Ser
					530				535				540			
	Ala	Ala	Asp	Met	Lys	Ser	Ala	Ile	Leu	Ser	Thr	Ile	Leu	Ser	Asp	Pro
					545				550				555			560
65	Glu	Ile	Glu	Val	Leu	Arg	Glu	Leu	Arg	Ser	Met	Pro	Pro	Arg	Pro	Ser
					565				570					575		
	Gly	Ile	Gln	Ala	Arg	Leu	Pro	Tyr	Tyr	Phe	Met	Pro	Tyr			
					580				585							

(2) INFORMATION FOR SEQ ID NO:400

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 313 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

336/ 490

1 Lys Glu His Val 5 Lys Val Glu Ala Ala 10 Thr Gln Thr Phe Ala Thr Ile
 20 25 30
 5 Thr Leu Gln Asn Tyr Phe Arg Met Tyr His Lys Leu Ala Gly Met Thr
 35 40 45
 Gly Thr Ala Glu Thr Glu Ala Gly Glu Leu Trp Asp Ile Tyr Lys Leu
 50 55 60
 Asp Val Val Val Ile Pro Thr Asn Lys Pro Ile Ala Arg Lys Asp Met
 65 70 75 80
 10 Asn Asp Arg Ile Tyr Lys Thr Ala Arg Glu Lys Tyr Ala Ala Val Ile
 85 90 95
 Glu Glu Ile Val Arg Leu Val Glu Glu Gly Arg Pro Val Leu Val Gly
 100 105 110
 15 Thr Thr Ser Val Glu Ile Ser Glu Leu Leu Ser Arg Met Leu Arg Leu
 115 120 125
 Arg Gly Ile Gln His Asn Val Leu Asn Ala Lys Leu His Gln Lys Glu
 130 135 140
 Ala Glu Ile Val Ala Gln Ala Gly Gln Lys Gly Thr Val Thr Ile Ala
 145 150 155 160
 20 Thr Asn Met Ala Gly Arg Gly Thr Asp Ile Lys Leu Ser Ala Glu Val
 165 170 175
 Lys Lys Ala Gly Glu Leu Ala Ile Ile Gly Thr Glu Arg His Glu Ser
 180 185 190
 25 Arg Arg Val Asp Arg Gln Leu Arg Gly Arg Ser Gly Arg Gln Gly Asp
 195 200 205
 Pro Gly Ser Ser Ile Phe Tyr Val Ser Leu Glu Asp His Leu Met Arg
 210 215 220
 Leu Phe Ala Thr Glu Lys Ile Ala Ser Leu Met Asp Arg Leu Gly Phe
 225 230 235 240
 30 Lys Glu Gly Glu Val Leu Glu Asn Asn Met Leu Ser Lys Ser Val Glu
 245 250 255
 Arg Ala Gln Lys Lys Val Glu Glu Asn Asn Phe Gly Ile Arg Lys His
 260 265 270
 Leu Leu Glu Tyr Asp Asp Val Met Asn Ser Gln Arg Glu Val Ile Tyr
 275 280 285
 35 Thr Arg Arg Arg His Ala Leu Met Gly Glu Arg Ile Gly Met Asp Val
 290 295 300
 Leu Asn Thr Ile Tyr Asp Val Cys Lys Ala Leu Ile Asp Asn Tyr Ala
 305 310 315 320
 40 Glu Ala Asn Asp Phe Glu Gly Phe Lys Glu Asp Leu Met Arg Ala Leu
 325 330 335
 Ala Ile Glu Ser Pro Ile Thr Gln Glu Ile Phe Arg Gly Lys Lys Ala
 340 345 350
 45 Glu Glu Leu Thr Asp Met Leu Phe Asp Glu Ala Tyr Lys Ser Phe Gln
 355 360 365
 Arg Lys Met Asp Leu Ile Ala Glu Val Ala His Pro Val Val His Gln
 370 375 380
 Val Phe Glu Thr Gln Ala Ala Val Tyr Glu Arg Ile Leu Ile Pro Ile
 385 390 395 400
 50 Thr Asp Gly Lys Arg Val Tyr Asn Ile Gly Cys Asn Leu Arg Glu Ala
 405 410 415
 Asp Glu Thr Gln Gly Lys Ser Ile Ile Lys Glu Phe Glu Lys Ala Ile
 420 425 430
 Val Leu His Thr Ile Asp Glu Ser Trp Lys Glu His Leu Arg Glu Met
 435 440 445
 55 Asp Glu Leu Arg Asn Ser Val Gln Asn Ala Ser Tyr Glu Asn Lys Asp
 450 455 460
 Pro Leu Leu Ile Tyr Lys Leu Glu Ser Tyr Glu Leu Phe Arg Lys Met
 465 470 475 480
 60 Val Glu Ala Met Asn Arg Lys Thr Val Ala Ile Leu Met Arg Ala Arg
 485 490 495
 Ile Pro Val Pro Glu Ala Pro Ser Gln Glu Glu Leu Glu His Arg Arg
 500 505 510
 65 Gln Ile Glu Ile Arg His Ala Thr Gln Gln Arg
 515 520

(2) INFORMATION FOR SEQ ID NO:402

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 375 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

WO 99/29870

PCT/AU98/01023

338/490

(A) NAME/KEY: misc_feature
(B) LOCATION: 1...362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403

5
Met Ile Tyr Leu Leu Leu Asp Thr Ile Thr Asn Arg Ala Gly Thr Glu
1 5 10 15
Arg Ala Val Ile Asn Leu Ala Asn Asn Leu His Ala Asn Gly His Arg
20 25 30
10 Val Ser Leu Val Ser Val Cys Thr Lys Glu Gly Glu Pro Ser Phe Gln
35 40 45
Val Glu Lys Gly Ile Glu Val His His Leu Gly Ile Arg Leu Tyr Gly
50 55 60
15 Asn Ala Leu Ala Arg Lys Thr Val Tyr Phe Lys Ala Tyr Arg Arg Ile
65 70 75 80
Lys Ala Leu Tyr Lys Lys Arg Glu Pro Val Leu Leu Ile Gly Thr Asn
85 90 95
Ile Phe Ile Asn Thr Ile Leu Ser Gln Ile Ser Asn Arg Gly Arg Ile
100 105 110
20 Phe Thr Ile Gly Cys Glu His Ile Ser Tyr Asp Ile Ala Arg Pro Ile
115 120 125
Thr Lys Arg Ile Arg Gly Phe Leu Tyr Ser Gly Leu Asp Ala Val Val
130 135 140
25 Ala Leu Thr Lys Arg Asp Gln Gln Ser Phe Glu Ala Ile Leu Arg Gly
145 150 155 160
Arg Ser Lys Ala Tyr Val Ile Pro Asn Gln Val Ser Phe Thr Thr Val
165 170 175
Gln Arg Asp Ala Thr Thr His Lys Gln Met Leu Ala Ile Gly Arg Leu
180 185 190
30 Thr Tyr Gln Lys Gly Phe Glu Phe Met Ile Glu Asp Ala Ser Arg Val
195 200 205
Leu Arg Glu Arg Pro Asp Trp Lys Leu Ile Ile Val Gly Asp Gly Glu
210 215 220
35 Asn Glu Ser Met Leu Arg Lys Glu Ile Ala Ser Arg Asn Met Glu Ser
225 230 235 240
Gln Ile Glu Ile His Pro Ser Thr Pro Glu Ile Arg Lys Tyr Tyr Glu
245 250 255
Ser Ser Ala Ile Tyr Leu Met Thr Ser Arg Phe Glu Gly Leu Pro Met
260 265 270
40 Val Leu Leu Glu Ala Glu Ala Tyr Ala Leu Pro Ile Ile Ser Tyr Asp
275 280 285
Cys Pro Thr Gly Pro Arg Glu Leu Ile Glu Asn Gly Arg Asn Gly Phe
290 295 300
45 Leu Val Pro Met Glu Ala His Glu Asp Phe Ala Asp Lys Leu Arg Leu
305 310 315 320
Leu Met Asp Asp Glu Thr Leu Arg Lys Lys Met Gly Gln Glu Ser Glu
325 330 335
Leu Met Val Lys Ser Tyr Ser Pro Ala Asn Ile Tyr Glu Cys Trp Lys
340 345 350
50 Lys Leu Phe Val Glu Ile Gly Tyr Met Asn
355 360

(2) INFORMATION FOR SEQ ID NO:404

55 (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 640 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
60 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
65 (A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...640
70

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404

Met Gly Lys Ile Ile Gly Ile Asp Leu Gly Thr Thr Asn Ser Cys Val
1 5 10 15
75 Ser Val Leu Glu Gly Asn Glu Pro Ile Val Ile Thr Asn Ser Glu Gly

WO 99/29870

PCT/AU98/01023

340/490

Pro Ser Asp Asp Lys Asn Val Thr Asp Val Arg Phe Glu Glu Val Lys
625 630 635 640

5 (2) INFORMATION FOR SEQ ID NO:405

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 449 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

15 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...449

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:405

25 Met Arg Tyr Asp Leu Ala Ile Ile Gly Gly Gly Pro Ala Gly Tyr Thr
1 5 10 15
Ala Ala Glu Arg Ala Ala Lys Gly Gly Leu Lys Thr Leu Leu Ile Glu
20 25 30
Lys Asn Ala Leu Gly Gly Val Cys Leu Asn Glu Gly Cys Ile Pro Thr
35 40 45
30 Lys Thr Leu Leu Tyr Ser Ala Lys Val Leu His Gln Ile Ala Thr Ala
50 55 60
Ser Lys Tyr Ala Val Ser Gly Thr Ala Asp Gly Leu Asp Leu Gly Lys
65 70 75 80
35 Val Ile Ala Arg Lys Gly Lys Ile Ile Arg Lys Leu Thr Ala Gly Ile
85 90 95
Arg Ser Arg Leu Thr Glu Ala Gly Val Glu Met Val Thr Ala Glu Ala
100 105 110
Thr Val Thr Gly Cys Asp Ala Asp Gly Ile Ile Gly Ile Thr Ala Gly
115 120 125
40 Glu Ala Gln Tyr Lys Ala Ala Asn Leu Leu Leu Cys Thr Gly Ser Glu
130 135 140
Thr Phe Ile Pro Pro Ile Pro Gly Val Glu Gln Thr Glu Tyr Trp Thr
145 150 155 160
45 Asn Arg Glu Ala Leu Gln Asn Lys Glu Ile Pro Thr Ser Leu Val Ile
165 170 175
Ile Gly Gly Gly Val Ile Gly Met Glu Phe Ala Ser Phe Phe Asn Gly
180 185 190
Ile Gly Thr Gln Val His Val Val Glu Met Leu Pro Glu Ile Leu Asn
195 200 205
50 Gly Ile Asp Pro Glu His Ala Ala Met Leu Arg Ala His Tyr Glu Lys
210 215 220
Glu Gly Ile Lys Phe Tyr Leu Gly His Lys Val Thr Ser Val Arg Asn
225 230 235 240
55 Gly Ala Val Thr Val Glu Tyr Glu Gly Glu Ser Lys Glu Ile Glu Gly
245 250 255
Glu Arg Ile Leu Met Ser Val Gly Arg Arg Pro Val Leu Gln Gly Phe
260 265 270
Glu Ser Leu Gly Leu Val Leu Ala Gly Lys Gly Val Lys Thr Asn Glu
275 280 285
60 Arg Met Gln Thr Ser Leu Pro Asn Val Tyr Ala Ala Gly Asp Ile Thr
290 295 300
Gly Phe Ser Leu Leu Ala His Thr Ala Val Arg Glu Ala Glu Val Ala
305 310 315 320
Val Asp Gln Ile Leu Gly Lys Thr Asp Glu Thr Met Ser Tyr Arg Ala
325 330 335
65 Val Pro Gly Val Val Tyr Thr Asn Pro Glu Val Ala Gly Val Gly Glu
340 345 350
Thr Glu Glu Ser Leu Arg Lys Ala Gly Arg Ala Tyr Thr Val Arg Arg
355 360 365
70 Leu Pro Met Ala Phe Ser Gly Arg Phe Val Ala Glu Asn Glu Gln Gly
370 375 380
Asn Gly Glu Cys Lys Leu Leu Leu Asp Glu Glu Asn Arg Leu Ile Gly
385 390 395 400
75 Ala His Leu Ile Gly Asn Pro Ala Gly Glu Leu Ile Val Thr Ala Ala
405 410 415

WO 99/29870

PCT/AU98/01023

342/ 490

Lys Gly Glu Tyr Asp Arg Ala Arg Thr Asn Val Leu Lys Arg Tyr Glu
 385 390 395 400
 Asn Gln Tyr Asn Glu Arg Asp Lys Arg Lys Asn Asn Ala Tyr Ala Asn
 405 410 415
 5 Glu Tyr Ser Thr Tyr Phe Thr Asp Gly Gly Tyr Ile Pro Gly Ile Glu
 420 425 430
 Val Glu Tyr Gln Thr Val Asn Ala Phe Ala Pro Gln Val Pro Leu Glu
 435 440 445
 Ala Phe Asn Gln Ala Ile Ala Gln Met Ile Asp Pro Val Lys Asn Ala
 10 455 460
 Val Val Thr Leu Thr Gly Pro Ser Lys Ala Glu Ala Lys Ile Pro Ser
 465 470 475 480
 Glu Ala Asp Phe Leu Ala Ala Phe Lys Ala Ala Arg Gln Gln Lys Val
 485 490 495
 15 Glu Ala Lys Lys Asp Glu Val Ser Asp Gln Lys Leu Met Glu Lys Ala
 500 505 510
 Pro Lys Ala Gly Lys Ile Val Ser Glu Lys Lys Asp Gln Lys Phe Gly
 515 520 525
 20 Thr Thr Glu Leu Thr Leu Ser Asn Gly Ile Lys Val Tyr Leu Lys Lys
 530 535 540
 Thr Asp Phe Lys Ser Asn Glu Ile Leu Met Ser Ala Leu Ser Pro Gly
 545 550 555 560
 Gly Ile Leu Ser Gly Lys His Ala Pro Asn Gln Ser Val Met Asn Ser
 565 570 575
 25 Phe Met Asn Val Gly Gly Leu Gly Asn Phe Asp Ala Ile Gln Leu Asp
 580 585 590
 Lys Val Leu Thr Gly Arg Ser Ala Ser Val Ser Pro Ser Leu Ser Leu
 595 600 605
 30 Leu Ser Glu Gly Leu Ser Gly Lys Thr Thr Val Glu Asp Met Glu Thr
 610 615 620
 Phe Phe Gln Leu Ile Tyr Leu Gln Met Thr Ala Asn Arg Lys Asp Pro
 625 630 635 640
 Glu Ala Phe Lys Ala Thr Gln Glu Lys Leu Tyr Asn Asn Leu Lys Asn
 645 650 655
 35 Gln Glu Ala Asn Pro Met Ala Ala Leu Met Asp Ser Ile Arg His Thr
 660 665 670
 Met Tyr Gly Asp Asn Pro Met Met Lys Pro Met Lys Ala Ala Asp Val
 675 680 685
 40 Glu Lys Val Asn Tyr Asp Gln Val Met Ala Phe Tyr Asn Glu Arg Phe
 690 695 700
 Ala Asp Ala Gly Asp Phe Met Phe Phe Phe Ile Gly Asn Leu Asp Glu
 705 710 715 720
 Ala Lys Met Lys Pro Leu Ile Glu Thr Tyr Leu Ala Ser Leu Pro Asn
 725 730 735
 45 Leu Lys Arg Gly Asp Lys Met Asn Lys Ala Gln Val Pro Ala Ala Arg
 740 745 750
 Ser Gly Lys Ile Asp Cys Lys Phe Glu Lys Glu Met Asp Thr Pro Ser
 755 760 765
 50 Thr Thr Ile Phe Asp Val Val Ser Gly Asn Val Glu Tyr Thr Leu Lys
 770 775 780
 Asn Ser Leu Leu Leu Glu Val Phe Ser Ala Val Met Asp Gln Val Tyr
 785 790 795 800
 Thr Ala Thr Val Arg Glu Lys Glu Gly Glu Ala Tyr Ser Val Ala Ala
 805 810 815
 55 Phe Gly Gly Leu Glu Gln Tyr Pro Gln Pro Lys Ala Leu Met Gln Ile
 820 825 830
 Tyr Phe Pro Thr Asp Pro Ala Arg Ala Glu Glu Met Asn Ala Ile Val
 835 840 845
 60 Phe Ala Glu Leu Glu Lys Leu Ala Lys Glu Gly Pro Asn Val Glu Tyr
 850 855 860
 Phe Lys Lys Thr Ile Glu Asn Leu Asn Lys Gln His Lys Glu Ser Leu
 865 870 875 880
 Arg Glu Asn Arg Phe Trp Leu Glu Ala Met Lys Ala Ser Phe Phe Glu
 885 890 895
 65 Gly Asn Asp Phe Ile Thr Asp Tyr Glu Ser Val Leu Asn Gly Leu Thr
 900 905 910
 Pro Ala Glu Leu Gln Lys Phe Ala Ala Asp Leu Leu Lys Gln Gln Asn
 915 920 925
 70 Arg Val Val Val Met Met Ala Pro Val Ala Lys Ala Gln
 930 935 940

(2) INFORMATION FOR SEQ ID NO:407

75 (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 684 amino acids

WO 99/29870

PCT/AU98/01023

344/ 490

465 470 475 480
Asn Asn Leu Ile Arg Lys Glu Glu Arg Ala Glu Val Lys Leu Ser Asp
485 490 495
5 Thr Glu Arg Ala Thr Leu Val Lys Leu Phe Glu Ala Arg Leu Pro Arg
500 505 510
5 Asp Glu Lys Lys His Phe Asn Val Ala Phe Glu Ser Leu Gly Ala Glu
515 520 525
Gly Glu Ala Ile Leu Ile Thr Gln Ala Glu Phe Met Arg Arg Met Arg
530 535 540
10 Asp Met Ala Gln Leu Gln Pro Gly Met Ser Phe Tyr Gly Glu Leu Pro
545 550 555
Asp Ser Tyr Asn Leu Val Leu Asn Thr Asp His Pro Leu Ile Asp Arg
560 565 570 575
15 Val Leu Ser Gly Glu Lys Glu Ser Val Glu Pro Ser Leu Thr Glu Leu
580 585 590
Arg Ala Lys Ile Ala Glu Leu Lys Ala Glu Glu Ala Lys Leu Leu Asp
595 600 605
Glu Glu Lys Gly Lys Lys Pro Glu Glu Ile Pro Val Ala Thr Lys Glu
610 615 620
20 Ala Lys Glu Asn Asn Ala Val Glu Gln Ala Lys Thr Glu Gly Ser Ile
625 630 635 640
Asn Asp Glu Leu Thr Lys Tyr Ala Gln Asp Asn Glu Leu Ile Gly Gln
645 650 655
25 Leu Ile Asp Leu Ala Leu Leu Gly Ser Gly Leu Leu Thr Gly Glu Ala
660 665 670
Leu Ala Glu Phe Ile Arg Arg Ser Gln Arg Leu Leu
675 680

(2) INFORMATION FOR SEQ ID NO:408

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 464 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408

Met Glu Lys Leu Ile Asp Ile Leu Val Val Asp Asp Asp Val Ala Val
1 5 10 15
50 Cys Ala Ala Leu Arg Leu Val Leu Lys Arg Ala Gly Tyr Asn Pro Val
20 25 30
Ile Ala Asn Ser Pro Asp Glu Ala Leu Ser Ile Met Arg Asn Pro Asp
35 40 45
55 Gly Gly Cys Lys Pro Ala Val Ile Leu Met Asp Met Asn Phe Ser Leu
50 55 60
Ser Thr Ser Gly Arg Glu Gly Leu Glu Leu Glu Lys Met Gln Ile
65 70 75 80
60 Phe Thr Ser Cys Pro Val Ile Leu Met Thr Ala Trp Ala Ser Ile Pro
85 90 95
Leu Ala Val Glu Gly Met Arg Leu Gly Ala Phe Asp Phe Ile Gly Lys
100 105 110
Pro Trp Asp Asn Asp Arg Leu Leu Arg Thr Ile Asp Thr Ala Leu His
115 120 125
65 Leu Ala Ala Pro Ser Ala Val Ala Asn Pro Ser Glu Gln Ser Asp Arg
130 135 140
Asp Thr Ala Arg Gln Pro Lys Ala Thr Val Gln Glu Asn Asp Pro Cys
145 150 155 160
Ala His Ile Ile Gly Arg Ser Asp Ala Ile Cys Lys Ile Lys Glu Arg
165 170 175
70 Ile Arg Arg Ile Ala Pro Thr His Ala Ser Val Leu Ile Thr Gly Glu
180 185 190
Ser Gly Thr Gly Lys Glu Leu Ile Ala Glu Ala Leu His Arg Gly Ser
195 200 205
75 Lys Arg Ala Ser Ala Pro Phe Val Lys Val Asn Leu Gly Gly Ile Pro

WO 99/29870

PCT/AU98/01023

346 / 490

180 185 190
 Ser Pro Glu Asn Ala Ala Ile Val Ile Thr His Tyr Gln Arg Leu Leu
 195 200 205
 Glu Tyr Ile Lys Pro Asp Phe Val His Val Leu Tyr Lys Gly Arg Ile
 210 215 220
 Val Lys Ser Gly Gly Ala Glu Leu Ala Leu Thr Leu Glu Glu Lys Gly
 225 230 235 240
 Tyr Asp Trp Ile Lys Glu Glu Ile Gly Glu
 245 250

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(2) INFORMATION FOR SEQ ID NO:410

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 461 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410

Met Ala Lys Glu Lys Thr Ile Tyr Val Cys Arg Ser Cys Gly Thr Lys
 1 5 10 15
 Tyr Ala Lys Trp Gln Gly Asn Cys Asn Ala Cys Gly Glu Trp Asn Cys
 20 25 30
 Ile Asp Glu Glu Lys Val Pro Ala Pro Ala Ser Gly Lys His Ala Ala
 35 40 45
 Lys Ser Phe Met Pro Arg Glu Gln Asp Asn Arg Pro Arg Leu Leu Gln
 50 55 60
 Asp Val Glu Ser Gly Asp Glu Glu Arg Ile Arg Leu Gly Asp Glu Glu
 65 70 75 80
 Phe Asp Arg Val Leu Gly Gly Gly Ile Val Lys Gly Ala Phe Val Leu
 85 90 95
 Leu Gly Gly Glu Pro Gly Ile Gly Lys Ser Thr Leu Ile Leu Gln Thr
 100 105 110
 Val Leu Arg Leu Pro Gln Leu Arg Thr Leu Tyr Val Ser Gly Glu Glu
 115 120 125
 Ser Ala Arg Gln Leu Lys Met Arg Ala Glu Arg Leu Gly Gln Ala Met
 130 135 140
 Asn Gly Cys Tyr Val Tyr Cys Glu Thr Asn Ile Glu Arg Ile Leu Ser
 145 150 155 160
 Arg Ala Glu Glu Leu Thr Pro Asp Leu Leu Val Ile Asp Ser Ile Gln
 165 170 175
 Thr Val Tyr Thr Glu Glu Met Glu Ser Ser Ala Gly Ser Val Gly Gln
 180 185 190
 Ile Arg Glu Cys Ala Ala Leu Leu Leu Lys Tyr Cys Lys Thr Thr Gly
 195 200 205
 Ile Pro Val Ile Val Ile Gly His Ile Thr Lys Glu Gly Ser Ile Ala
 210 215 220
 Gly Pro Lys Val Leu Glu His Ile Val Asp Thr Val Leu Leu Phe Asp
 225 230 235 240
 Gly Asp Lys His His Leu Tyr Arg Ile Leu Arg Gly Gln Lys Asn Arg
 245 250 255
 Tyr Gly Ser Thr Ser Glu Leu Gly Ile Tyr Glu Met Arg Gln Asp Gly
 260 265 270
 Leu Arg Gly Val Glu Asn Pro Ser Glu His Leu Ile Thr Arg Asn Arg
 275 280 285
 Glu Asp Leu Ser Gly Ile Ala Ile Ala Val Ala Met Glu Gly Ile Arg
 290 295 300
 Pro Ile Leu Ile Glu Ala Gln Ala Leu Val Ser Ser Ala Ile Tyr Ala
 305 310 315 320
 Asn Pro Gln Arg Ser Ala Thr Gly Phe Asp Ile Arg Arg Met Asn Met
 325 330 335
 Leu Leu Ala Val Leu Glu Lys Arg Ala Gly Phe Lys Leu Ile Gln Lys
 340 345 350
 Asp Val Phe Leu Asn Ile Ala Gly Gly Ile Lys Ile Ala Asp Pro Ala

WO 99/29870

PCT/AU98/01023

349/490

(ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...602
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:413

15	Met	Ile	Leu	Leu	Phe	Gly	Gly	Thr	Thr	Glu	Gly	Arg	Ala	Ala	Ala	Arg
	1				5					10					15	
	Val	Leu	Asp	Glu	Ala	Gly	Ser	Pro	Phe	Phe	Tyr	Ser	Thr	Lys	Gly	Asn
					20					25				30		
20	Leu	Gln	Glu	Ile	Gln	Ser	Ser	His	Gly	His	Arg	Leu	Thr	Gly	Ala	Met
					35				40					45		
	Thr	Val	Ala	Asp	Met	Val	Ser	Phe	Cys	Arg	Lys	Glu	Glu	Ile	Arg	Leu
					50				55					60		
	Ile	Val	Asp	Ala	Ala	His	Pro	Phe	Ala	Glu	Glu	Leu	His	Ala	Ser	Val
					65				70					75		80
25	Ala	Glu	Ala	Ser	Glu	Gln	Thr	Gly	Ile	Pro	Val	Val	Arg	Tyr	Glu	Arg
					85				90					95		
	Gln	Tyr	Pro	Pro	Arg	Glu	Glu	Gly	Ile	Val	Trp	Cys	Ala	Asn	Tyr	Asp
					100				105					110		
	Thr	Ala	Ala	Glu	Arg	Met	Leu	Gly	Asp	Gly	Val	Gln	Arg	Leu	Leu	Met
					115				120					125		
30	Leu	Thr	Gly	Val	Asn	Thr	Ile	Pro	Lys	Leu	Ala	Ala	Phe	Trp	Lys	Glu
					130				135					140		
	Arg	Thr	Thr	Phe	Cys	Arg	Ile	Leu	Lys	Arg	Asp	Glu	Ser	Val	Ala	Leu
					145				150					155		160
35	Ala	Glu	Lys	Asn	Gly	Phe	Pro	Ala	Glu	Arg	Ile	Val	Phe	Phe	Glu	Pro
					165				170					175		
	His	Ala	Asp	Glu	Glu	Leu	Met	Gln	Ala	Val	Arg	Pro	Asp	Ala	Ile	Ile
					180				185					190		
	Thr	Lys	Glu	Ser	Gly	Glu	Ser	Gly	Tyr	Phe	Arg	Glu	Lys	Ile	Glu	Ala
					195				200					205		
40	Ala	Arg	Arg	Met	Gly	Ile	Arg	Ile	Tyr	Ala	Val	Val	Arg	Pro	Pro	Leu
					210				215					220		
	Pro	Pro	Ser	Phe	Ile	Pro	Val	Gly	Gly	Pro	Val	Gly	Leu	Arg	Arg	Ala
					225				230					235		240
45	Val	Glu	Arg	Leu	Val	Pro	Gly	Phe	Phe	Ser	Leu	Arg	Ser	Gly	Phe	Thr
					245				250					255		
	Thr	Gly	Thr	Thr	Ala	Thr	Ala	Ala	Val	Val	Ala	Ala	Met	Tyr	Arg	Leu
					260				265					270		
50	Met	Gly	Leu	Gly	Ser	Leu	Ala	Glu	Ala	Pro	Val	Glu	Leu	Pro	Ser	Gly
					275				280					285		
	Glu	Ile	Val	Ser	Leu	Pro	Ile	Ala	Glu	Ile	Arg	Glu	Glu	Glu	Asp	Ala
					290				295					300		
	Val	Val	Ser	Ala	Val	Leu	Lys	Asp	Ala	Gly	Asp	Asp	Pro	Asp	Val	Thr
					305				310					315		320
55	Asn	Gly	Met	Ala	Val	Cys	Ala	Thr	Ile	Arg	Leu	Asn	Pro	Glu	His	Glu
					325				330					335		
	Glu	Val	Arg	Phe	Leu	Gln	Gly	Glu	Gly	Val	Gly	Val	Val	Thr	Leu	Pro
					340				345					350		
	Gly	Leu	Gly	Leu	Glu	Val	Gly	Gly	Pro	Ala	Ile	Asn	Leu	Val	Pro	Arg
					355				360					365		
60	Arg	Met	Met	Thr	Ala	Glu	Val	Arg	Arg	Leu	Tyr	Ala	Gln	Gly	Gly	Val
					370				375					380		
	Asp	Ile	Thr	Ile	Ser	Val	Pro	Glu	Gly	Arg	Glu	Ala	Ala	Thr	Gln	Thr
					385				390					395		400
65	Phe	Asn	Pro	Arg	Leu	Gly	Ile	Arg	Asp	Gly	Ile	Ser	Ile	Ile	Gly	Thr
					405				410					415		
	Ser	Gly	Val	Val	Lys	Pro	Phe	Ser	Ala	Glu	Ala	Phe	Val	Gly	Ala	Ile
					420				425					430		
	Arg	Lys	Gln	Val	Gly	Ile	Ala	Thr	Ala	Leu	Gly	Ala	Asn	His	Ile	Val
					435				440					445		
70	Leu	Asn	Ser	Gly	Ala	Lys	Ser	Glu	Arg	Tyr	Val	Lys	Gly	Ala	Tyr	Pro
					450				455					460		
	Ala	Leu	Ile	Pro	Gln	Ala	Phe	Val	Gln	Tyr	Gly	Asn	Phe	Val	Gly	Glu
					465				470					475		480
75	Ser	Leu	Ser	Cys	Val	Ala	Ser	Phe	Pro	Ser	Val	Arg	Ser	Val	Thr	Val

WO 99/29870

PCT/AU98/01023

350/490

485 490 495
Gly Ile Met Leu Gly Lys Ala Val Lys Leu Ala Glu Gly Tyr Leu Asp
500 505 510
5 Thr His Ser Lys Lys Val Val Met Asn Arg Arg Phe Leu His Glu Leu
515 520 525
Ala Arg Gln Ala Gly Cys Ser Glu Asp Ile His Ala Ile Ile Asp Ser
530 535 540
Leu Asn Leu Ala Arg Glu Leu Trp Thr Met Pro Ser Ala Glu Asp Ser
545 550 555
10 Asp Arg Leu Leu Arg Lys Ile Ala Glu Arg Ser Trp Glu Thr Cys Arg
565 570 575
Pro Ser Val Pro Ser Ala Glu Leu Glu Leu Leu Leu Ile Asp Glu Ser
580 585 590
15 Gly Ala Ile Arg Phe Arg Ile Gly Gly Glu
595 600

(2) INFORMATION FOR SEQ ID NO:414

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 443 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein

(iii) SYNTHETICAL: YES

(vi) ORIGINAL SOURCE:
30 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...443

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:414

Met Leu Arg Thr Phe Arg Ile Gly Gly Ile His Pro Pro Glu Asn Lys
1 5 10 15
40 Leu Ser Ala Gly Lys Pro Val Glu Val Leu Pro Ile Pro Ser Gln Val
20 25 30
Val Ile Pro Leu Gly Gln His Ile Gly Ala Pro Ala Thr Ala Thr Val
35 40 45
Lys Lys Gly Asp Glu Val Lys Val Gly Thr Ile Ile Ala Gln Ala Gly
50 55 60
45 Gly Phe Val Ser Ala Asn Ile His Ser Ser Val Ser Gly Lys Val Leu
65 70 75
Lys Ile Asp Asn Val Tyr Asp Ser Ser Gly Tyr Pro Lys Pro Ala Val
85 90 95
50 Phe Ile Ser Val Glu Gly Asp Glu Trp Glu Glu Gly Ile Asp Arg Ser
100 105 110
Pro Ala Ile Val Lys Glu Cys Asn Leu Asp Ala Lys Glu Ile Val Ala
115 120 125
Lys Ile Ser Ala Ala Gly Ile Val Gly Leu Gly Gly Ala Thr Phe Pro
130 135 140
55 Thr His Val Lys Leu Ser Pro Pro Pro Gly Asn Lys Ala Glu Ile Leu
145 150 155
Ile Ile Asn Ala Val Glu Cys Glu Pro Tyr Leu Thr Ser Asp His Val
165 170 175
60 Leu Met Leu Glu His Gly Glu Glu Ile Met Ile Gly Val Ser Ile Leu
180 185 190
Met Lys Ala Ile Gln Val Asn Lys Ala Val Ile Gly Val Glu Asn Asn
195 200 205
Lys Lys Asp Ala Ile Ala His Leu Thr Lys Leu Ala Thr Ala Tyr Pro
210 215 220
65 Gly Ile Glu Val Met Pro Leu Lys Val Gln Tyr Pro Gln Gly Gly Glu
225 230 235
Lys Gln Leu Ile Asp Ala Val Ile Arg Lys Gln Val Lys Ser Gly Ala
245 250 255
70 Leu Pro Ile Ser Thr Gly Ala Val Val Gln Asn Val Gly Thr Val Phe
260 265 270
Ala Val Tyr Glu Ala Val Gln Lys Asn Lys Pro Leu Val Glu Arg Ile
275 280 285
Val Thr Val Thr Gly Lys Lys Leu Ser Arg Pro Ser Asn Leu Leu Val
290 295 300
75 Arg Ile Gly Thr Pro Ile Ala Ala Leu Ile Glu Ala Ala Gly Gly Leu

WO 99/29870

PCT/AU98/01023

351/ 490

305 310 315 320
Pro Glu Asn Thr Gly Lys Ile Ile Gly Gly Gly Pro Met Met Gly Arg
325 330 335
5 Ala Leu Leu Ser Pro Asp Val Pro Val Thr Lys Gly Ser Ser Gly Val
340 345 350
Leu Ile Leu Asp Arg Glu Glu Ala Val Arg Lys Pro Met Arg Asp Cys
355 360 365
Ile Arg Cys Ala Lys Cys Val Gly Val Cys Pro Met Gly Leu Asn Pro
370 375 380
10 Ala Phe Leu Met Arg Asp Thr Leu Tyr Lys Ser Trp Glu Thr Ala Glu
385 390 395 400
Lys Gly Asn Val Val Asp Cys Ile Glu Cys Gly Ser Cys Ser Phe Thr
405 410 415
15 Cys Pro Ala Asn Arg Pro Leu Leu Asp Tyr Ile Arg Gln Ala Lys Lys
420 425 430
Thr Val Met Gly Ile Gln Arg Ala Arg Lys Gln
435 440

(2) INFORMATION FOR SEQ ID NO:415

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 479 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415

40 Met Lys Arg Ile Gln Leu Thr Leu Ile Ala Leu Phe Ala Ala Val Ala
1 5 10 15
Gly Leu Val Ala Gln Asn Ala Tyr Glu Gly Val Ile Ser Tyr Lys Ile
20 25 30
Ser Leu Asp Lys Thr Gly Asn Lys Val Val Leu Asn Gly Ala Ala Asp
35 40 45
45 Met Ser Asn Leu Lys Leu Lys Ser Thr Gln Met Ile Ile Val Thr Pro
50 55 60
Ile Leu Arg Ser Glu Asp Gly Thr Ser Arg Val Glu Phe Pro Ser Val
65 70 75 80
Val Ile Thr Gly Arg Asn Arg Thr Lys Ala Leu Lys Arg Glu Ile Ala
85 90 95
50 Phe Ser Ser Ala Leu Pro Gln Ala Lys His Ala Ala Gln Tyr Ile Arg
100 105 110
Arg His Asn Gly Lys Ser Glu Gln Phe Ala Phe Thr Gly Glu His Ala
115 120 125
55 Tyr Ala Ser Trp Met Met Asp Ala Lys Phe Val Val Arg Glu Glu Val
130 135 140
Arg Gly Cys Ala Lys Cys Pro Val Gly Leu Ser Ser Asn Ile Val Pro
145 150 155 160
Phe Asp Pro Leu Phe Asn Pro Ala Glu Ala Pro Tyr Leu Leu Ala His
165 170 175
60 Ile Thr Pro Ala Glu Glu Val Glu Lys Gln Arg Glu Ser Ser Phe Asp
180 185 190
Ala Tyr Ile Asn Phe Lys Val Asn Lys Ala Asp Val Leu Pro Glu Tyr
195 200 205
65 Arg Asn Asn Lys Ala Glu Leu Glu Lys Ile Lys Glu Phe Val Ser Thr
210 215 220
Val Lys Ala Asn Pro Asn Tyr Ser Val Asn Lys Met Ile Ile Glu Gly
225 230 235 240
Phe Ala Ser Pro Glu Ala Ser Ile Ala His Asn Lys Ala Leu Ser Glu
245 250 255
70 Arg Arg Ala Lys Arg Leu Ala Glu Glu Leu Val Arg Lys Tyr Gly Lys
260 265 270
Thr Leu Pro Asn Ile Thr Thr Glu Phe Gly Gly Glu Asp Trp Lys Gly
275 280 285
75 Leu Lys Leu Ala Ile Glu Lys Ser Asp Ile Ala Asp Arg Asp Arg Val

WO 99/29870

PCT/AU98/01023

352/ 490

290 295 300
 Leu Glu Ile Ile Asn Ser Asp Lys Tyr Ala Asp Asp Ala Arg Glu
 305 310 315 320
 Gln Ala Leu Lys Gln Leu Ser Ser Tyr Arg Tyr Ile Leu Asp Gln Ile
 325 330 335
 Tyr Pro Asn Leu Arg Arg Asn Thr Ile Thr Met Gly Tyr Ile Val Arg
 340 345 350
 Asp Tyr Thr Leu Glu Glu Ala Arg Glu Ile Ile Lys Thr Ala Pro Lys
 355 360 365
 Glu Leu Ser Glu Ala Glu Met Tyr Arg Val Ala Met Ser Tyr Pro Glu
 370 375 380
 Gly His Gln Glu Arg Leu Phe Ala Leu Asn Thr Thr Leu Lys Tyr Phe
 385 390 395 400
 Pro Glu Ser Val Thr Gly Arg Ile Asn Leu Ala Val Ala Ala Phe Asn
 405 410 415
 Gly Gly Asp Val Gln Gln Ala Ile Ala Leu Leu Ser Pro Ile Gln Thr
 420 425 430
 Glu Lys Gly Val Ser Asn Ile Leu Gly Ala Ala Tyr Ala Arg Thr Gly
 435 440 445
 Asp Phe Ala Arg Ala Glu Thr Phe Phe Arg Lys Ala Val Ala Glu Gly
 450 455 460
 Asp Ala Asn Ala Gln Arg Asn Leu Asp Met Leu Leu Gly Lys Lys
 465 470 475

5
 10
 15
 20
 25 (2) INFORMATION FOR SEQ ID NO:416
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 383 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 30
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 35
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 40
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...383
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:416
 45 Met Ala Glu Lys Arg Asp Tyr Tyr Glu Val Leu Gly Val Ser Lys Asn
 1 5 10 15
 Ala Thr Asp Asp Glu Leu Lys Lys Ala Tyr Arg Lys Lys Ala Ile Gln
 20 25 30
 Tyr His Pro Asp Lys Asn Pro Gly Asp Lys Glu Ala Glu Glu His Phe
 35 40 45
 Lys Glu Val Ala Glu Ala Tyr Asp Val Leu Ser Asp Pro Gln Lys Arg
 50 55 60
 Ser Gln Tyr Asp Gln Phe Gly His Ala Gly Leu Gly Gly Ala Ala Gly
 65 70 75 80
 Gly Gly Phe Ser Gly Gly Gly Met Ser Met Glu Asp Ile Phe Ser Arg
 85 90 95
 Phe Gly Asp Leu Phe Gly Gly Phe Gly Gly Phe Gly Phe Ser Asp
 100 105 110
 Met Gly Gly Gly Ser Arg Arg Arg Val Arg Arg Gly Ser Asp Leu Arg
 115 120 125
 Val Arg Val Lys Leu Ser Leu Ala Asp Ile Ser Lys Gly Val Glu Lys
 130 135 140
 Lys Val Lys Val Lys Lys Gln Val Val Cys Ser Lys Cys Arg Gly Asp
 145 150 155 160
 Gly Thr Glu Glu Ala Asn Gly Lys Thr Thr Cys Gln Thr Cys His Gly
 165 170 175
 Thr Gly Val Val Thr Arg Val Ser Asn Thr Phe Leu Gly Ala Met Gln
 180 185 190
 Thr Gln Ser Thr Cys Pro Thr Cys His Gly Glu Gly Glu Ile Ile Thr
 195 200 205
 Lys Pro Cys Ser Lys Cys Lys Gly Glu Gly Val Glu Ile Gly Glu Glu
 210 215 220
 Val Ile Ser Phe His Ile Pro Ala Gly Val Ala Glu Gly Met Gln Met
 225 230 235 240
 75 Ser Val Asn Gly Lys Gly Asn Ala Ala Pro Arg Gly Gly Val Asn Gly

WO 99/29870

PCT/AU98/01023

354/ 490

290

(2) INFORMATION FOR SEQ ID NO:418

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 356 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

15 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...356

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:419

Met Thr Ser Val Ser His Leu Arg Thr Ile Ser Val Ala Gly Ile Leu
1 5 10 15
25 Ala Ala Leu Gly Gly Ala Val Leu Ile Leu Phe Gly Val Asn Leu Phe
20 25 30
Leu Gly Ser Val Ala Ile Pro Met Ser Glu Ile Phe Arg His Leu Phe
35 40 45
30 Ser Asp Arg Pro Glu Gly Gly Glu Ala Leu Val His Tyr Asn Ile Leu
50 55 60
Trp Lys Ser Arg Leu Pro Glu Ala Leu Thr Ala Ala Phe Ala Gly Ala
65 70 75 80
Gly Leu Ser Val Ser Gly Leu Gln Met Gln Thr Val Phe Arg Asn Pro
85 90 95
35 Leu Ala Gly Pro Ser Val Leu Gly Ile Ser Ser Gly Ala Ser Leu Gly
100 105 110
Val Ala Leu Val Val Leu Leu Ser Gly Ser Leu Gly Val Ala Leu
115 120 125
40 Ser Ser Leu Gly Tyr Met Gly Glu Val Ala Met Asn Ile Ala Ala Ala
130 135 140
Val Gly Ser Leu Ala Val Met Gly Leu Ile Val Phe Val Ser Thr Lys
145 150 155 160
Val Arg Ser His Val Thr Leu Leu Ile Ile Gly Val Met Ile Gly Tyr
165 170 175
45 Val Ala Thr Ala Val Ile Gly Val Phe Lys Phe Phe Ser Ile Glu Glu
180 185 190
Asp Ile Arg Ala Tyr Val Ile Trp Gly Leu Gly Ser Phe Ser Arg Ala
195 200 205
Thr Asp Ser Gln Leu Ser Phe Phe Ala Ile Leu Met Leu Ile Phe Ile
210 215 220
50 Pro Ala Gly Met Leu Leu Val Lys Gln Leu Asn Leu Leu Leu Gly
225 230 235 240
Glu Ser Tyr Ala Arg Asn Leu Gly Leu Asn Thr Arg Arg Ala Arg Leu
245 250 255
55 Leu Val Ile Ser Ser Ala Gly Leu Leu Ile Ala Thr Val Thr Ala Tyr
260 265 270
Cys Gly Pro Ile Gly Phe Leu Gly Met Ala Val Pro His Leu Ala Arg
275 280 285
60 Val Ile Phe His Thr Ser Asp His Arg Ile Leu Met Pro Ala Thr Cys
290 295 300
Leu Ile Gly Ser Ala Leu Ala Leu Phe Cys Asn Ile Ile Ala Arg Met
305 310 315 320
Pro Gly Phe Glu Gly Ala Leu Pro Val Asn Ser Val Thr Ala Leu Val
325 330 335
65 Gly Ala Pro Ile Ile Val Thr Val Leu Phe Arg Arg Arg Arg Phe Lys
340 345 350
Glu Glu Thr Asp
355

70 (2) INFORMATION FOR SEQ ID NO:419

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 757 amino acids
(B) TYPE: amino acid
75 (D) TOPOLOGY: linear

355/ 490

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(iv) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...757

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419

15	Met Arg Thr Lys Thr Ile Phe Phe Ala Ile Ile Ser Phe Ile Ala Leu	1	5	10	15
	Leu Ser Ser Ser Leu Ser Ala Gln Ser Lys Ala Val Leu Thr Gly Ser	20	25	30	
20	Val Ser Asp Ala Glu Thr Gly Glu Pro Leu Ala Gly Ala Arg Ile Glu	35	40	45	
	Val Lys His Thr Asn Ile Val Ala Gly Ala Asp Ala Gly Gly His Phe	50	55	60	
	Glu Ile Lys Asn Leu Pro Ala Gly Gln His Thr Ile Ile Cys Ser Leu	65	70	75	
25	Gly Gly Tyr Gly Gln Lys Glu Glu Val Val Ala Ile Glu Ala Gly Gln	80	85	90	
	Thr Lys Thr Ile Ser Phe Ala Leu Arg Leu Arg Thr Asn Asn Leu Glu	95	100	105	
30	Glu Val Val Val Thr Gly Thr Gly Thr Arg Tyr Arg Leu Val Asp Ala	110	115	120	
	Pro Val Ala Thr Glu Val Leu Thr Ala Lys Asp Ile Ala Ser Phe Ser	125	130	135	
	Ala Pro Thr Ser Glu Ala Leu Leu Gln Gly Leu Ser Pro Ser Phe Asp	140	145	150	
35	Phe Gly Pro Asn Leu Met Gly Ser Phe Met Gln Leu Asn Gly Leu Ser	155	160	165	
	Ser Lys Tyr Ile Leu Ile Leu Ile Asp Gly Lys Arg Val Tyr Gly Asp	170	175	180	
	Val Gly Gly Gln Ala Asp Leu Ser Arg Ile Ser Pro Asp Gln Ile Glu	185	190	195	
40	Arg Ile Glu Leu Val Lys Gly Ala Ser Ser Ser Leu Tyr Gly Ser Asp	200	205	210	
	Ala Ile Ala Gly Val Ile Asn Val Ile Thr Lys Lys Asn Thr Asn Arg	215	220	225	
45	Leu Ser Ala Tyr Thr Ser His Arg Ile Ser Lys Tyr Asn Asp Arg Gln	230	235	240	
	Thr Asn Thr Ser Leu Asp Ile Asn Ile Gly Lys Phe Ser Ser Asn Thr	245	250	255	
	Asn Tyr Phe Phe Tyr His Thr Asp Gly Trp Gln Asn Ser Pro Phe Glu	260	265	270	
50	Ile Lys Lys Lys Lys Gly Ser Gly Glu Pro Val Leu Glu Glu Thr Tyr	275	280	285	
	Lys Lys Thr Phe Arg Ala Gln Glu Asn Gln Gly Val Ser Gln Ser Leu	290	295	300	
55	Ser Tyr Tyr Ala Thr Asn Asn Leu Ser Phe Ser Gly Asn Val Gln Tyr	305	310	315	
	Asn Lys Arg Gln Ile Phe Thr Pro Thr Phe Ser Glu Lys Lys Ala Tyr	320	325	330	
	Asp Met Asp Tyr Arg Ala Leu Thr Ala Ser Leu Gly Thr Asn Tyr Leu	335	340	345	
60	Phe Pro Asn Gly Leu His Thr Leu Ser Phe Asp Ala Val Tyr Asp Arg	350	355	360	
	Phe Arg Phe Gly Tyr Leu Tyr His Asp Lys Asp Ser Ser Glu Ser Leu	365	370	375	
	Ile Asn Asn Gln Gly Gln Thr Glu Gln Pro Thr Phe Phe Pro Gly Gln	380	385	390	
65	Leu Arg Asn Lys Asn Asp Gln Ile Arg Tyr Thr Ala Glu Ala Arg Gly	395	400	405	
	Val Phe Thr Leu Pro Tyr Ala Gln Lys Leu Thr Gly Gly Leu Glu Tyr	410	415	420	
70	Phe Arg Glu Glu Leu Ile Ser Pro Tyr Asn Leu Ile Thr Asp Lys Ala	425	430	435	
	Asp Ala Ser Thr Leu Ser Ala Tyr Val Gln Asp Glu Trp Lys Pro Leu	440	445	450	
75	Asp Trp Phe Asn Met Thr Ala Gly Phe Arg Leu Val His His Gln Glu	455	460	465	
		470	475	480	

356/ 490

485 490 495
 Phe Gly Thr Arg Met Thr Pro Lys Val Ser Ile Leu Ala Lys Tyr Gly
 500 505 510
 5 Phe Gly Thr Arg Met Thr Pro Lys Val Ser Ile Leu Ala Lys Tyr Gly
 515 520 525
 Leu Lys Glu Leu Phe Ala Arg Asn Glu Leu Thr Thr Met Gly Ser His
 530 535 540
 Asn Leu Tyr Leu Gly Asn Ala Asp Leu Lys Pro Gln Met Ser Asp Tyr
 545 550 555 560
 10 Tyr Ala Leu Gly Leu Glu Tyr Asn Gln Gly Pro Ile Ser Phe Ser Ala
 565 570 575
 Thr Val Tyr Asp Asn Glu Leu Arg Asn Leu Ile Ser Phe Met Asp Ile
 580 585 590
 15 Pro Thr Ser Pro Glu His Glu Ala Gln Gly Ile Lys Lys Thr Lys Gln
 595 600 605
 Tyr Ala Asn Ile Gly Lys Ala Arg Ser Arg Gly Leu Asp Val Leu Cys
 610 615 620
 Asp Ala Ser Ile Gly Trp Gly Ile Lys Leu Gly Ala Gly Tyr Ser Leu
 625 630 635 640
 20 Val Glu Ala Lys Asn Leu Gln Thr Asp Glu Trp Leu Glu Gly Ala Ala
 645 650 655
 Arg His Arg Ala Asn Val His Ala Asp Trp Val His Tyr Trp Gly Gln
 660 665 670
 25 Tyr Arg Leu Gly Val Ser Leu Phe Gly Arg Ile Gln Ser Glu Arg Tyr
 675 680 685
 Tyr Lys Asp Gly Asn Ala Pro Asp Tyr Thr Leu Trp Arg Leu Ala Thr
 690 695 700
 Ser His Arg Phe Ala His Phe Arg His Ile Ile Leu Asp Gly Thr Leu
 705 710 715 720
 30 Gly Ile Asp Asn Leu Phe Asp Tyr Val Asp Asp Arg Pro Met Gly Val
 725 730 735
 Asn Tyr Ala Thr Val Thr Pro Gly Arg Thr Phe Phe Ala Gln Ile Ala
 740 745 750
 35 Ile Arg Phe Asn Asn
 755

(2) INFORMATION FOR SEQ ID NO:420

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 331 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 45 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 50 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...331
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:420

Met Thr Asp Asn Lys Gln Arg Asn Ile Val Phe Pro Ala Phe Leu Leu
 1 5 10 15
 60 Leu Leu Gly Val Ile Ala Val Val Thr Ile Val Gly Phe Phe Met Leu
 20 25 30
 Arg Pro Ala Glu Glu Ile Ile Gln Gly Gln Ile Glu Val Thr Glu Tyr
 35 40 45
 Arg Val Ser Ser Lys Val Pro Gly Arg Ile Lys Glu Leu Arg Val Ser
 50 55 60
 65 Glu Gly Gln Gln Val Gln Ala Gly Asp Thr Leu Ala Val Ile Glu Ala
 65 70 75 80
 Pro Asp Val Ala Ala Lys Met Glu Gln Ala Lys Ala Ala Glu Ala Ala
 85 90 95
 70 Ala Gln Ala Gln Asn Ala Lys Ala Leu Lys Gly Ala Arg Ser Glu Gln
 100 105 110
 Ile Gln Ala Ala Tyr Glu Met Trp Gln Lys Ala Gln Ala Gly Val Ala
 115 120 125
 Ile Ala Thr Lys Thr His Gln Arg Val Gln Asn Leu Tyr Asp Gln Gly
 130 135 140
 75 Val Val Pro Ala Gln Lys Leu Asp Glu Ala Thr Ala Gln Arg Asp Ala

WO 99/29870

PCT/AU98/01023

357/490

145 150 155 160
Ala Ile Ala Thr Gln Lys Ala Ala Glu Ala Gln Tyr Asn Met Ala Arg
165 170 175
5 Asn Gly Ala Glu Arg Glu Asp Lys Leu Ala Ala Ser Ala Leu Val Asp
180 185 190
Arg Ala Arg Gly Ala Val Ala Glu Val Glu Ser Tyr Ile Asn Glu Thr
195 200 205
Tyr Leu Ile Ala Pro Arg Ala Gly Glu Val Ser Glu Ile Phe Pro Lys
210 215 220
10 Ala Gly Glu Leu Val Gly Thr Gly Ala Pro Ile Met Asn Ile Ala Glu
225 230 235 240
Met Gly Asp Met Trp Ala Ser Phe Ala Val Arg Glu Asp Phe Leu Ser
245 250 255
15 Ser Met Thr Met Gly Ala Val Leu Glu Thr Val Val Pro Ala Leu Asn
260 265 270
Glu Glu Lys Val Arg Phe Lys Ile Thr Phe Ile Lys Asn Met Gly Thr
275 280 285
Tyr Ala Ala Trp Lys Ala Thr Lys Thr Thr Gly Gln Tyr Asp Leu Lys
290 295 300
20 Thr Phe Glu Val Lys Ala Thr Leu Ala Asp Lys Asp Lys Ala Gln Lys
305 310 315 320
Leu Arg Pro Gly Met Ser Val Ile Ile Arg Lys
325 330

25 (2) INFORMATION FOR SEQ ID NO:421

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 amino acids

(E) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421

45 Met Arg Ile Val Ser Asn Phe Leu Phe Val Ser Phe Ser Val Leu Leu
1 5 10 15
Phe Ala Ser Cys Arg Ser Gln Arg Glu Lys Val Val Tyr Leu Gln Asp
20 25 30
50 Ile Gln Thr Phe Asn Arg Glu Ile Ile Ala Lys Pro Tyr Asp Val Lys
35 40 45
Ile Glu Lys Asp Asp Val Leu Asn Ile Leu Val Ser Ser Arg Asp Pro
50 55 60
Glu Leu Ser Thr Pro Tyr Asn Gln Val Leu Thr Thr Arg Ala Leu Ala
65 70 75 80
55 Arg Asn Gly Tyr Gly Thr Asn Ser Asn Glu Gly Phe Leu Val Asp Ser
85 90 95
Lys Gly Tyr Ile Asn Tyr Pro Ile Leu Gly Gln Ile Tyr Val Glu Gly
100 105 110
60 Leu Thr Arg Thr Glu Leu Glu Lys Glu Ile Gln Lys Arg Ile Ile Ser
115 120 125
Ser Gly Phe Ile Lys Asp Pro Thr Val Thr Val Gln Leu Gln Asn Phe
130 135 140
Lys Val Ser Val Leu Gly Glu Val Asn His Pro Gly Ser Met Ser Val
145 150 155 160
65 Lys Gly Glu Arg Ile Thr Leu Leu Glu Ala Ile Gly Met Ala Gly Asp
165 170 175
Leu Thr Ile Tyr Gly Arg Arg Asp Arg Val Phe Val Ile Arg Glu Thr
180 185 190
70 Asp Gly His Arg Glu Val Phe Gln Thr Asp Leu Arg Lys Ala Asp Leu
195 200 205
Leu Ala Ser Pro Val Tyr Tyr Leu His Gln Asn Asp Val Ile Tyr Val
210 215 220
Glu Pro Asn Asp Lys Lys Thr Gln Met Ser Glu Ile Asn Gln Asn Asn
225 230 235 240
75 Asn Val Asn Val Trp Leu Ser Val Thr Ser Thr Leu Val Ser Ile Ser

WO 99/29870

PCT/AU98/01023

358/ 490

Thr Leu Thr Ile Thr Ile Ile Asp Lys Thr Lys
245 250 255
260 265

5 (2) INFORMATION FOR SEQ ID NO:422

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 569 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...569

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:422

Met Lys Lys Thr Asn Leu Phe Leu Ser Leu Leu Val Ile Phe Ile Thr
1 5 10 15
Gly Ser Phe Met Thr Ala Cys Ala Gln Lys Ser Lys Thr Asn Lys Leu
20 25 30
Thr Glu Glu Asp Arg Ser Arg Asn Glu Tyr Val Gln Ser Met Asp Val
35 40 45
Leu Ser Asn Ile Ile Gly Asn Val Arg Leu Tyr Phe Val Asp Thr Ile
50 55 60
Ser Ile Lys His Met Thr Arg Arg Gly Ile Asp Ala Met Leu Gly Gly
65 70 75 80
Leu Asp Pro Tyr Thr Glu Tyr Ile Pro Tyr Glu Met Asp Glu Leu
85 90 95
Lys Leu Met Thr Thr Gly Glu Tyr Ala Gly Val Gly Ala Ile Ile Ser
100 105 110
Gln Arg Pro Asp Ser Ala Val Ile Ile Gln Arg Pro Met Glu Gly Met
115 120 125
Pro Ala Asp Glu Ala Gly Leu Ile Ala Gly Asp Arg Ile Leu Thr Ile
130 135 140
Asp Gly Lys Asp Phe Arg Lys Ser Thr Thr Pro Lys Val Ser Gln Ala
145 150 155 160
Leu Lys Gly Ile Ala Gly Thr Val Ala Lys Val Thr Val Met Arg Tyr
165 170 175
Gly Glu Thr Lys Pro Arg Thr Phe Ser Val Lys Arg Gln Lys Val Ile
180 185 190
Met Asn Ser Val Thr Tyr Ser Gly Met Leu Asp Gly Ser Ile Gly Tyr
195 200 205
Ile Arg Leu Asn Asn Phe Thr Asp Lys Ser Ala Glu Glu Val Arg Thr
210 215 220
Ala Leu Leu Asp Leu Arg Asp Lys Gln Gly Ala Lys Gly Leu Ile Leu
225 230 235 240
Asp Leu Arg Gly Asn Gly Gly Gly Leu Met Gln Ala Ala Ile Glu Ile
245 250 255
Val Asn Leu Phe Val Pro Lys Gly Lys Glu Val Val Thr Thr Lys Gly
260 265 270
Arg Ile Ala Glu Ser Ala Ser Val Phe Arg Thr Leu Thr Glu Pro Ile
275 280 285
Asp Thr Lys Leu Pro Ile Val Val Leu Ile Asp Gly Gln Ser Ala Ser
290 295 300
Ser Ser Glu Ile Val Ala Gly Ala Leu Gln Asp Met Asp Arg Ala Val
305 310 315 320
Leu Met Gly Gln Lys Ser Tyr Gly Lys Gly Leu Val Gln Thr Thr Arg
325 330 335
Gln Leu Pro Tyr Asn Gly Val Ile Lys Leu Thr Thr Ala Lys Tyr Tyr
340 345 350
Ile Pro Ser Gly Arg Cys Ile Gln Arg Leu Asp Tyr Ser Arg Thr Asn
355 360 365
Arg Thr Gly Met Ala Thr Ala Ile Pro Asp Ser Leu His Lys Ile Phe
370 375 380
Tyr Thr Ala Ala Gly Arg Arg Val Glu Asp Ala Gly Gly Ile Leu Pro
385 390 395 400
75 Asp Ile Glu Val Lys Gln Asp Thr Ala Ala Thr Leu Leu Tyr Tyr Met

WO 99/29870

PCT/AU98/01023

361/ 490

5 Glu Ile Asp Gln Asn Phe Ile Ala Ala Ile Leu Ala Ile Ile Gly Tyr
865 870 875 880
Ser Leu Asn Asp Thr Val Val Val Phe Asp Arg Ile Arg Glu Thr Met
885 890 895
Lys Leu Tyr Pro Asn Arg Asp Arg Tyr Gln Val Ile Asn Asp Ala Leu
900 905 910
Asn Ser Thr Leu Gly Arg Thr Leu Asn Thr Ser Leu Thr Thr Phe Ile
915 920 925
10 Val Met Leu Val Ile Phe Ile Phe Gly Gly Ala Thr Met Arg Ser Phe
930 935 940
Thr Phe Ser Ile Leu Leu Gly Ile Val Ile Gly Thr Tyr Ser Thr Leu
945 950 955 960
Phe Val Ala Thr Pro Leu Ala Tyr Glu Ile Gln Lys Arg Lys Leu Asn
965 970 975
15 Lys Ala Ala Lys Lys
980

(2) INFORMATION FOR SEQ ID NO:424

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1017 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- 25 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 30 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1017
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:424

Met Lys Arg Met Thr Leu Phe Phe Leu Cys Leu Leu Thr Ser Ile Gly
1 5 10 15
40 Trp Ala Met Ala Gln Asn Arg Thr Val Lys Gly Thr Val Ile Ser Ser
20 25 30
Glu Asp Asn Glu Pro Leu Ile Gly Ala Asn Val Val Val Gly Asn
35 40 45
45 Thr Thr Ile Gly Ala Ala Thr Asp Leu Asp Gly Asn Phe Thr Leu Ser
50 55 60
Val Pro Ala Asn Ala Lys Met Leu Arg Val Ser Tyr Ser Gly Met Thr
65 70 75 80
Thr Lys Glu Val Ala Ile Ala Asn Val Met Lys Ile Val Leu Asp Pro
85 90 95
50 Asp Ser Lys Val Leu Glu Gln Val Val Val Leu Gly Tyr Gly Thr Gly
100 105 110
Gln Lys Leu Ser Thr Val Ser Gly Ser Val Ala Lys Val Ser Ser Glu
115 120 125
Lys Leu Ala Glu Lys Pro Val Ala Asn Ile Met Asp Ala Leu Gln Gly
130 135 140
55 Gln Val Ala Gly Met Gln Val Met Thr Thr Ser Gly Asp Pro Thr Ala
145 150 155 160
Val Ala Ser Val Glu Ile His Gly Thr Gly Ser Leu Gly Ala Ser Ser
165 170 175
60 Ala Pro Leu Tyr Ile Val Asp Gly Met Gln Thr Ser Leu Asp Val Val
180 185 190
Ala Thr Met Asn Pro Asn Asp Phe Glu Ser Met Ser Val Leu Lys Asp
195 200 205
Ala Ser Ala Thr Ser Ile Tyr Gly Ala Arg Ala Ala Asn Gly Val Val
210 215 220
65 Phe Ile Gln Thr Lys Lys Gly Lys Met Ser Glu Arg Gly Arg Ile Thr
225 230 235 240
Phe Asn Ala Ser Tyr Gly Ile Ser Gln Ile Leu Asn Thr Lys Pro Leu
245 250 255
70 Asp Asn Met Met Thr Gly Asp Glu Leu Leu Asp Phe Gln Val Lys Ala
260 265 270
Gly Phe Trp Gly Asn Asn Gln Thr Val Gln Lys Val Lys Asp Met Ile
275 280 285
Leu Ala Gly Ala Glu Asp Leu Tyr Gly Asn Tyr Asp Ser Leu Lys Asp
290 295 300

WO 99/29870

PCT/AU98/01023

362/490

	Glu	Tyr	Gly	Lys	Thr	Leu	Phe	Pro	Val	Asp	Phe	Asn	His	Asp	Ala	Asp
	305					310					315					320
	Trp	Leu	Lys	Ala	Leu	Phe	Lys	Thr	Ala	Pro	Thr	Ser	Gln	Gly	Asp	Ile
				325						330					335	
5	Ser	Phe	Ser	Gly	Gly	Ser	Gln	Gly	Thr	Ser	Tyr	Tyr	Ala	Ser	Ile	Gly
				340						345					350	
	Tyr	Phe	Asp	Gln	Glu	Gly	Met	Ala	Arg	Glu	Pro	Ala	Asn	Phe	Lys	Arg
			355				360						365			
10	Tyr	Ser	Gly	Arg	Leu	Asn	Phe	Glu	Ser	Arg	Ile	Asn	Glu	Trp	Leu	Lys
			370				375					380				
	Val	Gly	Ala	Asn	Leu	Ser	Gly	Ala	Ile	Ala	Asn	Arg	Arg	Ser	Ala	Asp
			385			390					395					400
	Tyr	Phe	Gly	Lys	Tyr	Met	Gly	Ser	Gly	Thr	Phe	Gly	Val	Leu	Thr	
				405					410						415	
15	Met	Pro	Arg	Tyr	Tyr	Asn	Pro	Phe	Asp	Val	Asn	Gly	Asp	Leu	Ala	Asp
				420					425					430		
	Val	Tyr	Tyr	Met	Tyr	Gly	Ala	Thr	Arg	Pro	Ser	Met	Thr	Glu	Pro	Tyr
			435					440					445			
20	Phe	Ala	Lys	Met	Arg	Pro	Phe	Ser	Ser	Glu	Ser	His	Gln	Ala	Asn	Val
			450				455					460				
	Asn	Gly	Phe	Ala	Gln	Ile	Thr	Pro	Ile	Lys	Gly	Leu	Thr	Leu	Lys	Ala
			465				470				475					480
	Gln	Ala	Gly	Val	Asp	Ile	Thr	Asn	Thr	Arg	Thr	Ser	Ser	Lys	Arg	Met
				485						490					495	
25	Pro	Asn	Asn	Pro	Tyr	Asp	Ser	Thr	Pro	Leu	Gly	Glu	Arg	Arg	Glu	Arg
				500					505					510		
	Ala	Tyr	Arg	Val	Ser	Lys	Ser	Phe	Thr	Asn	Thr	Ala	Glu	Tyr	Lys	
			515				520					525				
30	Phe	Ser	Ile	Asp	Glu	Lys	His	Asp	Leu	Thr	Ala	Leu	Met	Gly	His	Glu
			530				535					540				
	Tyr	Ile	Glu	Tyr	Glu	Gly	Asp	Val	Ile	Gly	Ala	Ser	Ser	Lys	Gly	Phe
			545				550				555					560
	Glu	Ser	Asp	Lys	Leu	Met	Leu	Leu	Ser	Gln	Gly	Lys	Thr	Gly	Asn	Ser
				565							570				575	
35	Leu	Ser	Leu	Pro	Glu	His	Arg	Val	Ala	Glu	Tyr	Ala	Tyr	Leu	Ser	Phe
				580					585					590		
	Phe	Ser	Arg	Phe	Asn	Tyr	Gly	Phe	Asp	Lys	Trp	Met	Tyr	Ile	Asp	Phe
			595					600					605			
40	Ser	Val	Arg	Asn	Asp	Gln	Ser	Ser	Arg	Phe	Gly	Ser	Asn	Asn	Arg	Ser
				610				615					620			
	Ala	Trp	Phe	Tyr	Ser	Val	Gly	Gly	Met	Phe	Asp	Ile	Tyr	Asn	Lys	Phe
				625			630					635				640
	Ile	Gln	Glu	Ser	Asn	Trp	Leu	Ser	Asp	Leu	Arg	Leu	Lys	Met	Ser	Tyr
				645						650					655	
45	Gly	Thr	Thr	Gly	Asn	Ser	Glu	Ile	Gly	Asn	Tyr	Asn	His	Gln	Ala	Leu
				660					665					670		
	Val	Thr	Val	Asn	Asn	Tyr	Thr	Glu	Asp	Ala	Met	Gly	Leu	Ser	Ile	Ser
				675				680					685			
50	Thr	Ala	Gly	Asn	Pro	Asp	Leu	Ser	Trp	Glu	Lys	Gln	Ser	Gln	Phe	Asn
				690			695					700				
	Phe	Gly	Leu	Ala	Ala	Gly	Ala	Phe	Asn	Asn	Arg	Leu	Ser	Ala	Glu	Val
				705			710				715					720
	Asp	Phe	Tyr	Val	Arg	Thr	Thr	Asn	Asp	Met	Leu	Ile	Asp	Val	Pro	Met
				725						730					735	
55	Pro	Tyr	Ile	Ser	Gly	Phe	Phe	Ser	Gln	Tyr	Gln	Asn	Val	Gly	Ser	Met
				740					745						750	
	Lys	Asn	Thr	Gly	Val	Asp	Leu	Ser	Leu	Lys	Gly	Thr	Ile	Tyr	Gln	Asn
				755				760					765			
60	Lys	Asp	Trp	Asn	Val	Tyr	Ala	Ser	Ala	Asn	Phe	Asn	Tyr	Asn	Arg	Gln
				770				775					780			
	Glu	Ile	Thr	Lys	Leu	Phe	Phe	Gly	Leu	Asn	Lys	Tyr	Met	Leu	Pro	Asn
				785			790				795					800
	Thr	Gly	Thr	Ile	Trp	Glu	Ile	Gly	Tyr	Pro	Asn	Ser	Phe	Tyr	Met	Ala
				805						810					815	
65	Glu	Tyr	Ala	Gly	Ile	Asp	Lys	Lys	Thr	Gly	Lys	Gln	Leu	Trp	Tyr	Val
				820					825					830		
	Pro	Gly	Gln	Val	Asp	Ala	Asp	Gly	Asn	Lys	Val	Thr	Thr	Ser	Gln	Tyr
				835				840					845			
70	Ser	Ala	Asp	Leu	Glu	Thr	Arg	Ile	Asp	Lys	Ser	Val	Thr	Pro	Pro	Ile
				850			855					860				
	Thr	Gly	Gly	Phe	Ser	Leu	Gly	Ala	Ser	Trp	Lys	Gly	Leu	Ser	Leu	Asp
				865			870				875					880
	Ala	Asp	Phe	Ala	Tyr	Ile	Val	Gly	Lys	Trp	Met	Ile	Asn	Asn	Asp	Arg
				885						890					895	
75	Tyr	Phe	Thr	Glu	Asn	Ala	Gly	Gly	Leu	Met	Gln	Leu	Asn	Lys	Asp	Lys

WO 99/29870

PCT/AU98/01023

363/490

5 900 905 910
 Met Leu Leu Asn Ala Trp Thr Glu Asp Asn Lys Glu Thr Asp Val Pro
 915 920 925
 Lys Leu Gly Gln Ser Pro Gln Phe Asp Thr His Leu Leu Glu Asn Ala
 5 930 935 940
 Ser Phe Leu Arg Leu Lys Asn Leu Lys Leu Thr Tyr Val Leu Pro Asn
 945 950 955 960
 Ser Leu Phe Ala Gly Gln Asn Val Ile Gly Gly Ala Arg Val Tyr Leu
 10 965 970 975
 Met Ala Arg Asn Leu Leu Thr Val Thr Lys Tyr Lys Gly Phe Asp Pro
 980 985 990
 Glu Ala Gly Gly Asn Val Gly Lys Asn Gln Tyr Pro Asn Ser Lys Gln
 995 1000 1005
 Tyr Val Ala Gly Ile Gln Leu Ser Phe
 15 1010 1015

 (2) INFORMATION FOR SEQ ID NO:425

 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1014 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

 25 (ii) MOLECULE TYPE: protein

 (iii) HYPOTHETICAL: YES

 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 30 (vii) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1014

 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:425

 Met Thr Leu Phe Phe Leu Cys Leu Leu Thr Ser Ile Gly Trp Ala Met
 1 5 10
 Ala Gln Asn Arg Thr Val Lys Gly Thr Val Ile Ser Ser Glu Asp Asn
 40 20 25 30
 Glu Pro Leu Ile Gly Ala Asn Val Val Val Val Gly Asn Thr Thr Ile
 35 40 45
 Gly Ala Ala Thr Asp Leu Asp Gly Asn Phe Thr Leu Ser Val Pro Ala
 50 55 60
 45 Asn Ala Lys Met Leu Arg Val Ser Tyr Ser Gly Met Thr Thr Lys Glu
 65 70 75 80
 Val Ala Ile Ala Asn Val Met Lys Ile Val Leu Asp Pro Asp Ser Lys
 85 90 95
 50 Val Leu Glu Gln Val Val Val Leu Gly Tyr Gly Thr Gly Gln Lys Leu
 100 105 110
 Ser Thr Val Ser Gly Ser Val Ala Lys Val Ser Ser Glu Lys Leu Ala
 115 120 125
 Glu Lys Pro Val Ala Asn Ile Met Asp Ala Leu Gln Gly Gln Val Ala
 130 135 140
 55 Gly Met Gln Val Met Thr Thr Ser Gly Asp Pro Thr Ala Val Ala Ser
 145 150 155 160
 Val Glu Ile His Gly Thr Gly Ser Leu Gly Ala Ser Ser Ala Pro Leu
 165 170 175
 60 Tyr Ile Val Asp Gly Met Gln Thr Ser Leu Asp Val Val Ala Thr Met
 180 185 190
 Asn Pro Asn Asp Phe Glu Ser Met Ser Val Leu Lys Asp Ala Ser Ala
 195 200 205
 Thr Ser Ile Tyr Gly Ala Arg Ala Ala Asn Gly Val Val Phe Ile Gln
 210 215 220
 65 Thr Lys Lys Gly Lys Met Ser Glu Arg Gly Arg Ile Thr Phe Asn Ala
 225 230 235 240
 Ser Tyr Gly Ile Ser Gln Ile Leu Asn Thr Lys Pro Leu Asp Asn Met
 245 250 255
 70 Met Thr Gly Asp Glu Leu Leu Asp Phe Gln Val Lys Ala Gly Phe Trp
 260 265 270
 Gly Asn Asn Gln Thr Val Gln Lys Val Lys Asp Met Ile Leu Ala Gly
 275 280 285
 Ala Glu Asp Leu Tyr Gly Asn Tyr Asp Ser Leu Lys Asp Glu Tyr Gly
 290 295 300
 75 Lys Thr Leu Phe Pro Val Asp Phe Asn His Asp Ala Asp Trp Leu Lys

WO 99/29870

PCT/AU98/01023

364/ 490

	305			310			315		320
	Ala	Leu	Phe	Lys	Thr	Ala	Pro	Thr	Ser
									Gln
									Gly
									Asp
									Ile
									Ser
									Phe
									Ser
5	Gly	Gly	Ser	Gln	Gly	Thr	Ser	Tyr	Tyr
									Ala
									Ser
									Ile
									Gly
									Tyr
									Phe
									Asp
	Gln	Glu	Gly	Met	Ala	Arg	Glu	Pro	Ala
									Asn
									Phe
									Lys
									Arg
									Tyr
									Ser
									Gly
	Arg	Leu	Asn	Phe	Glu	Ser	Arg	Ile	Asn
									Glu
									Trp
									Leu
									Lys
									Val
									Gly
									Ala
10	Asn	Leu	Ser	Gly	Ala	Ile	Ala	Asn	Arg
									Arg
									Ser
									Ala
									Asp
									Tyr
									Phe
									Gly
	Lys	Tyr	Tyr	Met	Gly	Ser	Gly	Thr	Phe
									Gly
									Val
									Leu
									Thr
									Met
									Pro
									Arg
15	Tyr	Tyr	Asn	Pro	Phe	Asp	Val	Asn	Gly
									Asp
									Leu
									Ala
									Asp
									Val
									Tyr
									Tyr
	Met	Tyr	Gly	Ala	Thr	Arg	Pro	Ser	Met
									Thr
									Glu
									Pro
									Tyr
									Phe
									Ala
									Lys
	Met	Arg	Pro	Phe	Ser	Ser	Glu	Ser	His
									Gln
									Ala
									Asn
									Val
									Asn
									Gly
									Phe
20	Ala	Gln	Ile	Thr	Pro	Ile	Lys	Gly	Leu
									Thr
									Leu
									Lys
									Ala
									Gln
									Ala
									Gly
	Val	Asp	Ile	Thr	Asn	Thr	Arg	Thr	Ser
									Ser
									Lys
									Arg
									Met
									Pro
									Asn
									Asn
25	Pro	Tyr	Asp	Ser	Thr	Pro	Leu	Gly	Glu
									Arg
									Arg
									Glu
									Arg
									Ala
									Tyr
									Arg
	Asp	Val	Ser	Lys	Ser	Phe	Thr	Asn	Thr
									Ala
									Glu
									Tyr
									Lys
									Phe
									Ser
									Ile
	Asp	Glu	Lys	His	Asp	Leu	Thr	Ala	Leu
									Met
									Gly
									His
									Glu
									Tyr
									Ile
									Glu
30	Tyr	Glu	Gly	Asp	Val	Ile	Gly	Ala	Ser
									Ser
									Lys
									Gly
									Phe
									Glu
									Ser
									Asp
	Lys	Leu	Met	Leu	Leu	Ser	Gln	Gly	Lys
									Thr
									Gly
									Asn
									Ser
									Leu
									Ser
									Leu
35	Pro	Glu	His	Arg	Val	Ala	Glu	Tyr	Ala
									Tyr
									Leu
									Ser
									Phe
									Phe
									Ser
									Arg
	Phe	Asn	Tyr	Gly	Phe	Asp	Lys	Trp	Met
									Tyr
									Ile
									Asp
									Phe
									Ser
									Val
									Arg
	Asn	Asp	Gln	Ser	Ser	Arg	Phe	Gly	Ser
									Asn
									Asn
									Arg
									Ser
									Ala
									Trp
									Phe
40	Tyr	Ser	Val	Gly	Gly	Met	Phe	Asp	Ile
									Tyr
									Asn
									Lys
									Phe
									Ile
									Gln
									Glu
	Ser	Asn	Trp	Leu	Ser	Asp	Leu	Arg	Leu
									Lys
									Met
									Ser
									Tyr
									Gly
									Thr
									Thr
45	Gly	Asn	Ser	Glu	Ile	Gly	Asn	Tyr	Asn
									His
									Gln
									Ala
									Leu
									Val
									Thr
									Val
	Asn	Asn	Tyr	Thr	Glu	Asp	Ala	Met	Gly
									Leu
									Ser
									Ile
									Ser
									Thr
									Ala
									Gly
	Asn	Pro	Asp	Leu	Ser	Trp	Glu	Lys	Gln
									Ser
									Gln
									Phe
									Asn
									Gly
									Leu
50	Ala	Ala	G						

WO 99/29870

PCT/AU98/01023

365/ 490

5 Asn Ala Trp Thr Glu Asp Asn Lys Glu Thr Asp Val Pro Lys Leu Gly
915 920 925
Gln Ser Pro Gln Phe Asp Thr His Leu Leu Glu Asn Ala Ser Phe Leu
930 935 940
Arg Leu Lys Asn Leu Lys Leu Thr Tyr Val Leu Pro Asn Ser Leu Phe
945 950 955 960
Ala Gly Gln Asn Val Ile Gly Gly Ala Arg Val Tyr Leu Met Ala Arg
965 970 975
10 Asn Leu Leu Thr Val Thr Lys Tyr Lys Gly Phe Asp Pro Glu Ala Gly
980 985 990
Gly Asn Val Gly Lys Asn Gln Tyr Pro Asn Ser Lys Gln Tyr Val Ala
995 1000 1005
Gly Ile Gln Leu Ser Phe
1010
15 (2) INFORMATION FOR SEQ ID NO:426
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 821 amino acids
20 (P) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
25 (iii) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
30 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...821
35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:426
Met Lys Lys Lys Asn Phe Leu Leu Leu Gly Ile Phe Val Ala Leu Leu
1 5 10 15
Thr Phe Ile Gly Ser Met Gln Ala Gln Gln Ala Lys Asp Tyr Phe Asn
20 25 30
40 Phe Asp Glu Arg Gly Glu Ala Tyr Phe Ser Phe Lys Val Pro Asp Arg
35 40 45
Ala Val Leu Gln Glu Leu Ala Leu Ile Met Ser Ile Asp Glu Phe Asp
50 55 60
45 Pro Val Thr Asn Glu Ala Ile Ala Tyr Ala Ser Glu Glu Glu Phe Glu
65 70 75 80
Ala Phe Leu Arg Tyr Gly Leu Lys Pro Thr Phe Leu Thr Pro Pro Ser
85 90 95
Met Gln Arg Ala Val Glu Met Phe Asp Tyr Arg Ser Gly Glu Lys Tyr
100 105 110
50 Glu Trp Asn Ala Tyr Pro Thr Tyr Glu Ala Tyr Ile Ser Met Met Glu
115 120 125
Glu Phe Gln Thr Lys Tyr Pro Ser Leu Cys Thr Thr Ser Val Ile Gly
130 135 140
55 Lys Ser Val Lys Asp Arg Lys Leu Met Ile Cys Lys Leu Thr Ser Ser
145 150 155 160
Ala Asn Thr Gly Lys Lys Pro Arg Val Leu Tyr Thr Ser Thr Met His
165 170 175
Gly Asp Glu Thr Thr Gly Tyr Val Val Leu Leu Arg Leu Ile Asp His
180 185 190
60 Leu Leu Ser Asn Tyr Glu Ser Asp Pro Arg Ile Lys Asn Ile Leu Asp
195 200 205
Lys Thr Gln Val Trp Ile Cys Pro Leu Thr Asn Pro Asp Gly Ala Tyr
210 215 220
65 Arg Ala Gly Asn His Thr Val Gln Gly Ala Thr Arg Tyr Asn Ala Asn
225 230 235 240
Asn Val Asp Leu Asn Arg Asn Phe Lys Asp Asp Val Ala Gly Asp His
245 250 255
Pro Asp Gly Lys Pro Trp Gln Pro Glu Ala Thr Ala Phe Met Asp Leu
260 265 270
70 Glu Gly Asn Thr Ser Phe Val Leu Gly Ala Asn Ile His Gly Gly Thr
275 280 285
Glu Val Val Asn Tyr Pro Trp Asp Asn Lys Lys Glu Arg His Ala Asp
290 295 300
75 Asp Glu Trp Tyr Lys Leu Ile Ser Arg Asn Tyr Ala Ala Ala Cys Gln
305 310 315 320

WO 99/29870

PCT/AU98/01023

366/ 490

5 Ser Ile Ser Ala Ser Tyr Met Thr Ser Glu Thr Asn Ser Gly Ile Ile
325 330 335
Asn Gly Ser Asp Trp Tyr Val Ile Arg Gly Ser Arg Gln Asp Asn Ala
340 345 350
5 Asn Tyr Phe His Arg Leu Arg Glu Ile Thr Leu Glu Ile Ser Asn Thr
355 360 365
Lys Leu Val Pro Ala Ser Gln Leu Pro Lys Tyr Trp Asn Leu Asn Lys
370 375 380
10 Glu Ser Leu Leu Ala Leu Ile Glu Glu Ser Leu Tyr Gly Ile His Gly
385 390 395 400
Thr Val Thr Ser Ala Ala Asn Gly Gln Pro Leu Lys Cys Gln Ile Leu
405 410 415
15 Ile Glu Asn His Asp Lys Arg Asn Ser Asp Val Tyr Ser Asp Ala Thr
420 425 430
Thr Gly Tyr Tyr Val Arg Pro Ile Lys Ala Gly Thr Tyr Thr Val Lys
435 440 445
Tyr Lys Ala Glu Gly Tyr Pro Glu Ala Thr Arg Thr Ile Thr Ile Lys
450 455 460
20 Asp Lys Glu Thr Val Ile Met Asp Ile Ala Leu Gly Asn Ser Val Pro
465 470 475 480
Leu Pro Val Pro Asp Phe Thr Ala Ser Pro Met Thr Ile Ser Val Gly
485 490 495
Glu Ser Val Gln Phe Gln Asp Gln Thr Thr Asn Asn Pro Thr Asn Trp
500 505 510
25 Glu Trp Thr Phe Glu Gly Gly Gln Pro Ala Met Ser Thr Glu Gln Asn
515 520 525
Pro Leu Val Ser Tyr Ser His Pro Gly Gln Tyr Asp Val Thr Leu Lys
530 535 540
30 Val Trp Asn Ala Ser Gly Ser Asn Thr Ile Thr Lys Glu Lys Phe Ile
545 550 555 560
Thr Val Asn Ala Val Met Pro Val Ala Glu Phe Val Gly Thr Pro Thr
565 570 575
Glu Ile Glu Glu Gly Gln Thr Val Ser Phe Gln Asn Gln Ser Thr Asn
580 585 590
35 Ala Thr Asn Tyr Val Trp Ile Phe Asp Gly Gly Thr Pro Ala Thr Ser
595 600 605
Glu Asp Glu Asn Pro Thr Val Leu Tyr Ser Lys Ala Gly Gln Tyr Asp
610 615 620
40 Val Thr Leu Lys Ala Ile Ser Ala Ser Gly Glu Thr Val Lys Thr Lys
625 630 635 640
Glu Lys Tyr Ile Thr Val Lys Lys Ala Pro Val Pro Ala Pro Val Ala
645 650 655
Asp Phe Glu Gly Thr Pro Arg Lys Val Lys Lys Gly Glu Thr Val Thr
660 665 670
45 Phe Lys Asp Leu Ser Thr Asn Asn Pro Thr Ser Trp Leu Trp Val Phe
675 680 685
Glu Gly Gly Ser Pro Ala Thr Ser Thr Glu Gln Asn Pro Val Val Thr
690 695 700
50 Tyr Asn Glu Thr Gly Lys Tyr Asp Val Gln Leu Thr Ala Thr Asn Glu
705 710 715 720
Gly Gly Ser Asn Val Lys Lys Ala Glu Asp Tyr Ile Glu Val Ile Leu
725 730 735
Asp Asp Ser Val Glu Asp Ile Val Ala Gln Thr Gly Ile Val Ile Arg
740 745 750
55 Pro Gln Asn Gly Thr Lys Gln Ile Leu Ile Glu Ala Asn Ala Ala Ile
755 760 765
Lys Ala Ile Val Leu Tyr Asp Ile Asn Gly Arg Val Val Leu Lys Thr
770 775 780
60 Thr Pro Asn Gln Leu Arg Ser Thr Val Asp Leu Ser Ile Leu Pro Glu
785 790 795 800
Gly Ile Tyr Thr Ile Asn Ile Lys Thr Glu Lys Ser Ala Arg Thr Glu
805 810 815
Lys Ile His Ile Gly
820

65 (2) INFORMATION FOR SEQ ID NO:427

70 (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

75 (111) HYPOTHETICAL: YES

WO 99/29870

PCT/AU98/01023

368/ 490

5 Glu Arg Ile Val Asn Arg Lys Val Ser Arg Ile Leu Phe Asp Lys Arg
275 280 285
Ile Ile Ser Leu Asp Leu Ala Gln Met Val Ala Gly Thr Lys Tyr Arg
290 295 300
5 Gly Gln Phe Glu Glu Arg Leu Lys Ala Val Leu Asp Glu Leu Lys Lys
305 310 315 320
Asn Pro Gln Ile Ile Leu Phe Ile Asp Glu Ile His Thr Ile Val Gly
325 330 335
10 Ala Gly Ser Ala Ala Gly Ser Met Asp Thr Ala Asn Met Leu Lys Pro
340 345 350
Ala Leu Ala Arg Gly Gln Val Gln Cys Ile Gly Ala Thr Thr Leu Asp
355 360 365
Glu Tyr Arg Lys Asn Ile Glu Lys Asp Gly Ala Leu Glu Arg Arg Phe
370 375 380
15 Gln Lys Val Pro Ile Ala Pro Ser Thr Ala Glu Glu Thr Leu Thr Ile
385 390 395 400
Leu Gln Asn Ile Lys Glu Lys Tyr Glu Asp Tyr His Gly Val Arg Tyr
405 410 415
20 Thr Asp Glu Ala Ile Lys Ala Ala Val Glu Leu Thr Asp Arg Tyr Val
420 425 430
Ser Asp Arg Phe Phe Pro Asp Lys Ala Ile Asp Ala Met Asp Glu Ala
435 440 445
Gly Ala Ser Val His Ile Thr Asn Val Val Ala Pro Lys Glu Ile Glu
450 455 460
25 Ile Leu Glu Ala Glu Leu Ala Ser Val Arg Glu Asn Lys Leu Ser Ala
465 470 475 480
Val Lys Ala Gln Asn Tyr Glu Leu Ala Ala Ser Phe Arg Asp Gln Glu
485 490 495
30 Arg Arg Thr Gln Gln Gln Ile Ala Glu Glu Lys Lys Lys Trp Glu Glu
500 505 510
Gln Met Ser Lys His Arg Glu Thr Val Asp Glu Asn Val Val Ala His
515 520 525
Val Val Ala Leu Met Thr Gly Val Pro Ala Glu Arg Leu Ser Thr Gly
530 535 540
35 Glu Gly Glu Arg Leu Arg Thr Met Ala Asp Asp Leu Lys Thr Lys Val
545 550 555 560
Val Gly Gln Asp Thr Ala Ile Glu Lys Met Val His Ala Ile Gln Arg
565 570 575
40 Asn Arg Leu Gly Leu Arg Asn Glu Lys Lys Pro Ile Gly Ser Phe Leu
580 585 590
Phe Leu Gly Pro Thr Gly Val Gly Lys Thr Tyr Leu Ala Lys Lys Leu
595 600 605
Ala Glu Tyr Leu Phe Glu Asp Glu Asn Ala Met Ile Arg Val Asp Met
610 615 620
45 Ser Glu Tyr Met Glu Lys Phe Ser Val Ser Arg Leu Val Gly Ala Pro
625 630 635 640
Pro Gly Tyr Val Gly Tyr Glu Glu Gly Gly Gln Leu Thr Glu Arg Val
645 650 655
50 Arg Arg Lys Pro Tyr Ser Val Val Leu Leu Asp Glu Ile Glu Lys Ala
660 665 670
His Ala Asp Val Phe Asn Leu Leu Leu Gln Val Met Asp Glu Gly Gln
675 680 685
Leu Thr Asp Ser Leu Gly Arg Arg Val Asn Phe Lys Asn Thr Val Ile
690 695 700
55 Ile Ile Thr Ser Asn Val Gly Thr Arg Gln Leu Lys Asp Phe Gly Gln
705 710 715 720
Gly Ile Gly Phe Arg Ser Glu Lys Asp Glu Ala Asn Lys Glu His
725 730 735
60 Ser Arg Ser Val Ile Gln Lys Ala Leu Asn Lys Thr Phe Ser Pro Glu
740 745 750
Phe Leu Asn Arg Leu Asp Asp Ile Ile Leu Phe Asp Gln Leu Gly Lys
755 760 765
Thr Glu Ile Arg Arg Met Val Asp Ile Glu Leu Lys Ala Val Leu Ala
770 775 780
65 Arg Ile His Arg Ala Gly Tyr Asp Leu Val Leu Thr Asp Glu Ala Lys
785 790 795 800
Asp Val Ile Ala Thr Lys Gly Tyr Asp Leu Gln Tyr Gly Ala Arg Pro
805 810 815
70 Leu Lys Arg Thr Leu Gln Asn Glu Val Glu Asp Arg Leu Thr Asp Leu
820 825 830
Ile Leu Ser Gly Gln Ile Glu Lys Gly Gln Thr Leu Thr Leu Ser Ala
835 840 845
Arg Asp Gly Glu Ile Ile Val Gln Glu Gln Ala
850 855
75

370/490

(2) INFORMATION FOR SEQ ID NO:430

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 293 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...293
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:430
- | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Gln | Asn | Tyr | Phe | Lys | Arg | Val | Cys | Ser | Leu | Leu | Trp | Leu | Val |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Leu | Pro | Met | Leu | Ile | Met | Pro | Leu | Glu | Val | Ala | Ala | Gln | Glu | Ile | Ile |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Pro | Asn | Glu | Glu | Val | Leu | Glu | Ser | Leu | Thr | Phe | Val | Ala | Pro | Val | Glu |
| | | | 35 | | | | | 40 | | | | | 45 | | |
| Glu | Thr | Asp | Ala | Ile | Glu | Ala | Glu | Val | Glu | Ala | Leu | Gln | Glu | Ile | Val |
| | | | 50 | | | | | 55 | | | | | 60 | | |
| Ala | Thr | Glu | Glu | Ile | Ala | Glu | Gln | Ala | Val | Arg | Ser | Tyr | Thr | Tyr | Thr |
| | | | 65 | | | | | 70 | | | | | 75 | | |
| Val | Tyr | Arg | Asp | Gly | Val | Lys | Ile | Ala | Ser | Gly | Leu | Thr | Glu | Pro | Thr |
| | | | | 85 | | | | | | | | | 90 | | |
| Phe | Leu | Asp | Glu | Asp | Val | Pro | Ala | Gly | Glu | His | Thr | Tyr | Cys | Val | Glu |
| | | | | 100 | | | | | | | | | 105 | | |
| Val | Gln | Tyr | Gln | Gly | Gly | Val | Ser | Asp | Lys | Val | Cys | Val | Asp | Val | Glu |
| | | | | 115 | | | | | | | | | 120 | | |
| Val | Lys | Asp | Phe | Lys | Pro | Val | Thr | Asn | Leu | Thr | Gly | Thr | Ala | Ser | Asn |
| | | | | 130 | | | | | | | | | 135 | | |
| Asp | Glu | Val | Ser | Leu | Asp | Trp | Asp | Gly | Val | Glu | Glu | Lys | Ala | Glu | Glu |
| | | | | 145 | | | | | | | | | 150 | | |
| Pro | Ala | Ser | Asp | Lys | Ala | Val | Ser | Tyr | Asn | Val | Tyr | Lys | Asn | Gly | Thr |
| | | | | 165 | | | | | | | | | 170 | | |
| Leu | Ile | Gly | Asn | Thr | Ala | Glu | Thr | His | Tyr | Val | Glu | Thr | Gly | Val | Ala |
| | | | | 180 | | | | | | | | | 185 | | |
| Asn | Gly | Thr | Tyr | Ile | Tyr | Glu | Val | Glu | Val | Lys | Tyr | Pro | Asp | Gly | Val |
| | | | | 195 | | | | | | | | | 200 | | |
| Ser | Pro | Lys | Val | Ala | Val | Thr | Val | Thr | Val | Thr | Asn | Ser | Ser | Leu | Ser |
| | | | | 210 | | | | | | | | | 215 | | |
| Asn | Val | Asp | Gly | Gln | Ala | Pro | Tyr | Thr | Leu | Arg | Val | Glu | Gly | Lys | Lys |
| | | | | 225 | | | | | | | | | 230 | | |
| Ile | Ile | Ala | Glu | Ala | His | Gly | Met | Ile | Thr | Leu | Tyr | Asp | Ile | Asn | Gly |
| | | | | 245 | | | | | | | | | 250 | | |
| Arg | Thr | Val | Ala | Val | Ala | Pro | Asn | Arg | Leu | Glu | Tyr | Met | Ala | Gln | Thr |
| | | | | 260 | | | | | | | | | 265 | | |
| Gly | Phe | Tyr | Ala | Val | Arg | Phe | Asp | Val | Gly | Asn | Lys | His | His | Val | Ser |
| | | | | 275 | | | | | | | | | 280 | | |
| Lys | Ile | Gln | Val | Arg | | | | | | | | | 285 | | |
| | | | | 290 | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:431

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 312 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
(A) NAME/KEY: misc_feature

WO 99/29870

PCT/AU98/01023

371/490

(B) LOCATION 1...312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431

5 Met Ile Pro Leu Ser Glu Ser Phe Glu Ser Gly Ile Pro Ala Ile Trp
1 5 10 15
Lys Thr Ile Asp Ala Asp Gly Asp Gly Tyr Asn Trp Met His Leu Thr
20 25 30
10 Asn Phe Thr Gly Gln Ser Gly Leu Cys Val Ser Ser Ala Ser Tyr Ile
35 40 45
Gly Gly Val Gly Ala Leu Thr Pro Asp Asn Tyr Leu Ile Thr Pro Glu
50 55 60
Leu Lys Leu Pro Thr Asp Ala Leu Val Glu Ile Tyr Trp Val Cys
65 70 75 80
15 Thr Gln Asp Leu Thr Ala Pro Ser Glu His Tyr Ala Val Tyr Ser Ser
85 90 95
Ser Thr Gly Asn Asn Ala Ala Asp Phe Val Asn Leu Leu Tyr Glu Glu
100 105 110
20 Thr Leu Thr Ala Lys Arg Ile Gln Ser Pro Glu Leu Ile Arg Gly Asn
115 120 125
Arg Thr Gln Gly Val Trp Tyr Gln Arg Lys Val Val Leu Pro Asn Asp
130 135 140
Thr Lys Tyr Val Ala Phe Arg His Phe Asn Ser Thr Asp Asn Phe Trp
145 150 155 160
25 Leu Asn Leu Asp Glu Val Ser Ile Leu Tyr Thr Pro Leu Pro Arg Arg
165 170 175
Ala Pro Cys Pro His Pro Gly Gly Tyr Thr Tyr Ser Val Phe Arg Arg
180 185 190
30 Gly Gln Lys Ile Ala Ser Gly Leu Ser Ala Leu Ala Tyr Ile Asp Thr
195 200 205
Asp Val Pro Tyr Gly Thr Gln Asp Tyr Cys Val Gln Val Asn Tyr Leu
210 215 220
Gln Gly Asp Ser Tyr Lys Val Cys Lys Asn Ile Val Val Ala Asn Ser
225 230 235 240
35 Ala Asn Ile Tyr Gly Ala Asp Lys Pro Phe Ala Leu Thr Val Val Gly
245 250 255
Lys Thr Ile Val Ala Ser Ala Phe Lys Gly Glu Ile Thr Leu Tyr Asp
260 265 270
40 Ile Arg Gly Arg Leu Ile Ala Ser Gly Cys Asp Thr Leu Arg Tyr Lys
275 280 285
Ala Glu Asn Gly Phe Tyr Leu Ile Lys Ile Gln Val Asn Gly Thr Val
290 295 300
Tyr Thr Glu Lys Ile Gln Ile Gln
305 310

(2) INFORMATION FOR SEQ ID NO:432

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 843 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1...843

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432

65 Met Lys Lys Ser Phe Leu Leu Ala Ile Val Met Leu Phe Gly Ile Ala
1 5 10 15
Met Gln Gly His Ser Ala Pro Val Thr Lys Glu Arg Ala Leu Ser Leu
20 25 30
70 Ala Arg Leu Ala Leu Arg Gln Val Ser Leu Arg Met Gly Gln Thr Ala
35 40 45
Val Ser Asp Lys Ile Ser Ile Asp Tyr Val Tyr Arg Gln Gly Asp Ala
50 55 60
75 Glu Arg Gly Ile Thr Ser Gln Glu Glu Gly Ser Pro Ala Tyr Phe Tyr
65 70 75 80

372/ 490

Val Ala Asn Arg Gly Asn Asn Glu Gly Tyr Ala Leu Val Ala Ala Asp
85 90 95
Asp Arg Ile Pro Thr Ile Leu Ala Tyr Ser Pro Ile Gly Arg Phe Asp
100 105 110
5 Met Asp Ser Met Pro Asp Asn Leu Arg Met Trp Leu Gln Ile Tyr Asp
115 120 125
Gln Glu Ile Gly Leu Ile Leu Ser Gly Lys Ala Gln Leu Asn Glu Glu
130 135 140
10 Ile Leu Arg Thr Glu Gly Val Pro Ala Glu Val His Ala Leu Met Asp
145 150 155 160
Asn Gly His Phe Ala Asn Asp Pro Met Arg Trp Asn Gln Gly Tyr Pro
165 170 175
Trp Asn Asn Lys Glu Pro Leu Leu Pro Asn Gly Asn His Ala Tyr Thr
180 185 190
15 Gly Cys Val Ala Thr Ala Ala Ala Gln Ile Met Arg Tyr His Ser Trp
195 200 205
Pro Leu Gln Gly Glu Gly Ser Phe Asp Tyr His Ala Gly Ser Leu Val
210 215 220
20 Gly Asn Trp Ser Gly Thr Phe Gly Glu Met Tyr Asp Trp Ile Asn Met
225 230 235 240
Pro Gly Asn Pro Asp Leu Asp Asn Leu Thr Gln Ser Gln Val Asp Ala
245 250 255
Tyr Ala Thr Leu Met Arg Asp Val Ser Ala Ser Val Ser Met Ser Phe
260 265 270
25 Tyr Glu Asn Gly Ser Gly Thr Tyr Ser Val Tyr Val Val Gly Ala Leu
275 280 285
Arg Asn Asn Phe Arg Tyr Lys Arg Ser Leu Gln Leu His Val Arg Ala
290 295 300
30 Leu Tyr Thr Ser Gln Glu Trp His Asp Met Ile Arg Gly Glu Leu Ala
305 310 315 320
Ser Gly Arg Pro Val Tyr Tyr Ala Gly Asn Asn Gln Ser Ile Gly His
325 330 335
Ala Phe Val Cys Asp Gly Tyr Ala Ser Asp Gly Thr Phe His Phe Asn
340 345 350
35 Trp Gly Trp Gly Gly Val Ser Asn Gly Phe Tyr Lys Leu Thr Leu Leu
355 360 365
Ser Pro Thr Ser Leu Gly Ile Gly Gly Glu Gly Ile Gly Phe Thr Ile
370 375 380
40 Tyr Gln Glu Ile Ile Thr Gly Ile Glu Pro Ala Lys Thr Pro Ala Glu
385 390 395 400
Ala Gly Thr Asp Ala Leu Pro Ile Leu Ala Leu Lys Asp Ile Glu Ala
405 410 415
Glu Tyr Lys Ser Glu Ser Gly Leu Asn Val Gly Tyr Ser Ile Tyr Asn
420 425 430
45 Thr Gly Glu Glu Gln Ser Asn Leu Asp Leu Gly Tyr Arg Leu Asn Lys
435 440 445
Ala Asp Gly Glu Val Ile Glu Val Lys Thr Ser Ser Ile Asn Ile Ser
450 455 460
50 Trp Tyr Gly Tyr Gly Glu His Pro Glu Ser Phe Ser Leu Ala Pro Asn
465 470 475 480
Gln Leu Ser Gln Gly Ile Asn Thr Ile Thr Leu Leu Tyr Arg Arg Thr
485 490 495
Gly Thr Glu Gln Trp Glu Pro Val Arg His Ala Gln Gly Gly Tyr Val
500 505 510
55 Asn Ser Ile Lys Val Asn Thr Thr Asp Pro Asn Asn Val Val Val Thr
515 520 525
Val Asp Asn Asn Glu Gly Lys Leu Ser Ile Val Pro Asn Ser Phe Val
530 535 540
60 Ala Asp Leu Asn Ser Tyr Glu His Ser Thr Ile Thr Val Gln Phe Asn
545 550 555 560
Ser Asp Ser Pro Asp Glu Ile Arg Thr Pro Val Ala Phe Ala Leu Ser
565 570 575
Thr Gly Ala Thr Ala Asp Asp Val Ile Ser Leu Gly Trp Val Met Ala
580 585 590
65 Glu Val Pro Gly Gly Ser Ser Asn Tyr Pro Val Val Trp Ser Lys Asp
595 600 605
Val Leu Thr Leu Ser Glu Gly Asp Tyr Thr Leu Trp Tyr Arg Phe Ser
610 615 620
70 Ile Asn Asn Gln Lys Asp Glu Trp Lys Lys Ile Gly Ser Val Ser Val
625 630 635 640
Lys Thr Pro Thr Glu Tyr Thr His Pro Leu Phe Glu Val Gly His Asn
645 650 655
Gln Thr Ser Thr Tyr Thr Leu Asp Met Ala His Asn Arg Val Leu Pro
660 665 670
75 Asp Phe Thr Leu Lys Asn Leu Gly Leu Pro Phe Asn Gly Glu Leu Val

373/490

675 680 685
 Val Val Phe Arg Gln Thr Gln Ser Ser Ser Gly Ser Leu Trp Ala Ala
 690 695 700
 5 Gln Glu Thr Val His Ile Lys Gln Gly Glu Thr Phe Val Tyr Lys Pro
 705 710 715 720
 Val Val Glu Gly Pro Ile Pro Asp Gly Ser Tyr Arg Ala Thr Leu His
 725 730 735
 Ala Phe Val Asn Gly Gln Gln Gln Leu Tyr Leu Lys Gly Lys Arg Asn
 740 745 750
 10 Tyr Thr Val Lys Ile Val Asn Gly Thr Ala Val Glu Ala Ile Glu Ser
 755 760 765
 Ser Glu Glu Ile Arg Val Phe Pro Asn Pro Ala Arg Asp Tyr Val Glu
 770 775 780
 15 Ile Ser Ala Pro Cys Ile Pro Gln Glu Thr Ser Ile Ile Leu Phe Asp
 785 790 795 800
 Leu Ser Gly Lys Ile Val Met Lys Asn Ser Leu Ser Ala Gly His Gly
 805 810 815
 Arg Met Asp Val Ser Arg Leu Pro Asn Gly Ala Tyr Ile Leu Lys Val
 820 825 830
 20 Asp Gly Tyr Thr Thr Lys Ile Asn Ile Val His
 835 840
 (2) INFORMATION FOR SEQ ID NO:433
 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 290 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 30 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 35 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...290
 40 (xii) SEQUENCE DESCRIPTION: SEQ ID NO:433
 Met Lys Lys Leu Phe Leu Ser Leu Thr Ser Leu Val Met Val Phe Ala
 1 5 10 15
 45 Val Ala Ser Cys Asp Ile Ile Asp Lys Asp Gln Thr Leu Leu Pro Ala
 20 25 30
 Pro Thr Asn Val Thr Pro Asp Asn Pro Asp Asp Asn Pro Ser Glu Ile
 35 40 45
 50 Asp Ile Thr Gln Thr His Thr Glu Lys Tyr Val Leu Ala Glu Glu Phe
 50 55 60
 Thr Gly Gln Lys Cys Leu Asn Cys Pro Lys Gly His Arg Lys Leu Ala
 65 70 75 80
 Ala Leu Lys Glu Gln Tyr Gly Lys Arg Leu Thr Val Val Gly Ile His
 85 90 95
 55 Ala Gly Pro Gly Ser Leu Val Pro Pro Leu Phe Arg Thr Glu Ala Gly
 100 105 110
 Asp Ala Tyr Tyr Ser Lys Phe Ala Asn Asn Thr Pro Leu Pro Ala Leu
 115 120 125
 60 Met Val Ser Arg Lys Lys Phe Gly Ser Ser Tyr Val Tyr Asp Lys Ser
 130 135 140
 Tyr Lys Thr Trp Asp Val Pro Ile Ala Glu Gln Met Glu Gln Lys Ala
 145 150 155 160
 Lys Ile Asn Ile Phe Ala Val Ala Glu Tyr Thr Asp Thr Gln Lys Ile
 165 170 175
 65 Lys Val Thr Val Lys Gly Lys Ile Leu Glu Gly Asn Thr Leu Pro Lys
 180 185 190
 Ser Met Val Gln Val Tyr Leu Leu Glu Asp Lys Leu Ile Ala Pro Gln
 195 200 205
 70 Val Asp Gly Asn Thr Thr Val Glu Asn Tyr Glu His Asn His Val Leu
 210 215 220
 Arg Gly Ala Val Asn Gly Ile Trp Gly Glu Glu Phe Val Asn Leu Lys
 225 230 235 240
 Asp Tyr Leu Tyr Thr Tyr Ala Val Glu Pro Leu Ser Gly Met Ser Phe
 245 250 255
 75 Val Ala Glu Asn Tyr Ser Ile Val Ala Phe Val Tyr Asp Val Gln Thr

WO 99/29870

PCT/AU98/01023

374/ 490

5 Phe Glu Val Tyr Asp Val Val His Val Lys Ile Asn Pro Gln Ser Asp
260 265 270
275 280 285
Gly Lys
290

(2) INFORMATION FOR SEQ ID NO:434

10 (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 223 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

20 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...223

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:434

30 Met Lys Lys Ser Ser Val Val Ala Ser Val Leu Ala Val Ala Leu Val
1 5 10 15
Phe Ala Gly Cys Gly Leu Asn Asn Met Ala Lys Gly Gly Leu Ile Gly
20 25 30
Ala Gly Val Gly Gly Ala Ile Gly Ala Gly Val Gly Asn Val Ala Gly
35 40 45
Asn Thr Ala Val Gly Ala Ile Val Gly Thr Ala Val Gly Gly Ala Ala
50 55 60
Gly Ala Leu Ile Gly Lys Lys Met Asp Lys Gln Lys Lys Glu Leu Glu
65 70 75 80
Ala Ala Val Pro Asp Ala Thr Ile Gln Thr Val Asn Asp Gly Glu Ala
85 90 95
Ile Leu Val Thr Phe Asp Ser Gly Ile Leu Phe Ala Thr Asn Ser Ser
100 105 110
Thr Leu Ser Pro Asn Ser Arg Thr Ala Leu Thr Lys Phe Ala Ala Asn
115 120 125
Met Asn Lys Asn Pro Asp Thr Asp Ile Arg Ile Val Gly His Thr Asp
130 135 140
Asn Thr Gly Ser Asp Lys Ile Asn Asp Pro Leu Ser Glu Arg Arg Ala
145 150 155 160
Ala Ser Val Tyr Ser Phe Leu Asn Ser Gln Gly Val Ser Met Ser Arg
165 170 175
Met Ala Ala Glu Gly Arg Gly Ser His Glu Pro Val Ala Asp Asn Ser
180 185 190
Thr Val Ala Gly Arg Ser Ala Asn Arg Arg Val Glu Val Tyr Ile Leu
195 200 205
Pro Asn Ala Lys Met Ile Glu Gln Ala Gln Gln Gly Thr Leu Lys
210 215 220

55 (2) INFORMATION FOR SEQ ID NO:435

60 (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 337 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

65 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

70 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...337

75 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:435

375 / 490

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Met Ser Lys Lys Ser Ile Leu Leu Leu Cys Cys Ser Leu Cys Phe Ile
1      5      10      15
Ser Ala Thr Lys Ala Val Thr Pro Val Arg Asn Val Arg Asn Ser Gln
20      25      30
5 Val Asn Ser Lys Ala Lys Thr Glu Arg Thr Lys Pro Ser Asp Ser Val
35      40      45
Arg Tyr Ile Ser Asn Met Ile Ala Asp Arg Leu Glu Phe Arg Asn Lys
50      55      60
10 Ile Ser Ser Glu Lys Glu Val Arg Lys Ala Glu Tyr Glu Asn Arg Leu
65      70      75      80
Ala Met Glu Ala Leu Asn Tyr Pro Ala Ile Asp Leu Tyr Gly Glu Asp
85      90      95
Ser Trp Ser Glu Tyr Val Asn Pro Phe Val Gly Ala Gly Thr Asp Val
100      105      110
15 Glu Ile Pro Asn Ser Tyr Asp Ile Asp Cys Ser Ser Phe Val Met Pro
115      120      125
Val Glu Asp Lys Gln Val Thr Ser Gln Phe Gly Tyr Arg Arg Arg Phe
130      135      140
20 Gly Arg Met His Tyr Gly Ile Asp Leu Ser Val Asn Arg Gly Asp Thr
145      150      155      160
Ile Arg Ala Ala Phe Asp Gly Lys Val Arg Val Arg Ser Tyr Glu Ala
165      170      175
Arg Gly Tyr Gly Tyr Tyr Ile Val Leu Arg His Pro Asn Gly Leu Glu
180      185      190
25 Thr Val Tyr Gly His Met Ser Arg Gln Leu Val Asp Glu Asn Gln Ile
195      200      205
Val Arg Ala Gly Gln Pro Ile Gly Leu Gly Gly Ser Thr Gly Arg Ser
210      215      220
30 Thr Gly Pro His Leu His Phe Glu Thr Arg Phe Met Gly Ile Pro Ile
225      230      235      240
Asn Pro Ser Thr Ile Ile Asp Phe Asp Asn Gly Val Pro Leu Arg Asp
245      250      255
Ile Tyr Thr Phe Lys Arg Gly Ser Asn Ser Arg Tyr Ala Lys Ala Ser
260      265      270
35 Lys Thr Ser Ser Arg Tyr Ala Lys Lys Gly Lys Lys Gly Arg Gln Ala
275      280      285
Ser Ser Pro Met Thr Tyr Arg Ile Lys Lys Gly Asp Thr Leu Glu Thr
290      295      300
40 Ile Ala Lys Arg His Gly Thr Ser Val Gln Lys Leu Cys Ala Thr Asn
305      310      315      320
Gly Ile Gly Lys Ser Lys Ile Leu Thr Pro Gly Lys Ala Leu Arg Ile
325      330      335
Lys

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- 45 (2) INFORMATION FOR SEQ ID NO:436
- 50 (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 151 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 55 (11) MOLECULE TYPE: protein
- (11) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
- 60 (1x) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...151
- 65 (x1) SEQUENCE DESCRIPTION: SEQ ID NO:436

```

Met Ala Lys Ile Asn Phe Tyr Ala Glu Gly Val Ser Leu Pro Arg Ile
1      5      10      15
Arg Arg Arg Ile Val Gly Lys Trp Ile Ala Glu Val Cys Ser Arg Tyr
20      25      30
70 Gly Lys Ala Val Gly Glu Ile Ser Tyr Leu Phe Cys Asp Asp Glu Tyr
35      40      45
Ile Leu Lys Ala Asn Gln Glu Phe Leu Asp His Asp Tyr Tyr Thr Asp
50      55      60
75 Ile Ile Thr Phe Asp Ser Cys Glu Ala Asp Thr Val Asn Gly Asp Leu
65      70      75      80

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376/ 490

Leu Ile Ser Leu Asp Thr Val Arg Ser Asn Ala Arg Ala Leu Asp Leu
 85 90 95
 Arg Tyr Glu Asp Glu Leu His Arg Val Ile Ile His Gly Ile Leu His
 100 105 110
 5 Leu Cys Gly Leu Lys Asp Lys Ser Lys Lys Asp Glu Ala Gln Met Arg
 115 120 125
 Ala Ala Glu Glu Lys Ala Leu Val Met Leu Arg Glu Thr Ile Gly Ser
 130 135 140
 10 Glu Leu Ser Leu Leu His Thr
 145 150

(2) INFORMATION FOR SEQ ID NO:437

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 391 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...391
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:437

Met Lys Val Lys Tyr Leu Met Leu Thr Leu Val Gly Ala Ile Ala Leu
 1 5 10 15
 35 Asn Ala Ser Ala Gln Glu Asn Thr Val Pro Ala Thr Gly Gln Leu Pro
 20 25 30
 Ala Lys Asn Val Ala Phe Ala Arg Asn Lys Ala Gly Ser Asn Trp Phe
 35 40 45
 Val Thr Leu Gln Gly Gly Val Ala Ala Gln Phe Leu Asn Asp Asn Asn
 50 55 60
 40 Asn Lys Asp Leu Met Asp Arg Leu Gly Ala Ile Gly Ser Leu Ser Val
 65 70 75 80
 Gly Lys Tyr His Ser Pro Phe Phe Ala Thr Arg Leu Gln Ile Asn Gly
 85 90 95
 45 Gly Gln Ala His Thr Phe Leu Gly Lys Asn Gly Glu Gln Glu Ile Asn
 100 105 110
 Thr Asn Phe Gly Ala Ala His Phe Asp Phe Met Phe Asp Val Val Asn
 115 120 125
 Tyr Phe Ala Pro Tyr Arg Glu Asn Arg Phe Phe His Leu Ile Pro Trp
 130 135 140
 50 Val Gly Val Gly Tyr Gln His Lys Phe Ile Gly Ser Glu Trp Ser Lys
 145 150 155 160
 Asp Asn Val Glu Ser Leu Thr Ala Asn Val Gly Val Met Met Ala Phe
 165 170 175
 55 Arg Leu Gly Lys Arg Val Asp Phe Val Ile Glu Ala Gln Ala His
 180 185 190
 Ser Asn Leu Asn Leu Ser Arg Ala Tyr Asn Ala Lys Lys Thr Pro Val
 195 200 205
 Phe Glu Asp Pro Ala Gly Arg Tyr Tyr Asn Gly Phe Gln Gly Met Ala
 210 215 220
 60 Thr Ala Gly Leu Asn Phe Arg Leu Gly Ala Val Gly Phe Asn Ala Ile
 225 230 235 240
 Unk Pro Met Asp Tyr Ala Leu Ile Asn Asp Leu Asn Gly Gln Ile Asn
 245 250 255
 65 Arg Leu Arg Ser Glu Val Glu Glu Leu Ser Lys Arg Pro Val Ser Cys
 260 265 270
 Pro Glu Cys Pro Glu Val Thr Pro Val Thr Lys Thr Glu Asn Ile Leu
 275 280 285
 Thr Glu Lys Ala Val Leu Phe Arg Phe Asp Ser His Val Val Asp Lys
 290 295 300
 70 Asp Gln Leu Ile Asn Leu Tyr Asp Val Ala Gln Phe Val Lys Glu Thr
 305 310 315 320
 Asn Glu Pro Ile Thr Val Val Gly Tyr Ala Asp Pro Thr Gly Asn Thr
 325 330 335
 75 Gln Tyr Asn Glu Lys Leu Ser Glu Arg Arg Ala Lys Ala Val Val Asp
 340 345 350

WO 99/29870

PCT/AU98/01023

377/ 490

5 Val Leu Thr Gly Lys Tyr Gly Val Pro Ser Glu Leu Ile Ser Val Glu
355 360 365
Trp Lys Gly Asp Ser Thr Gln Pro Phe Ser Lys Lys Ala Trp Asn Arg
370 375 380
Val Val Ile Val Arg Ser Lys
385 390

(2) INFORMATION FOR SEQ ID NO:438

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 385 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- 15 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
- 20 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
(iii) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION: 1...385
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:438

Met Thr Tyr Arg Ile Met Lys Ala Lys Ser Leu Leu Leu Ala Leu Ala
1 5 10 15
Gly Leu Ala Cys Thr Phe Ser Ala Thr Ala Gln Glu Ala Thr Thr Gln
20 25 30
Asn Lys Ala Gly Met His Thr Ala Phe Gln Arg Asp Lys Ala Ser Asp
35 40 45
His Trp Phe Ile Asp Ile Ala Gly Gly Ala Gly Met Ala Leu Ser Gly
50 55 60
Trp Asn Asn Asp Val Asp Phe Val Asp Arg Leu Ser Ile Val Pro Thr
65 70 75 80
Phe Gly Ile Gly Lys Trp His Glu Pro Tyr Phe Gly Thr Arg Leu Gln
85 90 95
Phe Thr Gly Phe Asp Ile Tyr Gly Phe Pro Gln Gly Ser Lys Glu Arg
100 105 110
Asn His Asn Tyr Phe Gly Asn Ala His Leu Asp Phe Met Phe Asp Leu
115 120 125
Thr Asn Tyr Phe Gly Val Tyr Arg Pro Asn Arg Val Phe His Ile Ile
130 135 140
Pro Trp Ala Gly Ile Gly Phe Gly Tyr Lys Phe His Ser Glu Asn Ala
145 150 155 160
Asn Gly Glu Lys Val Gly Ser Lys Asp Asp Met Thr Gly Thr Val Asn
165 170 175
Val Gly Leu Met Leu Lys Phe Arg Leu Ser Arg Val Val Asp Phe Asn
180 185 190
Ile Glu Gly Gln Ala Phe Ala Gly Lys Met Asn Phe Ile Gly Thr Lys
195 200 205
Arg Gly Lys Ala Asp Phe Pro Val Met Ala Thr Ala Gly Leu Thr Phe
210 215 220
Asn Leu Gly Lys Thr Glu Trp Thr Glu Ile Val Pro Met Asp Tyr Ala
225 230 235 240
Leu Val Asn Asp Leu Asn Asn Gln Ile Asn Ser Leu Arg Gly Gln Val
245 250 255
Glu Glu Leu Ser Arg Arg Pro Val Ser Cys Pro Glu Cys Pro Glu Pro
260 265 270
Thr Gln Pro Thr Val Thr Arg Val Val Asp Asn Val Val Tyr Phe
275 280 285
Arg Ile Asn Ser Ala Lys Ile Asp Arg Asn Gln Glu Ile Asn Val Tyr
290 295 300
Asn Thr Ala Glu Tyr Ala Lys Thr Asn Asn Ala Pro Ile Lys Val Val
305 310 315 320
Gly Tyr Ala Asp Glu Lys Thr Gly Thr Ala Ala Tyr Asn Met Lys Leu
325 330 335
Ser Glu Arg Arg Ala Lys Ala Val Ala Lys Met Leu Glu Lys Tyr Gly
340 345 350
Val Ser Ala Asp Arg Ile Thr Ile Glu Trp Lys Gly Ser Ser Glu Gln
355 360 365
Ile Tyr Glu Glu Asn Ala Trp Asn Arg Ile Val Val Met Thr Ala Ala
370 375 380

WO 99/29870

PCT/AU98/01023

378/490

Glu
385

- 5 (2) INFORMATION FOR SEQ ID NO:439
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 190 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- 10 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 15 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
(A) NAME/KEY: misc feature
20 (B) LOCATION: 1...190
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:439

25 Met Glu Phe Phe Met Leu Phe Ile Ala Ala Val Phe Val Asn Asn Val
1 5 10 15
Val Leu Ser Gln Phe Leu Gly Ile Cys Pro Phe Leu Gly Val Ser Lys
20 25 30
Lys Val Asp Thr Ser Ile Gly Met Gly Ala Ala Val Thr Phe Val Leu
35 40 45
Ala Leu Ala Thr Leu Val Thr Phe Leu Ile Gln Lys Phe Val Leu Asp
50 55 60
Arg Phe Gly Leu Gly Phe Met Gln Thr Ile Ala Phe Ile Leu Val Ile
65 70 75 80
Ala Ala Leu Val Gln Met Val Glu Ile Ile Leu Lys Lys Val Ser Pro
85 90 95
Pro Leu Tyr Gln Ala Leu Gly Val Phe Leu Pro Leu Ile Thr Thr Asn
100 105 110
Cys Cys Val Leu Gly Val Ala Ile Leu Val Ile Gln Lys Asp Tyr Thr
115 120 125
40 Leu Leu Gln Ser Phe Val Tyr Ala Ile Ser Thr Ala Ile Gly Phe Thr
130 135 140
Leu Ala Met Val Thr Phe Ala Gly Ile Arg Glu Gln Leu Asp Met Thr
145 150 155 160
45 Asn Leu Pro Lys Ala Met Lys Gly Ile Pro Ser Ala Leu Leu Ala Ala
165 170 175
Glu Ile Leu Ala Met Ala Phe Met Gly Phe Ser Gly Ile Ala
180 185 190

- 50 (2) INFORMATION FOR SEQ ID NO:440
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 186 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- 55 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 60 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
65 (B) LOCATION: 1...186
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:440

70 Met Leu Phe Ile Ala Ala Val Phe Val Asn Asn Val Val Leu Ser Gln
1 5 10 15
Phe Leu Gly Ile Cys Pro Phe Leu Gly Val Ser Lys Lys Val Asp Thr
20 25 30
Ser Ile Gly Met Gly Ala Ala Val Thr Phe Val Leu Ala Leu Ala Thr
35 40 45
75 Leu Val Thr Phe Leu Ile Gln Lys Phe Val Leu Asp Arg Phe Gly Leu

WO 99/29870

PCT/AU98/01023

379/ 490

50 55 60
Gly Phe Met Gln Thr Ile Ala Phe Ile Leu Val Ile Ala Ala Leu Val
65 70 75 80
Gln Met Val Glu Ile Ile Leu Lys Lys Val Ser Pro Pro Leu Tyr Gln
85 90 95
Ala Leu Gly Val Phe Leu Pro Leu Ile Thr Thr Asn Cys Cys Val Leu
100 105 110
Gly Val Ala Ile Leu Val Ile Gln Lys Asp Tyr Thr Leu Leu Gln Ser
115 120 125
10 Phe Val Tyr Ala Ile Ser Thr Ala Ile Gly Phe Thr Leu Ala Met Val
130 135 140
Thr Phe Ala Gly Ile Arg Glu Gln Leu Asp Met Thr Asn Leu Pro Lys
145 150 155 160
Ala Met Lys Gly Ile Pro Ser Ala Leu Leu Ala Ala Gly Ile Leu Ala
15 165 170 175
Met Ala Phe Met Gly Phe Ser Gly Ile Ala
180 185

(2) INFORMATION FOR SEQ ID NO:441

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 833 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441

40 Met Lys Gln Leu Asn Ile Ile Ser Phe Ile Ile Ala Phe Leu Phe Leu
1 5 10 15
Gly Thr Ser Ala Ser Ala Gln Gln Ser Gly Gly Ser Val Thr Gly Thr
20 25 30
Val Val Asp Lys Ser Ser Lys Glu Pro Ile Ala Tyr Val Gln Val Phe
35 40 45
45 Val Lys Gly Thr Thr Leu Gly Thr Ser Thr Asp Ala Asn Gly Asn Tyr
50 55 60
Ser Ile Lys Gly Ile Pro Ser Gly Asn Gln Thr Ile Val Ala Arg Leu
65 70 75 80
50 Met Gly Tyr Ser Thr Cys Glu Glu Lys Val His Ile Glu Lys Gly Gly
85 90 95
Ser Arg His Val Asp Leu Tyr Leu Thr Glu Glu Ile Leu Ser Leu Asp
100 105 110
Gly Val Val Val Ser Ala Asn Arg Asn Glu Thr Phe Arg Arg Gln Ala
115 120 125
55 Pro Ser Leu Val Thr Val Leu Ser Pro Glu Leu Phe Leu Lys Thr Asn
130 135 140
Ser Thr Asn Leu Ser Gln Gly Leu Lys Phe Gln Pro Gly Leu Arg Val
145 150 155 160
60 Glu Asp Asn Cys Gln Asn Cys Gly Phe Asn Gln Val Arg Ile Asn Gly
165 170 175
Leu Glu Gly Ala Tyr Ser Gln Ile Leu Ile Asp Ser His Pro Ile Phe
180 185 190
Ser Ser Leu Ala Gly Val Tyr Gly Leu Glu Gln Met Pro Ala Asn Met
195 200 205
65 Ile Glu Arg Val Glu Val Ile Arg Gly Gly Gly Ser Ala Leu Phe Gly
210 215 220
Ser Asn Ala Val Gly Gly Val Ile Asn Val Ile Thr Lys Glu Pro Leu
225 230 235 240
70 Arg Asn Ser Ala Glu Ile Ser His Ser Thr Met Thr Phe Asp His Ala
245 250 255
Lys Gly Trp Gly Ser Phe Gln Asn Thr Thr Gln Phe Asn Gly Ser Met
260 265 270
Leu Thr Glu Asp Arg Lys Ala Gly Val Met Val Phe Gly Gln His Asn
275 280 285
75 Tyr Arg Pro Gly Gln Asp Ile Asp Gly Asp Asn Phe Thr Glu Leu Pro

WO 99/29870

PCT/AU98/01023

380/ 490

290 295 300
 Asn Leu Arg Asn Arg Ser Leu Gly Phe Arg Ser Tyr Tyr Lys Thr Gly
 305 310 315 320
 5 Leu Tyr Ser Lys Ala Thr Leu Glu Tyr His Ser Met Gln Glu Tyr Arg
 325 330 335
 Arg Gly Gly Asp Arg Leu Asp Asn Pro Pro Phe Glu Ala Gln Ile Ala
 340 345 350
 Glu Tyr Leu Gln His Tyr Ile Asn Gly Gly Ser Phe Lys Phe Asp Gln
 355 360 365
 10 Gly Phe Ser Gly Gly Lys Asp Phe Phe Ser Leu Tyr Ala Ser Ala Gln
 370 375 380
 Asp Val Gln Arg Arg Ser Tyr Tyr Gly Gly Gly Asp Tyr Thr Glu Asn
 385 390 395 400
 15 Leu Leu Asn Gly Ala Val Gln Ser Gly Ser Thr Glu Ser Asp Glu Tyr
 405 410 415
 Asn Asp Ala Phe Thr Ala Leu Thr Ser Tyr Gly Thr Thr Lys Gly Phe
 420 425 430
 Asp Leu Gln Gly Gly Gly Met Tyr Arg His Thr Phe Gly Glu Asn Trp
 435 440 445
 20 Asp Phe Thr Gly Gly Leu Glu Tyr Ile Tyr Gly Gln Leu Asp Asp Arg
 450 455 460
 Ser Gly Tyr Arg Pro Ser Lys Ile Asp Gln Asn Thr Ser Thr Phe Ser
 465 470 475 480
 25 Gln Tyr Asp Gln Leu Glu Tyr Lys Thr Glu Lys Leu Ser Ala Leu Ile
 485 490 495
 Gly Ala Arg Ile Asp Tyr Val Leu Leu Asn Gln Asp Gly Lys Arg Tyr
 500 505 510
 Ile Asp Pro Leu Phe Ile Phe Ser Pro Arg Ala Asn Val Arg Tyr Asn
 515 520 525
 30 Pro Asn Lys Asn Leu Ser Phe Arg Leu Ser Tyr Ser Glu Gly Phe Arg
 530 535 540
 Ala Pro Gln Tyr Phe Asp Glu Asp Leu His Val Glu Leu Ala Gly Gly
 545 550 555 560
 35 Thr Pro Ile Ser Arg Val Leu Ser Pro Asn Leu Lys Glu Glu Arg Ser
 565 570 575
 Arg Ser Ile Ser Ala Ser Phe Asp Tyr Tyr His Arg Ala Asp Glu Trp
 580 585 590
 Gln Phe Asn Ile Met Gly Glu Ala Phe Ser Thr Phe Ile Ser Asn Gln
 595 600 605
 40 Phe Lys Pro Ser Asp Lys Val Glu Thr Thr Ser Asp Gly Lys Glu Trp
 610 615 620
 Ile Ile Arg Thr Ile Tyr Asn Asp Lys Asp Gly Val Ser Lys Val Tyr
 625 630 635 640
 45 Gly Val Asn Leu Glu Gly Arg Ile Ala Tyr Asn Lys Ser Phe Asp Leu
 645 650 655
 Gln Leu Gly Gly Thr Trp Gln Arg Ser Arg Tyr Gly Ser Ile Tyr Thr
 660 665 670
 Ala Val Glu Ala Asp Lys Thr Thr Gly Gln Ala Glu Ile Ser Val Lys
 675 680 685
 50 Asp Tyr Val Arg Thr Pro Asn Leu Tyr Gly Tyr Phe Val Ala Thr Val
 690 695 700
 Arg Pro Thr Glu His Phe Ala Ile Asn Leu Ser Gly Thr Phe Thr Gly
 705 710 715 720
 55 Lys Met Asp Val Val His Glu Ala Tyr Glu Gly Asp Ile Pro Ala Glu
 725 730 735
 His Ile Ala Pro Asp Gly Ser Phe Asp Phe Glu Met Asn Gly Gln Gln
 740 745 750
 Phe Lys Gly Leu Ala Glu Gly His Ala Lys Leu Val Lys Thr Pro Ala
 755 760 765
 60 Phe Ala Asp Ile Asp Leu Lys Leu Ser His Asp Phe His Leu Ala Ser
 770 775 780
 Thr Met Thr Leu Glu Leu Asn Ala Gly Ile Gln Asn Ile Phe Asn Ser
 785 790 795 800
 65 Tyr Gln Lys Asp Thr Asp Lys Gly Pro Gly Arg Ala Ser Thr Tyr Val
 805 810 815
 Tyr Gly Pro Met Gln Pro Arg Arg Ile Phe Val Gly Thr Lys Ile Asn
 820 825 830
 Phe

70

(2) INFORMATION FOR SEQ ID NO:442

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 891 amino acids

(B) TYPE: amino acid

75

SUBSTITUTE SHEET (Rule 26) (RO/AU)

WO 99/29870

PCT/AU98/01023

381/ 490

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

10 (ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442

15 Met Tyr Lys Lys Ile Ile Ala Val Ala Ala Leu Phe Cys Ala Ser Ile
1 5 10 15
Gly Ile Leu Lys Gly Gln Ser Ser Asp Leu Thr Pro Gln Asp Thr Ile
20 Tyr Ser Pro Glu Ile Ser Tyr Ala Lys Pro Ile His Lys Thr Ile Ala
35 40 45
Ser Ile Glu Ile Glu Gly Met Arg Ser Phe Asp Asp Phe Val Leu Arg
50 55 60
Asn Leu Ser Gly Leu Ala Val Gly Asp Glu Val Leu Ile Pro Gly Asp
25 65 70 75 80
Ala Met Ser Ala Ala Val Asn Arg Ile Met Arg Gln Gly Tyr Phe Ser
85 90 95
Asn Val Arg Ile Ile Ala Asp Lys Tyr Val Gly Asn Lys Val Tyr Leu
100 105 110
30 Lys Ile Ile Val Thr Glu Arg Pro Arg Ile Ser Lys Val Thr Phe Ser
115 120 125
Gly Val Lys Lys Ser Glu Arg Glu Asp Leu Glu Met Lys Ile Gly Leu
130 135 140
35 Arg Glu Gly Ile Gln Met Thr Arg Asn Asn Glu Asp Lys Val Arg Gln
145 150 155 160
Ile Val Gln Lys Tyr Phe Ser Glu Lys Gly Tyr Arg Asp Ala Ser Ile
165 170 175
Arg Ile Thr Gln Glu Pro Asp Leu Ser Lys Asp Gly Phe Val Asn Val
180 185 190
40 Leu Ile Ser Ile Glu Lys Lys Ser Lys Thr Lys Val Asn Glu Ile Tyr
195 200 205
Phe Ser Gly Asn Lys Ala Leu Ser Asn His Lys Leu Arg Met Ala Met
210 215 220
45 Lys Asn Thr Asn Ala Lys Phe Ser Leu Arg Lys His Ile Arg Ser Ser
225 230 235 240
Phe Leu Lys Leu Phe Ser Thr His Lys Phe Val Glu Glu Ser Tyr Arg
245 250 255
Glu Asp Leu Val Arg Leu Ile Glu Lys Tyr Gln Glu Tyr Gly Tyr Arg
260 265 270
50 Asp Ala Glu Ile Leu Thr Asp Ser Val Val Lys Ala Pro Asp Gly Lys
275 280 285
Arg Val Asp Ile Tyr Leu Asn Ile Glu Glu Gly Gln Lys Tyr Tyr Ile
290 295 300
55 Lys Asp Val Asn Phe Val Gly Asn Ser Gln Tyr Pro Ser Glu Tyr Leu
305 310 315 320
Glu Arg Val Leu Gly Ile Lys Ser Gly Asp Val Tyr Asn Gln Arg Arg
325 330 335
Leu Ala Lys Arg Leu Asn Glu Asp Glu Asp Ala Val Gly Asn Leu Tyr
340 345 350
60 Tyr Asn Asn Gly Tyr Ile Phe Ala Trp Val Asp Pro Val Glu Thr Asn
355 360 365
Val Val Gly Asp Ser Val Ser Leu Asp Ile Arg Ile Ala Glu Gly Lys
370 375 380
65 Gln Ala Asn Ile Asn Lys Val Ile Ile Lys Gly Asn Thr Val Val Tyr
385 390 395 400
Glu Asp Val Val Arg Arg Glu Leu Tyr Thr Lys Pro Gly Gln Leu Phe
405 410 415
Ser Arg Glu Asp Ile Ile Asn Ser Ile Arg Leu Ile Asn Gln Leu Gly
420 425 430
70 His Phe Asp Ala Glu Lys Ser Ile Pro Arg Pro Ile Pro Asn Pro Glu
435 440 445
Thr Gly Thr Val Asp Ile Glu Tyr Asp Leu Val Pro Arg Ser Ser Asp
450 455 460
75 Gln Leu Glu Leu Ser Val Gly Trp Ser Gln Ser Gly Leu Leu Phe Arg
465 470 475 480

WO 99/29870

PCT/AU98/01023

382/490

5 Gly Ala Ile Lys Phe Thr Asn Phe Ser Val Gly Asn Leu Leu His Pro
485 490 495
Ser Met Tyr Lys Lys Gly Ile Ile Pro Gln Gly Asp Gly Gln Thr Leu
500 505 510
10 Ser Leu Ser Ala Gln Thr Asn Gly Lys Tyr Tyr Gln Gln Tyr Ser Val
515 520 525
Thr Phe Met Asp Pro Trp Phe Gly Gly Lys Arg Pro Asp Met Phe Ser
530 535 540
Phe Ser Ala Phe Tyr Ser Lys Thr Thr Ala Ile Asp Ser Lys Phe Tyr
545 550 555 560
Asn Ser Asn Ala Gly Asn Tyr Tyr Asn Ala Tyr Tyr Asn Ser Tyr Tyr
565 570 575
Asn Asn Tyr Asn Ser Tyr Tyr Asn Gly Met Ser Asn Tyr Thr Gly Asp
580 585 590
15 Leu Tyr Thr Gln Ala Ser Asp Pro Asp Arg Ser Leu Gln Met Leu Gly
595 600 605
Thr Ser Ile Gly Tyr Gly Lys Arg Leu Thr Trp Pro Asp Asn Trp Phe
610 615 620
20 Gln Ile Tyr Thr Ser Leu Asn Tyr Thr Tyr Arg Leu Arg Asn Trp
625 630 635 640
Ser Tyr Asn Thr Phe Gln Asn Phe His His Gly Ser Ala Asn Asp Leu
645 650 655
Asn Leu Glu Leu Arg Leu Ser Arg Thr Ser Ile Asp Asn Pro Ile Tyr
660 665 670
25 Thr Arg Ser Gly Ser Asp Phe Met Val Ser Val Ala Ala Thr Leu Pro
675 680 685
Tyr Ser Leu Trp Asp Asn His Asp Tyr Ala Ser Gln Asn Leu Ser Val
690 695 700
30 Ser Asp Arg Tyr Arg Phe Ile Glu Tyr His Lys Trp Lys Phe Arg Gly
705 710 715 720
Arg Val Phe Thr Pro Leu Leu Asn Pro Ala Thr His Lys Tyr Thr Pro
725 730 735
Val Leu Met Ser Arg Val Glu Gly Ala Val Leu Gly Ser Tyr Asn Ser
740 745 750
35 Asn Lys Lys Ser Pro Phe Gly Thr Phe Tyr Met Gly Gly Asp Gly Met
755 760 765
Ser Ser Tyr Tyr Gly Gly Tyr Met Asn Glu Thr Ile Gly Leu Arg Gly
770 775 780
40 Tyr Lys Asn Gly Ser Ile Ala Gly Asn Asn Tyr Asp Tyr Ala Tyr Ala
785 790 795 800
Tyr Met Arg Leu Thr Met Glu Leu Arg Phe Pro Ile Leu Phe Glu Asn
805 810 815
Ser Phe Asn Ala Trp Leu Leu Ala Phe Ala Glu Ala Gly Asn Ala Trp
820 825 830
45 Arg Ser Ile Asp Asn Tyr Asn Pro Phe Asn Leu Lys Arg Ser Ala Gly
835 840 845
Val Gly Lcu Arg Val Thr Leu Pro Met Val Gly Met Leu Gly Ile Asp
850 855 860
50 Trp Gly Tyr Gly Phe Asp Arg Pro Asp Asn Ser Leu Gln Arg Gly Gly
865 870 875 880
Ser Asn Val His Phe Val Leu Gly Gln Glu Phe
885 890

(2) INFORMATION FOR SEQ ID NO:443

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION: 1...174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443

Met Asn Gly Asp Met Lys Arg Phe Leu Ile Leu Ile Gly Phe Ala Leu
1 5 10 15

383/490

Ala Val Ala Phe Ser Gly Phe Ser Gln Lys Phe Ala Leu Val Asp Met
 20 25 30
 Glu Tyr Ile Leu Arg Asn Ile Pro Asp Tyr Glu Met Met Asn Glu Gln
 35 40 45
 5 Leu Glu Gln Val Ser Lys Lys Trp Gln Asn Glu Ile Glu Ala Leu Glu
 50 55 60
 Asn Glu Ala Gln Ser Met Tyr Lys Lys Tyr Gln Ser Asp Leu Val Phe
 65 70 75 80
 10 Leu Ser Ala Ala Gln Lys Lys Thr Gln Glu Glu Ala Ile Val Lys Lys
 85 90 95
 Glu Gln Gln Ala Ser Glu Leu Lys Arg Lys Tyr Phe Gly Pro Glu Gly
 100 105 110
 Glu Leu Tyr Lys Lys Arg Ser Asp Leu Met Lys Pro Ile Gln Asp Glu
 115 120 125
 15 Ile Trp Asn Ala Ile Lys Glu Ile Ala Lys Arg Asn Asn Tyr Gln Met
 130 135 140
 Val Leu Asp Arg Gly Thr Ser Gly Ile Ile Phe Ala Ser Pro Ser Ile
 145 150 155 160
 20 Asp Ile Ser Asp Leu Val Leu Ser Lys Met Gly Phe Ser Lys
 165 170

(2) INFORMATION FOR SEQ ID NO:444

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Porphyromonas gingivalis*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...170
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:444

Met Lys Arg Phe Leu Ile Leu Ile Gly Phe Ala Leu Ala Val Ala Phe
 1 5 10 15
 45 Ser Gly Phe Ser Gln Lys Phe Ala Leu Val Asp Met Glu Tyr Ile Leu
 20 25 30
 Arg Asn Ile Pro Asp Tyr Glu Met Met Asn Glu Gln Leu Glu Gln Val
 35 40 45
 Ser Lys Lys Trp Gln Asn Glu Ile Glu Ala Leu Glu Asn Glu Ala Gln
 50 55 60
 Ser Met Tyr Lys Lys Tyr Gln Ser Asp Leu Val Phe Leu Ser Ala Ala
 65 70 75 80
 Gln Lys Lys Thr Gln Glu Glu Ala Ile Val Lys Lys Glu Gln Gln Ala
 85 90 95
 55 Ser Glu Leu Lys Arg Lys Tyr Phe Gly Pro Glu Gly Glu Leu Tyr Lys
 100 105 110
 Lys Arg Ser Asp Leu Met Lys Pro Ile Gln Asp Glu Ile Trp Asn Ala
 115 120 125
 Ile Lys Glu Ile Ala Lys Arg Asn Asn Tyr Gln Met Val Leu Asp Arg
 130 135 140
 60 Gly Thr Ser Gly Ile Ile Phe Ala Ser Pro Ser Ile Asp Ile Ser Asp
 145 150 155 160
 Leu Val Leu Ser Lys Met Gly Phe Ser Lys
 165 170

65 (2) INFORMATION FOR SEQ ID NO:445

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 163 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES

384/ 490

(v1) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445

10 Met Lys Lys Phe Phe Leu Met Leu Leu Met Ala Leu Pro Leu Ser Leu
1 5 10 15
Leu Ala Gln Lys Val Ala Val Val Asn Thr Glu Glu Ile Ile Ser Lys
20 25 30
Met Pro Glu Gln Val Ala Ala Thr Lys Gln Leu Asn Glu Leu Ala Glu
15 35 40 45
Lys Tyr Arg Leu Asp Leu Lys Ser Met Asp Asp Glu Phe Ala Lys Lys
50 55 60
Thr Glu Glu Phe Val Lys Glu Lys Asp Ser Leu Leu Glu Asn Ile Arg
65 70 75 80
20 Asn Arg Arg Gln Gln Glu Leu Gln Asp Ile Gln Thr Arg Tyr Gln Gln
85 90 95
Ser Tyr Glu Thr Met Gln Glu Asp Leu Gln Lys Arg Gln Gln Gln Leu
100 105 110
Phe Ala Pro Ile Gln Gln Lys Val Ala Asp Ala Ile Lys Lys Val Gly
115 120 125
25 Asp Glu Glu Asn Cys Ala Tyr Ile Met Glu Ala Gly Met Met Leu Tyr
130 135 140
Thr Gly Ala Thr Ala Ile Asp Leu Thr Ala Lys Val Lys Ala Lys Leu
145 150 155 160
30 Gly Ile Lys

(2) INFORMATION FOR SEQ ID NO:446

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 827 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...827

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:446

Met Lys Glu Ala Ile Pro Arg Lys Asn Lys Tyr Ile Lys Leu Asn Gly
1 5 10 15
55 Ile Tyr Arg Leu Ser Phe Ile Leu Leu Cys Cys Leu Leu Cys Ser Gln
20 25 30
Ala Ala Met Ala Gln Gly Val Arg Val Ser Gly Tyr Val Leu Asp Arg
35 40 45
60 Gly Glu Lys Pro Ile Pro Phe Ala Gly Val Lys Val Arg Gly Thr Gly
50 55 60
Thr Gly Ala Thr Thr Asn Leu Lys Gly Tyr Tyr Glu Phe Arg Met Lys
65 70 75 80
Ala Thr Thr Asp Ser Ile Thr Ile Glu Phe Ser Ser Met Gly Tyr Gln
85 90 95
65 Gly Val Ser Arg Ser Phe Pro Ser Leu Thr Lys Asp Thr Arg Leu Asn
100 105 110
Val Arg Leu Ala Glu Ala Glu Met Glu Leu Ser Ser Val Thr Val Gln
115 120 125
70 Ala Thr Lys Arg Arg Leu Asn Thr Met Glu Arg Val Asn Thr Arg Asp
130 135 140
Leu Arg Val Asn Ala Gly Pro Thr Gly Gly Val Glu Ser Leu Ile Ser
145 150 155 160
Thr Tyr Ala Gly Val Thr Gln Asn Asn Glu Leu Ser Ser Gln Tyr Ser
165 170 175
75 Val Arg Gly Gly Ser Tyr Asp Glu Asn Met Val Tyr Val Asn Gly Val

WO 99/29870

PCT/AU98/01023

387/ 490

5 Gln Pro Val Asn Ser Ser Ala Asp Asp Phe Gly Leu Ala Val Glu Pro
385 390 395 400
Lys Gly Lys Asn Lys Glu Glu Ala Leu Pro Asp Asn Gly Val Lys Gly
405 410 415
Val Phe Cys Ser Asn Arg Gly Asp Ala Arg Gly Trp Pro His Leu Phe
420 425 430
His Phe Glu Leu Pro Ala Ile Tyr Thr Glu Ile Gln Gly Tyr Val Met
435 440 445
10 Asp Arg Glu Glu Asn Pro Ile Ala Gly Ala Thr Val Arg Ile Val Gly
450 455 460
Glu Arg Gly Pro Val Gly Gln Gly Phe Val Thr Thr Arg Asp Asp Gly
465 470 475 480
Ser Tyr Lys Met Ser Val Gln Gly Asp Thr Arg Tyr Val Met Leu Ala
485 490 495
15 Gly Ala Ser Gly Tyr Leu Asn Gln Tyr Val Glu Leu Lys Trp Asp Thr
500 505 510
Ala Lys Gln Ser Glu Thr Tyr Tyr Val Asp Phe Phe Leu Ala Ser Arg
515 520 525
20 Glu Lys Ala Glu Gly Leu Gln Asn Ile Phe Tyr Asp Phe Asp Lys Ala
530 535 540
Thr Leu Arg Pro Glu Ser Met Lys Ser Leu Asp Glu Leu Ile Arg Ile
545 550 555 560
Leu Thr Asp Asn Pro Asp Ile Arg Ile Glu Leu Gly Ser His Ala Asp
565 570 575
25 Arg Lys Gly Pro Asp Ala Tyr Asn Leu Gly Leu Ser Asp Arg Arg Ala
580 585 590
Lys Ser Val Val Asp Tyr Leu Thr Ser Arg Gly Ile Ala Ala Asp Arg
595 600 605
30 Leu Thr Trp Lys Gly Tyr Gly Lys Ser Val Pro Lys Thr Val Thr Ala
610 615 620
Lys Ile Ala Glu Arg His Asp Phe Leu Lys Glu Gly Asp Val Leu Thr
625 630 635 640
Glu Glu Phe Val Ala Pro Leu Thr Glu Glu Gln Gln Ser Val Cys Asp
645 650 655
35 Gln Leu Asn Arg Arg Thr Glu Phe Arg Val Ile Glu Glu Glu Leu Arg
660 665 670

(2) INFORMATION FOR SEQ ID NO:448

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 708 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
45 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
50 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...708
55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:448

Met Lys Lys Phe Phe Phe Ala Leu Leu Ser Ile Gly Ile Ser Ala Gln
1 5 10 15
60 Ala Phe Ala Lys Thr Asp Asn Val Pro Thr Asp Ser Leu Arg Val His
20 25 30
Asn Leu Gln Thr Val Thr Val Tyr Ser Thr Arg Thr Ala Val Pro Leu
35 40 45
65 Lys Lys Ile Pro Ala Lys Met Glu Leu Ile Ser Ser Arg Asn Ile Lys
50 55 60
Gln Ser Gly Phe Asn Asn Met Thr Asp Ile Leu Lys Thr Gln Ser Ser
65 70 75 80
Leu Asp Val Ile Gln Tyr Pro Gly Phe Ser Ser Asn Ile Gly Ile Arg
85 90 95
70 Gly Phe Lys Pro Ser Gly Lys Tyr Val Thr Val Leu Val Asn Gly Ile
100 105 110
Pro Ala Gly Thr Asp Asn Ile Ser Thr Leu Asn Thr Ser Asn Ile Glu
115 120 125
75 Gln Ile Glu Ile Leu Lys Gly Pro Phe Ser Ser Ile Tyr Gly Thr Asn
130 135 140

WO 99/29870

PCT/AU98/01023

388/490

Ala Met Gly Gly Val Val Asn Ile Ile Thr His Lys Ser Lys Asp Lys
145 150 155 160
Ile His Gly Asn Val Ser Leu Phe Gly Gly Ser Tyr Gln Thr Met Ala
165 170 175
5 Gly Ser Phe Asn Leu Gly Gly Arg Phe Glu Asp Ile Phe Ser Phe Asp
180 185 190
Leu Ser Leu Gly Leu Asp Lys Gln Asn Lys Asp Tyr Lys Thr Gly Ser
195 200 205
10 Asn Asn Phe Leu Ser Leu Ser Lys Leu Glu Glu Ala Ile Val Asp Val
210 215 220
Asn Ala Thr Lys Asn Lys Lys Met Lys Gly Ser Asp Tyr Thr Val Ala
225 230 235 240
Thr Gly Arg Leu Arg Phe Gly Ile Asp Phe Thr Pro Glu Trp Ser Leu
245 250 255
15 Asn Leu Tyr Gln Asn Val Phe Leu Gly Asp Ala Ile Pro Val Gly Gly
260 265 270
Ser Ile Trp Gly Val Tyr Gly Glu Ser Lys Lys Asn Leu Asn Arg Ser
275 280 285
20 Ser Thr Ser Phe Glu Leu Leu Gly Lys His Gly Cys His Thr Leu Gln
290 295 300
Phe Ser Pro Tyr Phe Asn Ile Glu Lys Ser Glu Asn Tyr Asn Asn Ala
305 310 315 320
Asp Pro Thr Gly Phe Ile Asn Tyr Lys Ser Asp Tyr Tyr Thr Tyr Gly
325 330 335
25 Ala Leu Leu Gln Asp Lys Ile Ser Phe Gly Gly Gln Asn Ile Val Leu
340 345 350
Gly Val Asp Ser Arg Asn Met Thr Met Glu Ser Glu Arg Phe Glu Gln
355 360 365
30 Ala Gly Val Asn Thr Lys Pro Tyr Asn Pro Gly Tyr Ala Thr Asn Asn
370 375 380
Ile Gly Leu Phe Gly Gln Ala Asn Phe Tyr Leu Leu Asn Asp Ala Leu
385 390 395 400
Ser Ile Ser Ala Gly Ala Arg Ala Asp Phe Met Phe Phe Asp Leu Lys
405 410 415
35 Ala Asn Glu Tyr Leu Asn Asn Glu Ala Lys Gln Glu Thr His Asn Val
420 425 430
Ile Asn Pro Asn Val Gly Ile Lys Tyr Glu Phe Val Lys Gly Leu Thr
435 440 445
40 Ala His Gly Thr Phe Gly Ser Ala Phe Ser Ala Pro Asp Ala Phe Gln
450 455 460
Lys Ala Gly Gln Tyr Val Gly Pro Phe Gly Thr Thr Ile Gly Asn Pro
465 470 475 480
Asp Leu Lys Pro Glu Lys Ser Met Thr Trp Asp Phe Gly Ile Gly Tyr
485 490 495
45 Ser Asn Ala Arg Cys Gly Ile Gln Ala Asp Val Thr Leu Thr Tyr Phe
500 505 510
His Thr Asp His Lys Asp Leu Ile Leu Ser Ser Pro Asp Tyr Ala Asn
515 520 525
50 Asn Ile Thr Thr Tyr Ile Asn Ala Asp Lys Ala Arg Met Ser Gly Ile
530 535 540
Glu Ala Leu Leu Ser Tyr Asp Phe Gly Ser Leu Phe Ala Asn Lys Phe
545 550 555 560
Ser Leu Arg Ala Phe Ala Asn Ala Thr Ile Met Leu Asn Ser Glu Met
565 570 575
55 Lys Lys Ser Gln Thr Asp Ala Pro Trp Ser Glu Met Tyr Tyr Val Arg
580 585 590
Lys Gln Asn Ile Thr Phe Gly Ile Glu Tyr Arg Gly Lys Glu Gly Leu
595 600 605
60 Glu Val Met Leu Asn Gly Arg Phe Met Gly Arg Arg Ile Glu Gln Asn
610 615 620
Trp Tyr Ala Tyr Tyr Pro Glu Val Arg Pro Glu Leu Gln Gln Leu Leu
625 630 635 640
Ala Ala Glu Glu Pro Glu Leu Ala Ala Gln Gly Leu Leu Arg His Pro
645 650 655
65 Gln Ala Met Val Phe Asn Ala Ser Ala Tyr Tyr His Met Asn Lys Tyr
660 665 670
Leu Thr Phe Gly Val Asn Leu Asn Asn Ile Leu Asp Glu Leu Tyr Thr
675 680 685
70 Glu Lys Asp Gly Tyr His Met Pro Gly Arg Asn Ile Met Gly Lys Val
690 695 700
Met Val Asn Phe
705

(2) INFORMATION FOR SEQ ID NO:449

75

WO 99/29870

PCT/AU98/01023

389/490

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 462 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1...462

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:449

20 Met Asn Arg Phe Ser Asn His Trp Pro Cys Ile Leu Val Gly Phe Val
 1 5 10 15
 Leu Trp Phe Val Ser Ala Ser Arg Thr Val Ala Gln Asn Ala Ser Glu
 20 25 30
 Thr Thr Val Ser Tyr Asp Thr Asp Thr Ala Val Leu Ser Glu Ala Asp
 35 40 45
 25 Val Leu Arg Ile Ala Leu Ser Glu Asn Ala Thr Val Lys Val Ala Asp
 50 55 60
 Met Asp Val Arg Lys Gln Glu Tyr Ala Arg Arg Ala Ala Arg Ala Asp
 65 70 75 80
 30 Leu Phe Pro Lys Val Asp Leu Asn Gly Val Tyr Ser His Thr Leu Lys
 85 90 95
 Lys Gln Val Leu Tyr Ile Asp Met Pro Gly Phe Ser Ser Ser Glu Gly
 100 105 110
 Ile Glu Met Gly Arg Thr His Asn Thr Gln Gly Gly Val Asn Val Ser
 115 120 125
 35 Met Pro Leu Val Ser Ala Gln Leu Trp Lys Ser Ile Ala Met Thr Gly
 130 135 140
 Glu Gln Leu Asp Leu Ala Leu Glu Lys Ala Arg Ser Ser Arg Ile Asp
 145 150 155 160
 40 Leu Val Ala Glu Val Lys Lys Ala Tyr Leu Ser Val Leu Leu Ala Glu
 165 170 175
 Asp Ser Tyr Gly Val Phe Lys Arg Ser Tyr Asp Asn Ala Leu Ala Asn
 180 185 190
 Tyr Lys Asn Ile Ser Asp Lys Phe Asp Arg Gly Leu Val Ala Glu Tyr
 195 200 205
 45 Asp Lys Ile Arg Ala Asn Val Gln Val Arg Asn Ile Glu Pro Asn Leu
 210 215 220
 Leu Gln Ala Gln Asn Ser Val Ala Leu Ala Leu Trp Gln Leu Lys Val
 225 230 235 240
 50 Leu Met Ser Met Glu Val Glu Thr Pro Ile Arg Leu Ser Gly Ser Leu
 245 250 255
 Ser Asp Tyr Lys Glu Gln Val Tyr Thr Gly Tyr Phe Ala Ala Asp Thr
 260 265 270
 Leu Ile Ser Asn Asn Ser Ser Leu Arg Gln Leu Asp Ile Gln Arg Arg
 275 280 285
 55 Leu Ala Val Ser Ala Asp Lys Leu Asn Lys Tyr Ser Phe Leu Pro Thr
 290 295 300
 Leu Asn Leu Gly Gly Gln Tyr Thr Tyr Ser Leu Asn Ser Asn Asp Ile
 305 310 315 320
 60 Lys Phe Trp Gly Glu Gly Gln Arg Trp Thr Pro Phe Ser Thr Ile Ser
 325 330 335
 Leu Ser Leu Tyr Ile Pro Ile Phe Asn Gly Gly Lys Arg Leu Tyr Asn
 340 345 350
 Val Lys Gln Ser Ala Leu Ser Ile Arg Gln Ile Asp Leu Gln Arg Arg
 355 360 365
 65 His Ile Glu Gln Ser Ile Arg Met Gly Ile Lys Asn Gln Asn Asp Arg
 370 375 380
 Leu Arg Thr Cys Met Gln Arg Phe Val Ala Ser Glu Glu Ala Val Arg
 385 390 395 400
 70 Ser Ala Glu Lys Gly Tyr Gln Ile Ala Glu Lys Arg-Tyr Gln Thr Gly
 405 410 415
 Glu Gly Thr Leu Val Glu Leu Asn Asp Ala Asp Val Ala Leu Leu Gln
 420 425 430
 Ala Arg Leu Asn Tyr Asn Gln Ala Ile Phe Asp Phe Met Thr Ala Lys
 435 440 445
 75 Ala Glu Leu Asp Lys Met Asn Gly Met Gly Ile Pro Glu Gln

WO 99/29870

PCT/AU98/01023

390/ 490

450 455 460

(2) INFORMATION FOR SEQ ID NO:450

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 492 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

15 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...492

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:450

Met Trp Gly Asp Ser His Gly Val Ala Pro Asn Gln Val Arg Arg Thr
1 5 10 15
25 Leu Val Lys Val Ala Leu Ser Glu Ser Leu Pro Pro Gly Ala Lys Gln
20 25 30
Ile Arg Ile Gly Phe Ser Leu Pro Lys Glu Thr Glu Glu Lys Val Thr
35 40 45
30 Ala Leu Tyr Leu Leu Val Ser Asp Ser Leu Ala Val Arg Asp Leu Pro
50 55 60
Asp Tyr Lys Gly Arg Val Ser Tyr Asp Ser Phe Pro Ile Ser Lys Glu
65 70 75 80
Asp Arg Thr Thr Ala Leu Ser Ala Asp Ser Val Ala Gly Arg Arg Phe
85 90 95
35 Phe Tyr Leu Ala Ala Asp Ile Gly Pro Val Ala Ser Phe Ser Arg Ser
100 105 110
Asp Thr Leu Thr Ala Arg Val Glu Glu Val Ala Val Asp Gly Arg Pro
115 120 125
40 Leu Pro Leu Lys Glu Leu Ser Pro Ala Ser Arg Arg Leu Tyr Arg Gly
130 135 140
Tyr Glu Ala Leu Phe Val Pro Gly Asp Gly Gly Ser Arg Asn Tyr Arg
145 150 155 160
Ile Pro Ala Ile Leu Lys Thr Ala Asn Gly Thr Leu Ile Ala Met Ala
165 170 175
45 Asp Arg Arg Lys Tyr Asn Gln Thr Asp Leu Pro Glu Asp Ile Asp Ile
180 185 190
Val Met Arg Arg Ser Thr Asp Gly Gly Lys Ser Trp Ser Asp Pro Arg
195 200 205
50 Ile Ile Val Gln Gly Glu Gly Arg Asn His Gly Phe Gly Asp Val Ala
210 215 220
Leu Val Gln Thr Gln Ala Gly Lys Leu Leu Met Ile Phe Val Gly Gly
225 230 235 240
Val Gly Leu Trp Gln Ser Thr Pro Asp Arg Pro Gln Arg Thr Tyr Ile
245 250 255
55 Ser Glu Ser Arg Asp Glu Gly Leu Thr Trp Ser Pro Pro Arg Asp Ile
260 265 270
Thr His Phe Ile Phe Gly Lys Asp Cys Ala Asp Pro Gly Arg Ser Arg
275 280 285
60 Trp Leu Ala Ser Phe Cys Ala Ser Gly Gln Gly Leu Val Leu Pro Ser
290 295 300
Gly Arg Ile Thr Phe Val Ala Ala Ile Arg Glu Ser Gly Gln Glu Tyr
305 310 315 320
Val Leu Asn Asn Tyr Val Leu Tyr Ser Asp Asp Glu Gly Asp Thr Trp
325 330 335
65 Gln Leu Ser Asp Cys Ala Tyr Arg Arg Gly Asp Glu Ala Lys Leu Ser
340 345 350
Leu Met Pro Asp Gly Arg Val Leu Met Ser Ile Arg Asn Gln Gly Arg
355 360 365
70 Gln Glu Ser Arg Gln Arg Phe Phe Ala Leu Ser Ser Asp Asp Gly Leu
370 375 380
Thr Trp Glu Arg Ala Lys Gln Phe Glu Gly Ile His Asp Pro Gly Cys
385 390 395 400
Asn Gly Ala Met Leu Gln Val Lys Arg Asn Gly Arg Asp Gln Val Leu
405 410 415
75 His Ser Leu Pro Leu Gly Pro Asp Gly Arg Arg Asp Gly Ala Val Tyr

WO 99/29870

PCT/AU98/01023

391/490

5 Leu Phe Asp 420 His Val Ser Gly Arg Trp Ser Ala Pro Val Val Val Asn
435 440 445
Ser Gly Ser Ser Ala Tyr Ser Asp Met Thr Leu Leu Ala Asp Gly Thr
450 455 460
Ile Gly Tyr Phe Val Glu Glu Gly Asp Glu Ile Ser Leu Val Phe Ile
465 470 475 480
Arg Phe Val Leu Asp Asp Leu Phe Asp Val Arg Gln
485 490

10 (2) INFORMATION FOR SEQ ID NO:451

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 245 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

25 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...245

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:451

Met Lys Lys Glu Lys Leu Trp Ile Ala Ile Val Ala Gly Leu Ala Phe
1 5 10 15
Val Leu Gly Leu Tyr Ala Leu Gly Arg Ser Val Ala Gln Leu Arg Arg
20 25 30
35 Ser Gln Pro Ser Val Thr Val Thr Gly Met Ala Glu Arg Asn Phe Lys
35 40 45
Ser Asp Leu Ile Val Trp Thr Ala Ser Tyr Gln Leu Gln Met Met Asp
50 55 60
40 Leu Glu Ser Ala Tyr Lys Ala Leu Lys Glu Lys Gln Ile Leu Val Ala
65 70 75 80
Asp Tyr Leu Lys Asn Lys Gln Leu Pro Asp Ser Ser Tyr Ile Phe Ser
85 90 95
Ser Val Ala Ile Ser Lys Glu Tyr Asn Tyr Tyr Tyr Asp Pro Arg Gln
100 105 110
45 Glu Gln Asn Val Arg Thr Phe Ala Gly Tyr Leu Leu Ser Gln Thr Val
115 120 125
Thr Val Thr Ser Gln Asp Ile Glu His Val Glu Lys Ile Ser Arg Asp
130 135 140
50 Ile Thr Glu Leu Ile Asn Gln Gly Val Glu Ile Thr Ser Asp Arg Pro
145 150 155 160
Ala Tyr Tyr Tyr Thr Lys Leu Asn Asp Leu Lys Val Glu Met Leu Arg
165 170 175
Asn Ala Ser Glu Asp Ala Phe Asn Arg Ala Ser Val Ile Ala Glu Gly
180 185 190
55 Ser Gly Ser Ser Val Gly Lys Met Leu Ser Ser Ser Met Gly Val Phe
195 200 205
Gln Ile Val Gly Leu Asn Ser Asn Glu Asp Tyr Ser Trp Gly Gly Ser
210 215 220
60 Phe Asn Thr Ser Ser Lys Met Lys Thr Ala Ser Ile Thr Val Lys Ala
225 230 235 240
Ser Phe Ala Leu Lys
245

65 (2) INFORMATION FOR SEQ ID NO:452

70 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 276 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

75 (vi) ORIGINAL SOURCE:

392/490

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452

Met Lys Lys Thr Ile Ala Ile Ile Ala Ser Ala Leu Leu Ala Leu Gly
1 5 10 15
Ala Val Gly Cys Lys Lys Asn Ala Asp Thr Thr Ala Val Ser Glu Lys
20 25 30
Asp Ser Ile Ala Leu Ser Met Gly Ile Leu Tyr Gly Gln Asp Phe Ala
35 40 45
15 Asn Gln Phe Glu Met Ser Arg Leu Gln Gly Gln Pro Ile Asp Ser Val
50 55 60
Ala Phe Leu Asp Gly Phe Lys Tyr Gly Ile Asp Thr Thr Arg Phe Ser
65 70 75 80
Tyr Asn Leu Gly Ala Ile Tyr Ala Ser Asn Ile Ala Arg Gln Leu Ala
85 90 95
20 His Asp Ser Ile Asp Ile Asp Lys Phe Tyr Ala Ala Met Arg Ala Ala
100 105 110
Leu Leu Lys Asp Thr Val Ser Ile Ala Met Lys Pro Ala Asp Ala Gln
115 120 125
25 Ala Phe Met Gln Arg Ile Gln Ala Lys Lys Gln Arg Glu Asn Asn Met
130 135 140
Lys Gln Phe Gly Gln Asn Ile Glu Lys Gly Asn Glu Tyr Ile Asp Thr
145 150 155 160
Phe Lys Lys Glu Asp Gly Val Thr Val Thr Thr Gly Leu Ala Tyr
165 170 175
30 Lys Thr Leu Gln Glu Gly Thr Gly Ala Thr Pro Ser Leu Ala Asp Thr
180 185 190
Val Arg Val Lys Tyr Val Gly Thr Leu Val Asp Gly Lys Glu Phe Asp
195 200 205
35 Lys Asn Glu Glu Gly Ile Glu Phe Ala Val Thr Gly Val Ile Lys Gly
210 215 220
Trp Thr Glu Met Leu Gln Leu Met Lys Val Gly Gln Lys Val Arg Val
225 230 235 240
Val Ile Pro Gln Glu Leu Ala Tyr Gly Glu Thr Gly Asn Tyr Thr Ile
245 250 255
40 Glu Pro Phe Ser Thr Leu Thr Phe Glu Met Glu Leu Ile Gly Ile Lys
260 265 270
Pro Gly Lys Lys
275

(2) INFORMATION FOR SEQ ID NO:453

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 775 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(iv) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1...775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453

Met Lys Val Leu Arg Gln Val Phe Leu Pro Ile Leu Phe Val Leu Leu
1 5 10 15
Thr Gly Ala Cys Ser Thr Thr Lys Asn Leu Pro Glu Gly Glu Gln Leu
20 25 30
70 Tyr Ile Gly Met Gly Lys Thr Gln Ile Leu Arg Gln Asp Lys Ser His
35 40 45
Ala Gly Gln Gln Ala Leu Thr Glu Val Glu Ser Thr Leu Lys Val Thr
50 55 60
Pro Asn Gly Ala Ile Phe Gly Ser Ala Ser Ala Ser Leu Pro Lys Ile
65 70 75 80

WO 99/29870

PCT/AU98/01023

393/490

Pro Phe Gly Leu Trp Leu Tyr Asn Ser Phe Val Gly Asp Ser Thr Val
85 90 95
Ile Ser Lys Trp Ile Phe Asp Lys Phe Ala Ala Lys Pro Val Phe Ile
100 105 110
5 Ser Gln Val Lys Ser Asp Ser Arg Ala Lys Val Ala Thr Asn Ile Leu
115 120 125
Arg Glu His Gly Tyr Phe Asp Ala Lys Val Lys Ser Ser Val Thr Thr
130 135 140
10 Leu Lys Lys Asp Ser Leu Lys Ala Lys Ile Ser Tyr Thr Val Asp Met
145 150 155 160
Ala Ser Pro Tyr His Tyr Asp Ser Ile Ile Pro Lys Pro Ile Ser Thr
165 170 175
Phe Pro Asp Ser Ile Leu Ala Tyr Arg Gln Thr Pro Ser Leu Ile Arg
180 185 190
15 Lys Gly Asp Gln Phe Asn Leu Ala Lys Leu His Glu Glu Arg Gln Thr
195 200 205
Ile Ser Ala Leu Leu Arg Asp Asn Gly Tyr Tyr Tyr Phe Arg Pro Gln
210 215 220
20 Asp Ile Ile Tyr Glu Ala Asp Thr Leu Leu Val Arg Gly Ala Val Cys
225 230 235 240
Leu Arg Ala Lys Leu Ser Glu Asp Thr Pro Pro Gln Ala Met Arg Pro
245 250 255
Trp Arg Ile Gly Lys Arg Thr Ala Val Leu Leu Gly Met Asn Gly Glu
260 265 270
25 Ser Pro Thr Asp Ser Leu Glu Val Glu Asp Met Lys Val Leu Tyr Tyr
275 280 285
Arg Lys Met Pro Val Arg Pro Lys Ile Leu Ala Lys Arg Phe Arg Phe
290 295 300
30 Phe Ser Gly Asn Leu Tyr Arg Gln Lys Asp Asp Glu Thr Thr Arg Lys
305 310 315 320
Ser Leu Ala Arg Leu Gly Ala Phe Ser Val Ile Asp Leu Asn Phe Leu
325 330 335
Gln Arg Asp Ser Ile Ser Gly Leu Leu Asp Val Arg Leu Leu Thr Thr
340 345 350
35 Leu Asp Lys Pro Trp Asp Ala Ser Leu Glu Thr Leu Phe Thr Ser Lys
355 360 365
Ser Asn Asp Phe Ile Gly Pro Gly Leu Asn Phe Ala Leu Ala Arg Arg
370 375 380
40 Asn Val Phe Gly Gly Gly Gly Asn Leu Ser Trp Asn Ile Gly Gly Ser
385 390 395 400
Tyr Glu Trp Glu Thr Gly Asn Arg Pro Glu Asn Ser Ser Asn Arg Leu
405 410 415
Ile Asp Ile Asn Ser Tyr Asn Met Asn Thr Ala Val Asn Leu Ser Phe
420 425 430
45 Pro Ser Ile Val Phe Pro Gly Leu Leu Asp Lys Tyr Tyr Tyr Pro
435 440 445
Thr Thr Thr Thr Phe Gln Ala Ser Ala Thr Ala Leu Asn Arg Ala His
450 455 460
50 Tyr Phe Ser Met Tyr Ser Phe Gly Phe Ser Thr Thr Tyr Glu Phe Gln
465 470 475 480
Pro Ser Lys Glu His Arg His Ala Ile Phe Pro Leu Lys Leu Asn Tyr
485 490 495
Asn Leu Leu Gly His Gln Thr Glu Thr Phe Gln Ala Ile Thr Ala Asn
500 505 510
55 Asn Pro Pro Leu Leu Ser Leu Gln Ser Gln Phe Leu Ala Gln Met
515 520 525
Gly Tyr Ile Tyr Thr Phe Asn Lys Ser Val Ser Glu Lys Ser Pro His
530 535 540
60 His Leu Trp Met Gln Phe Gly Leu Ser Glu Ala Gly Asn Leu Leu Asn
545 550 555 560
Leu Ile Tyr Leu Ala Ala Gly Lys Lys Tyr Ser Asp Thr Lys Asn Phe
565 570 575
Val Gly Val Pro Phe Ser Gln Phe Ile Lys Ala Thr Gly Glu Leu Arg
580 585 590
65 Tyr Ser Tyr Thr Ile Asp Arg Asn Gln Ser Leu Ala Thr Arg Phe Gly
595 600 605
Thr Gly Val Ile Tyr Ser Tyr Gly Asn Met Arg Val Ala Pro Tyr Ser
610 615 620
70 Glu Gln Phe Tyr Val Gly Gly Ala Asn Ser Ile Arg Ala Phe Thr Val
625 630 635 640
Arg Ser Ile Gly Pro Gly Arg Phe Asn Pro Asp Ser Asp Asn Gln Tyr
645 650 655
Ser Tyr Leu Asp Gln Val Gly Glu Phe Lys Leu Glu Ala Asn Val Glu
660 665 670
75 Tyr Arg Gly Lys Leu Phe Gly Asp Leu His Ala Ala Val Phe Leu Asp

394/ 490

675
 Ala Gly Asn Val Trp Leu Leu Arg Glu Asp Ser Ser Arg Pro Gly Gly
 690 695 700
 5 Ala Leu Ser Glu Val Gly Ser Val Ser Asn Phe Leu Asn Ser Ile Ala
 705 710 715 720
 Leu Gly Thr Gly Val Gly Leu Arg Tyr Asp Leu Ala Phe Leu Val Val
 725 730 735
 Arg Val Asp Val Gly Phe Gly Leu His Leu Pro Tyr Asn Thr Gly Lys
 740 745 750
 10 Lys Gly Tyr Tyr Asn Ile Pro Arg Phe Lys Asp Ala Ile Gly Phe His
 755 760 765
 Leu Ala Val Gly Tyr Pro Phe
 770 775

15 (2) INFORMATION FOR SEQ ID NO:451
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 774 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...774
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:454

35 Met Ser Ser His Ser Val Arg Tyr Leu Ile Gl, Ile Ala Gly Cys Leu
 1 5 10 15
 Leu Leu Met Leu Ala Ser Ser Cys Ser Val Thr Arg Tyr Val Pro Asp
 20 25 30
 40 Gly Ser Arg Leu Leu Asp Arg Val Thr Ile Ala Ser Glu Thr Gly Ser
 35 40 45
 Ile Ala Leu Pro Glu Asp Ile Arg Asp Tyr Thr Leu Gln Gln Pro Asn
 50 55 60
 Tyr Arg Leu Phe Gly Met Thr Arg Trp Leu Leu Arg Val Tyr Ser Ser
 65 70 75 80
 45 Ser Asn Pro Asn Ser Asn Ser Trp Trp Asn Arg Ser Leu Arg Lys Met
 85 90 95
 Gly Glu Pro Pro Val Leu Ile Asp Ser Val Leu Thr Asp Arg Thr Ala
 100 105 110
 50 Asn Arg Leu Ala Lys Ala Met Ala Gly Asp Gly Phe Leu Asp Ala Thr
 115 120 125
 Ala Arg Ala Val Val Asp Thr Gly Leu Tyr Lys Lys Ala Arg Ile Thr
 130 135 140
 Tyr Leu Ile Gln Pro Gly Ser Arg Tyr Tyr Ile Arg Asn Met Ala Leu
 145 150 155 160
 55 Asp Val Lys Asn Pro Leu Leu Pro Pro Val Ala Leu Gly Asn Ser Leu
 165 170 175
 Pro Ser Ala Tyr Lys Val Gly Ile Ser Glu Gly Ser Pro Leu Ser Pro
 180 185 190
 60 Ile Val Leu Asp Glu Glu Arg Lys Ala Ile Ala Arg His Met Arg Asn
 195 200 205
 Asn Gly Phe Trp Lys Phe Ser Ala Glu Asp Val Tyr Tyr Glu Ala Asp
 210 215 220
 Thr Thr Val Ser Gly Gly Ser Gly Thr Lys Ser Ala Asp Leu Lys Leu
 225 230 235 240
 65 Val Val Asn Gly Ile Gly Arg Tyr Pro Tyr Arg Ile Gly Arg Val Phe
 245 250 255
 Phe His Ala Asp Tyr Asp Pro Leu Glu Ser Asp Phe Arg Val Gln Glu
 260 265 270
 70 Leu Pro Arg Ile Asp Ser Ile Ser Arg Gly Asp Tyr Thr Val Tyr Tyr
 275 280 285
 Gly Ser Arg Gly Arg Tyr Ile Arg Ala Ser Ala Leu Thr Arg Ser Val
 290 295 300
 Ser Val Thr Pro Gly Ala Phe Phe Cys Glu Asp Asp Val Glu Arg Ser
 305 310 315 320
 75 Tyr Ile Lys Leu Asn Ala Leu Pro Ile Val Arg Asn Val Asn Ile Arg

WO 99/29870

PCT/AU98/01023

395/ 490

5 Phe Val Glu His 325 Asn Gly Lys Asp Glu Ile Ala Leu Ala 335 Asp Ser Ser
 Arg Leu Val Asp Cys Tyr Ile Leu Thr Val Pro Ala Lys Ser Lys Ser 340 345 350
 Phe Glu Ala Glu Val Leu Gly Thr Asn Ser Ala Gly Asp Phe Gly Ala 355 360 365
 Ala Leu Ser Leu Gly Phe Thr Asp Arg Asn Leu Phe Arg Gly Ala Glu 370 375 380
 10 Met Phe Asn Ile Lys 390 Leu Lys Gly Ala Tyr Glu Ala Ile Arg Lys Gly 385 395 400
 Ser His Ser Phe Met Glu Tyr Gly Val Glu Ser Ser Leu Arg Phe Pro 405 410 415
 Arg Leu Leu Phe Pro Phe Ile Ser Asp Glu Thr Arg Arg Arg Leu Arg 420 425 430
 15 Ala Ser Thr Glu Trp Lys Ile Gly Tyr Asn Tyr Gln Thr Arg Pro Glu 435 440 445
 Phe Asp Arg Val Ile Leu Ser Ala Gln Leu Asn Tyr Ser Trp Gln Thr 450 455 460
 20 Tyr Leu His Asn Arg Leu Arg His Thr Ile Arg Leu Leu Asp Val Asp 465 470 475
 Tyr Leu His Leu Pro Tyr Ile Asp Pro Asp Phe Ala Gln Ser Leu Pro 480 485 490
 25 Pro Thr Thr Ala Leu Tyr Asn Tyr Thr Glu Gln Phe Ile Leu Gly Ser 495 500 505
 Ala Tyr Ile Leu Asn Tyr Thr Thr Ala Ser Ser Met Glu Arg Thr Val 510 515 520
 Ser Asn Pro Phe Thr Ala Arg Phe Ser Ile Gln Thr Ala Gly Asn Leu 525 530 535
 30 Leu Gln Ala Ile Ser Tyr Leu Thr Asp Ser Pro Lys Asp Glu His Gly 540 545 550
 Leu Tyr Lys Met Phe Gly Leu His Tyr Ala Gln Phe Val Lys Leu Asp 555 560 565
 Leu Asp Leu Ala Lys Thr Val Leu Leu Glu Lys Asp Asn Thr Leu Ala 570 575 580
 35 Leu His Leu Gly Phe Gly Leu Ala Phe Pro Tyr Gly Ser Asn Ser Val Arg 585 590 595
 Ile Pro Phe Glu Leu Arg Tyr Phe Ala Gly Gly Ser Asn Ser Val Arg 600 605 610
 40 Gly Trp Ser Val Arg Thr Leu Gly Pro Gly Ser Met Lys Met Thr Pro 615 620 625
 Asp Lys Thr Phe Phe Asp Gln Met Gly Asp Ile Arg Leu Asp Leu Asn 630 635 640
 Val Glu Tyr Arg Thr Lys Leu Phe Trp Lys Phe Arg Ala Ala Phe 645 650 655
 45 Val Asp Ala Gly Asn Val Trp Thr Ile Lys Glu Tyr Glu Asn Gln Glu 660 665 670
 Asp Gly Leu Phe Arg Phe Asp Arg Phe Tyr Lys Glu Ile Ala Leu Ala 675 680 685
 50 Tyr Gly Leu Gly Leu Arg Leu Asp Phe Asp Tyr Phe Leu Val Arg Leu 690 695 700
 Asp Ala Gly Leu Lys Ala Tyr Asp Pro Gln Gln Thr Gly Arg Tyr Lys 705 710 715
 55 Trp Ala Ile Thr Arg Pro Asn Leu Ser Ser Asn Phe Ala Trp His Ile 720 725 730
 Ala Val Gly Tyr Pro Phe 735 740 745 750 755 760 765 770

- 60 (2) INFORMATION FOR SEQ ID NO:455
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 867 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 65 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 70 (i) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
- (ii) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...867
- 75

WO 99/29870

PCT/AU98/01023

397/ 490

Trp Lys Ser Phe Leu Pro Trp Ser Gly Lys Ala Gly Leu Ser Tyr Lys
580 585 590
Phe Ala Gln Gly His Asn Val Phe Ala Asn Gly Gly Phe Phe Thr Arg
595 600 605
5 Ala Pro Leu Phe Gly Asn Ile Tyr Ala Ala Gly Ala Ile Ile Pro Asn
610 615 620
Asp Lys Ala Asn Met Glu Lys Val Leu Thr Gly Glu Val Gly Tyr Gly
625 630 635 640
10 Phe Thr Asn His Lys Asn Phe Glu Phe Asn Ile Asn Gly Tyr Tyr Thr
645 650 655
Lys Trp Met Asp Arg Val Thr Ser Lys Arg Ile Gly Asn Glu Tyr Val
660 665 670
Tyr Leu Asn Gly Val Asp Ala Val His Cys Gly Val Glu Ala Glu Val
675 680 685
15 Ser Tyr Arg Pro Ile Arg Gln Ile Asp Leu Arg Gly Met Phe Ser Leu
690 695 700
Gly Asp Trp Thr Trp Gln Asn Asn Val Ser Tyr Thr Ser Tyr Asp Glu
705 710 715 720
20 Ala Gly Asn Glu Thr Gly Gln Asp Ile Thr Tyr Ile Lys Gly Leu His
725 730 735
Val Gly Asp Ala Ala Gln Met Thr Ala Ala Val Ser Ala Arg Ile Glu
740 745 750
Leu Phe Lys Gly Phe His Val Ile Gly Lys Tyr Asn Phe Leu Gly Lys
755 760 765
25 Asn Tyr Ala Gly Phe Asn Pro Ala Thr Arg Asn Ala Gln Gln Tyr Glu
770 775 780
Ala Asp Gly Lys Glu Ile Val Glu Ser Trp Lys Leu Pro Asp Val Gly
785 790 795 800
30 Leu Phe Asp Leu Ser Ala Ser Tyr Asn Phe Lys Leu Gly Ser Leu Ser
805 810 815
Thr Thr Phe Tyr Phe Asn Met Asp Asn Val Ala Asp Lys Arg Tyr Val
820 825 830
Ser Asp Ala Asp Asp Asn Ile Ile Gly Lys Lys His Asp Glu Ala Ser
835 840 845
35 Ala Leu Val Trp Tyr Gly Phe Gly Arg Thr Trp Ser Thr Gly Ile Arg
850 855 860
Val Asn Phe
865
40 (2) INFORMATION FOR SEQ ID NO:456
(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 431 amino acids
(B) TYPE: amino acid
45 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
50 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc_feature
55 (B) LOCATION 1...431
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456
60 Met Lys Phe Ser Ile Arg Leu Phe Leu Cys Ile Ile Phe Leu Leu Ser
1 5 10 15
Ala Phe Ile Leu Pro Ala Leu Gly Gln Lys Ser Lys Gln Val Gln Arg
20 25 30
65 Leu Glu Lys Gln Arg Lys Glu Ala Leu Lys Ala Ile Glu Lys Thr Asp
35 40 45
Arg Glu Leu Arg Asn Thr Lys Lys Asp Lys Gln Asp Lys Gln Lys His
50 55 60
Leu Asn Leu Leu Asn Lys Gln Val Ala Gln Arg Lys Gln Met Val Gln
65 70 75 80
70 Leu Leu Asp Asn Glu Val Lys Glu Leu Gln Ser Asp Ile Asp Ser Met
85 90 95
Thr Gly Val Cys His Gln Leu Ser Val Glu Glu Lys Ala Arg Ser Asp
100 105 110
75 Glu Tyr Ala Gln Ala Leu Gln Ser Met Gln Lys Arg Lys Arg Ser Leu
115 120 125

WO 99/29870

PCT/AU98/01023

401/490

Phe Arg Arg Gly Gly Asp Arg Ile Asp Leu Pro Pro His Val Val Gly
 340 345 350
 Val Ala Glu Gln Thr Asp His Ser Val Phe Ser Gly Asn Leu Lys Tyr
 355 360 365
 5 Asp Leu Phe Ser Ser Asn Tyr Lys His His Phe Gln Ala Tyr Thr Ser
 370 375 380
 Gly Gln Ile Val Asn Arg Lys Ser Tyr Tyr Gly Gly Ile Gly Glu Ile
 385 390 395 400
 10 Asp Val Asn Gly His Pro Gly Gly Thr Glu Gly Tyr Pro Ile Pro Gln
 405 410 415
 Asp Gln Tyr Gly Asn Asn Tyr Gly Val Thr Lys Gly Lys Thr Tyr Met
 420 425 430
 Gly Gly Ile Gln Tyr Ser Tyr Asp Leu Asp Lys Phe Leu Leu Met Pro
 435 440 445
 15 Ser Gln Leu Leu Phe Gly Ala Glu Tyr Thr Arg Asp Glu Leu Asn Asp
 450 455 460
 Val Met Pro Ile Leu Ser Trp Gln Thr Gly Glu Asp Ala Asn Gly Asn
 465 470 475 480
 20 Thr Ile Pro Leu Tyr Pro Glu Leu Asp Gln Asn Ile Asn Asn Tyr Ser
 485 490 495
 Leu Phe Gly Gln Asn Glu Trp Lys Asn Asp Arg Trp Ser Ile Leu Val
 500 505 510
 Gly Ala Arg Leu Asp Lys His Ser Glu Val Lys Asp Met Ile Leu Ser
 515 520 525
 25 Pro Arg Thr Thr Leu Arg Phe Asn Val Asn Pro Asp Ile Asn Leu Arg
 530 535 540
 Ala Thr Tyr Ala Lys Gly Phe Arg Ala Pro Gln Val Phe Asp Glu Asp
 545 550 555 560
 30 Leu His Val Gly Val Val Gly Gly Glu Ala Gln Lys Val Phe Asn Asp
 565 570 575
 Pro Asn Leu Lys Pro Glu Ile Ser His Ala Phe Ser Leu Ser Ala Asp
 580 585 590
 Met Tyr His Arg Phe Gly Asn Val Gln Thr Asn Phe Leu Val Glu Gly
 595 600 605
 35 Phe Tyr Thr Arg Leu Leu Asp Val Phe Thr Asn Glu Glu Gln Pro Asp
 610 615 620
 Gln His Asp Gly Ile Lys Arg Tyr Thr Arg Ile Asn Gly Ser Gly Ala
 625 630 635 640
 40 Lys Val Phe Gly Leu Asn Leu Glu Gly Lys Val Ala Tyr Lys Ser Phe
 645 650 655
 Gln Leu Gln Ala Gly Leu Thr Leu Ala Ser Asn Lys Tyr Asp Glu Ala
 660 665 670
 Gln Glu Trp Gly Leu Asn Thr Val Lys Asp Thr Asn Gly Ala Phe Val
 675 680 685
 45 Thr Glu Ala Asn Ala Asn Gly Gln Gln Glu Tyr Lys Asn Glu Ser Met
 690 695 700
 Thr Asp Thr Gln Ile Thr Arg Thr Pro Ser Val Tyr Gly Tyr Phe Thr
 705 710 715 720
 50 Leu Ala Tyr Asn Pro Ala His Ser Trp Asn Ile Ala Leu Thr Gly Ala
 725 730 735
 Tyr Thr Gly Gln Met Tyr Val Pro His Ala Ile Glu Tyr Gly Val Lys
 740 745 750
 Ser Ala Glu Leu Asp Ile Met Gln Asn Asn Pro Glu Ile Thr Asp Glu
 755 760 765
 55 Thr Gly Lys Ala Pro Arg Ile Asp Glu Leu Lys Lys Thr Pro Ala Phe
 770 775 780
 Phe Asp Leu Gly Leu Lys Val Gly Tyr Asp Phe His Val Phe Gln Ala
 785 790 795 800
 60 Thr Glu Val Gln Leu Tyr Val Gly Met Asn Asn Ile Phe Asn Ser Phe
 805 810 815
 Gln Lys Asp Phe Asp Arg Gly Ala Ala Arg Asp Ser Gly Tyr Ile Tyr
 820 825 830
 Gly Pro Thr Gln Pro Arg Thr Gly Tyr Met Gly Leu Val Lys Phe
 835 840 845

(2) INFORMATION FOR SEQ ID NO:460

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 202 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

WO 99/29870

PCT/AU98/01023

402/ 490

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

5 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460

10 Met Thr Val Lys Arg Ala Val Arg Ile Ala Leu Leu Thr Leu Ile Gly
1 5 10 15
Ile Leu Phe Ser Ser Pro Ser Leu Val Arg Ala Gln Ser Leu Phe Ser
20 25 30
15 Thr Glu His Val Leu Gln Leu Tyr Asn Lys Ile Leu Tyr Gly Glu Ser
35 40 45
Ala Ala Asp Thr Val Ala Glu Lys Thr Ala Gly Glu Ser Ala Phe Pro
50 55 60
Phe Ile Asp Lys Leu Ile Asn Leu Gly Arg Thr Phe Leu Gly Lys Pro
65 70 75 80
20 Tyr Arg Tyr Arg Gly Pro Ser Pro Trp Pro Met Asp Cys Ser Gly Tyr
85 90 95
Val Ser Tyr Leu Tyr Ser Lys Phe Asp Ile Lys Leu Pro Arg Gly Ala
100 105 110
25 Ala Ala Gln Ser Gln Tyr Thr Asn Pro Ile Glu Arg Glu Asp Val Arg
115 120 125
Pro Gly Asp Leu Leu Phe Phe Lys Gly Arg Asn Ala Arg Ser Asn Arg
130 135 140
Ile Gly His Val Ala Leu Val Val Ser Val Asp Glu Asp Asp Ile Thr
145 150 155 160
30 Met Met His Ser Arg Asn Ser Arg Gly Ile Val Ile Glu Lys Leu Asn
165 170 175
Arg Ser Ala Tyr Phe Ser Arg Arg Leu Val Ser Tyr Gly Arg Val Pro
180 185 190
35 Gly Ala Lys Arg Val Ile Pro Arg Lys Ser
195 200

(2) INFORMATION FOR SEQ ID NO:461

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 455 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES

50 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...455

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:461

60 Met Lys Arg Thr Ile Leu Leu Thr Ala Leu Thr Val Leu Ser Ser Leu
1 5 10 15
Ser Leu Leu Arg Ala Gln Asn Glu Ser Glu Ala Ser Thr Asn Pro Met
20 25 30
Ser Gly Leu Ser Leu Glu Asp Cys Ile Arg Ile Ala Lys Glu Arg Asn
35 40 45
65 Leu Asn Leu Arg Arg Gln Glu Ile Glu Gln Glu Asn Arg Ile Ile Ser
50 55 60
Leu Asp Ala Ala Arg His Ser Phe Leu Pro Ser Val Asn Ala Gly Ile
65 70 75 80
Gly His Asn Tyr Ser Phe Gly Arg Ser Lys Asp Lys Thr Gly Val Thr
85 90 95
70 Val Asp Arg Ser Ser Met Asn Thr Asn Leu Ser Ile Gly Ala Ser Val
100 105 110
Glu Val Phe Ser Gly Thr Arg Arg Leu His Asp Leu Lys Gln Gln Lys
115 120 125
75 Tyr Asn Val Glu Asp Gly Ile Ala Arg Leu Gln Lys Ala Arg Glu Asp
130 135 140

WO 99/29870

PCT/AU98/01023

403/ 490

Leu Ser Leu Gln Ile Ala Ala Leu Tyr Ile Asn Leu Leu Phe Arg Gln
145 150 155 160
Glu Met Thr Arg Thr Ala Glu Thr Gln Leu Ala Leu Ile Arg Glu Gln
165 170 175
5 Arq Asn Arg Thr Ala Glu Met Val Arg Val Gly Lys Trp Ala Glu Gly
180 185 190
Lys Leu Leu Asp Ile Asn Ala Gln Met Ala Lys Asp Glu Gln Leu Leu
195 200 205
10 Val Gln Tyr Arq Ser Glu Glu Glu Leu Ala Arg Leu Asp Leu Gly Gln
210 215 220
Ala Leu Glu Leu Glu His Pro Glu Ser Ile Ala Val Lys Ala Pro Asp
225 230 235 240
Thr Asp Val Leu Val Ala Glu Arg Leu Gly Ser Leu Leu Ala Pro Glu
245 250 255
15 Glu Ile Tyr Arg Thr Ala Leu Gly Leu Lys Pro Ala Leu His Ser Ser
260 265 270
Glu Leu Gln Ile Ala Ser Ala Arg Glu Gly Leu Ala Ser Ala Arg Ala
275 280 285
20 Ala Tyr Phe Pro Thr Leu Ser Leu Ser Ala Gly Tyr Ser Asn Gly Tyr
290 295 300
Phe Arg Asp Leu Gly Lys Glu Tyr Ala Ala Ile Asn Pro Ser Phe Ser
305 310 315 320
Glu Gln Trp Lys Asn Asn Gly Ser Tyr Ser Ile Gly Leu Ser Leu Asn
325 330 335
25 Ile Pro Ile Phe Ser Ala Met Gln Thr Gln Asp Arg Val Arg Ser Ser
340 345 350
Arg Leu Gln Ile Arg Ser Ser Glu Leu Arg Leu Val Glu Glu Lys Lys
355 360 365
30 Ala Leu Tyr Lys Glu Ile Arg Gln Ala Tyr Ser Asn Ala Val Ala Ala
370 375 380
Asp Lys Ala Ile Ala Ala Glu Asn Ser Lys Ala Ala Thr Leu Lys
385 390 395 400
Ala Tyr Glu Tyr Ala Arg Asp Ser Phe Glu Ala Gly Arg Leu Ser Ala
405 410 415
35 Tyr Glu Tyr Ala Glu Ala Lys Thr Lys Tyr Ala Leu Ser Gln Val Glu
420 425 430
Glu Leu Arg Ala Lys Tyr Asp Phe Ile Tyr Lys Ala Lys Val Leu Asp
435 440 445
40 Phe Tyr Gln Gly Lys Asp Phe 455
450

(2) INFORMATION FOR SEQ ID NO:462

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 444 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
50 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
55 (A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...444
60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:462

Met Arg Phe Gln His Tyr Leu Ile Cys Thr Ala Ala Val Ala Ala Leu
1 5 10 15
65 Ala Ala Asn Pro Leu Thr Gly Gln Ser Asn Met Thr Leu Glu Glu Cys
20 25 30
Ile Asp Tyr Ala Arg Arg His Ser Ser Ala Val Ala Leu Ser Ala Ala
35 40 45
Glu Leu Glu Gln Ser Lys Ala Asp Tyr Leu Gln Ala Val Gly Asn Phe
50 55 60
70 Leu Pro Arg Val Ser Ala Gly Thr Gly Ala Ser Trp Asn Phe Gly Arg
65 70 75 80
Gly Leu Asp Ala Glu Thr Asn Thr Tyr Thr Asp Ile Asn Ser Phe Asn
85 90 95
75 Asn Ser Tyr Ser Ile His Ala Thr Met Thr Leu Phe Asp Gly Leu Gln
100 105 110

WO 99/29870

PCT/AU98/01023

405 / 490

	Ser	His	Ile	Ser	Ser	Ile	Gly	Asp	Val	Asp	Val	Tyr	Arg	Leu	Gln	Phe
				100					105					110		
	Lys	Leu	Glu	Gly	Ala	Lys	Ala	Ile	Thr	Leu	Tyr	Tyr	Asp	Ala	Phe	Asn
				115					120					125		
5	Ile	Pro	Glu	Gly	Gly	Arg	Leu	Tyr	Ile	Tyr	Thr	Pro	Asp	His	Glu	Ile
				130					135					140		
	Val	Leu	Gly	Ala	Tyr	Thr	Asn	Ala	Thr	His	Arg	Arg	Asn	Gly	Ala	Phe
				145					150					155		160
10	Ala	Thr	Glu	Pro	Val	Pro	Gly	Ser	Glu	Leu	Ile	Met	Asp	Tyr	Glu	Val
					165					170					175	
	Ser	Arg	Gly	Gly	Thr	Leu	Pro	Asp	Ile	Lys	Ile	Ser	Gly	Ala	Gly	Tyr
					180					185					190	
	Ile	Phe	Asp	Lys	Val	Gly	Gly	Arg	Pro	Val	Thr	Asp	Asn	His	Tyr	Gly
				195					200					205		
15	Ile	Gly	Glu	Asp	Asp	Ser	Asp	Ser	Asp	Cys	Glu	Ile	Asn	Ile	Asn	Cys
				210					215					220		
	Pro	Glu	Gly	Ala	Asp	Trp	Gln	Ala	Glu	Lys	Asn	Gly	Val	Val	Gln	Met
					225				230					235		240
	Ile	Met	Val	Lys	Gly	Gln	Tyr	Ile	Ser	Met	Cys	Ser	Gly	Asn	Leu	Leu
					245					250					255	
20	Asn	Asn	Thr	Lys	Gly	Asp	Phe	Thr	Pro	Leu	Ile	Ile	Ser	Ala	Gly	His
				260					265						270	
	Cys	Ala	Ser	Ile	Thr	Thr	Asn	Phe	Gly	Val	Thr	Gln	Ser	Glu	Leu	Asp
				275					280					285		
25	Lys	Trp	Ile	Phe	Thr	Phe	His	Tyr	Glu	Lys	Arg	Gly	Cys	Ser	Asn	Gly
				290					295					300		
	Thr	Leu	Ala	Ile	Phe	Arg	Gly	Asn	Ser	Ile	Ile	Gly	Ala	Ser	Met	Lys
				305					310					315		320
30	Ala	Phe	Leu	Pro	Ile	Lys	Gly	Lys	Ser	Asp	Gly	Leu	Leu	Leu	Gln	Leu
					325					330					335	
	Asn	Asp	Glu	Val	Pro	Leu	Arg	Tyr	Arg	Val	Tyr	Tyr	Asn	Gly	Trp	Asp
				340					345						350	
	Ser	Thr	Pro	Asp	Ile	Pro	Ser	Ser	Gly	Ala	Gly	Ile	His	His	Pro	Ala
				355					360					365		
35	Gly	Asp	Ala	Met	Lys	Ile	Ser	Ile	Leu	Lys	Lys	Thr	Pro	Ala	Leu	Asn
				370					375					380		
	Thr	Trp	Ile	Ser	Ser	Ser	Gly	Ser	Gly	Gly	Thr	Asp	Asp	His	Phe	Tyr
				385					390					395		400
40	Phe	Lys	Tyr	Asp	Gln	Gly	Gly	Thr	Glu	Gly	Gly	Ser	Ser	Gly	Ser	Ser
					405					410					415	
	Leu	Phe	Asn	Gln	Asn	Lys	His	Val	Val	Gly	Thr	Leu	Thr	Gly	Gly	Ala
				420					425					430		
	Gly	Asn	Cys	Gly	Gly	Thr	Glu	Phe	Tyr	Gly	Arg	Leu	Asn	Ser	His	Trp
				435					440					445		
45	Asn	Glu	Tyr	Ala	Ser	Asp	Gly	Asn	Thr	Ser	Arg	Met	Asp	Ile	Tyr	Leu
				450					455					460		
	Asp	Pro	Gln	Asn	Asn	Gly	Gln	Thr	Thr	Ile	Leu	Asn	Gly	Thr	Tyr	Arg
				465					470					475		480
	Asp	Gly	Tyr	Lys	Pro	Leu	Pro	Ser	Val	Pro	Arg	Leu	Leu	Leu	Gln	Ser
					485					490					495	
50	Thr	Gly	Asp	Gln	Val	Glu	Leu	Asn	Trp	Thr	Ala	Val	Pro	Ala	Asp	Gln
				500					505					510		
	Tyr	Pro	Ser	Ser	Tyr	Gln	Val	Glu	Tyr	His	Ile	Phe	Arg	Asn	Gly	Lys
				515					520					525		
55	Glu	Ile	Ala	Thr	Thr	Lys	Glu	Leu	Ser	Tyr	Ser	Asp	Ala	Ile	Asp	Glu
				530					535					540		
	Ser	Ile	Ile	Gly	Ser	Gly	Ile	Ile	Arg	Tyr	Glu	Val	Ser	Ala	Arg	Phe
				545					550					555		560
	Ile	Tyr	Pro	Ser	Pro	Leu	Asp	Gly	Val	Glu	Ser	Tyr	Lys	Asp	Thr	Asp
					565					570					575	
60	Lys	Thr	Ser	Ala	Asp	Leu	Ala	Ile	Gly	Asp	Ile	Gln	Thr	Lys	Leu	Lys
				580					585					590		
	Pro	Asp	Val	Thr	Pro	Leu	Pro	Gly	Gly	Gly	Val	Ser	Leu	Ser	Trp	Lys
				595					600					605		
65	Val	Pro	Phe	Leu	Ser	Gln	Leu	Val	Ser	Arg	Phe	Gly	Glu	Ser	Pro	Asn
				610					615					620		
	Pro	Val	Phe	Lys	Thr	Phe	Glu	Val	Pro	Tyr	Val	Ser	Ala	Ala	Ala	Ala
				625					630					635		640
	Gln	Thr	Pro	Asn	Pro	Pro	Val	Gly	Val	Val	Ile	Ala	Asp	Lys	Phe	Met
					645					650					655	
70	Ala	Gly	Thr	Tyr	Pro	Glu	Lys	Ala	Ala	Ile	Ala	Ala	Val	Tyr	Val	Met
				660					665					670		
	Pro	Ser	Ala	Pro	Asp	Ser	Thr	Phe	His	Leu	Phe	Leu	Lys	Ser	Asn	Thr
				675					680					685		
75	Asn	Arg	Arg	Leu	Gln	Lys	Val	Thr	Thr	Pro	Ser	Asp	Trp	Gln	Ala	Gly

407 / 490

180 185 190
 Val Val Gly Asn Ile Gln Ala Lys Phe Arg Asn Ser Val Thr Lys Gly
 195 200 205
 Phe Leu Thr Thr Glu Ala Gln Glu Ile Pro Ala Ala Ala Ser Tyr Lys
 210 215 220
 Thr Ser Glu Tyr Leu Asp Ile Ala Glu Ser Ala Pro Ala Asn Ser Ile
 225 230 235 240
 His Phe Tyr Ser Tyr Tyr Asn Lys Trp Thr Leu Ser Thr Pro Glu Lys
 245 250 255
 10 Arg Pro Glu Phe Phe Ile Met Val Lys Phe Lys Lys Thr Gly Gln Pro
 260 265 270
 Asp Asn Thr Ala Lys Pro Tyr Tyr Arg Val Pro Leu Glu Ser Gln
 275 280 285
 15 Asp Asn Gln Val Lys Ser Asn Val Leu Tyr Asn Leu Asn Val Lys Ile
 290 295 300
 Glu Ile Leu Gly Ser Leu Gln Glu Pro Glu Ala Val Ser Val Asn Gly
 305 310 315 320
 Thr Leu Ala Ile Glu Glu Trp Ile Leu His Gln Asp Ala Phe Asn Leu
 325 330 335
 20 Pro Ala Thr Asn Tyr Leu Ile Val Glu Gln His Glu Ile Phe Met Asn
 340 345 350
 Asn Val Asn Thr Tyr Ser Val Lys Tyr Gln Thr Ser Gln Lys Pro Ile
 355 360 365
 25 Ser Ile Ser Ile Gln Ser Val Thr Phe Ser Tyr Val Ser Ser Asp Gly
 370 375 380
 Thr Gln His Asn Asp Leu Val Ala Ser Ser Ser Asp Gln Tyr Pro Thr
 385 390 395 400
 Ile Thr Ser Asp Asn Thr Ser Ile Ile Ile Thr Ser Lys Ile Pro Val
 405 410 415
 30 Asn Asn Val Pro Lys Lys Ile Val Phe Glu Val Thr Asn Gly Val Ala
 420 425 430
 Gly Leu Lys Glu Thr Val Thr Val Leu Gln Tyr Pro Ala Gln Phe Ile
 435 440 445
 35 Val Asn Thr Leu Gly Thr Ala Ser Ala Trp Arg Pro Asp Gly Ser Leu
 450 455 460
 Ala Pro Gly Leu Asn Asn Lys Ala Ile Tyr His Val Val Val Leu Val
 465 470 475 480
 Pro Pro Glu Asn Leu Phe Glu Asp Gly Thr Gln Thr Ile Ile Gly Tyr
 485 490 495
 40 Pro Pro Thr Glu Thr Ile Ser Phe His Lys Lys Glu Asn Asn Thr Tyr
 500 505 510
 Pro Ile Val Trp Ser Asp Thr Asn Thr Thr Lys Gln Asp Leu Glu Thr
 515 520 525
 45 Ser Arg Met Ile Ser Pro Ser Phe Glu Leu Ala Ser Gln Leu Gly Ala
 530 535 540
 Thr Leu Pro Met Pro Tyr Leu Glu Tyr Trp Pro Gly Thr Ser Tyr Leu
 545 550 555 560
 Leu Asp Tyr Ser Gly Asn Tyr Asn Asn Lys Arg Tyr Ala Leu Phe Asn
 565 570 575
 50 Cys Ala Phe Tyr Trp Glu Lys Arg Lys Val Asn Asn Glu Glu Ile Lys
 580 585 590
 Phe Asp Asp Trp Arg Leu Pro Thr Glu Ala Glu Ile Lys Leu Ile Asp
 595 600 605
 55 Lys Leu Gln His Asn Glu Gln Ser Ala Val Gln Ala Ile Met Thr Gly
 610 615 620
 Asn Tyr Tyr Trp Asp Ser Tyr Ser Ala Asn Gly Ser Tyr Lys Met Gln
 625 630 635 640
 Gly Gly Gly Gly Gln Gly Asn Ser Ser Lys Ala Tyr Val Arg Cys Val
 645 650 655
 60 Arg Asp Val Lys Lys Pro Ile Arg Asp Lys Lys Ser Gly Lys
 660 665 670

(2) INFORMATION FOR SEQ ID NO:465

- 65 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1282 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 70 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 75 (A) ORGANISM: Porphyromonas gingivalis

WO 99/29870

PCT/AU98/01023

408/490

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1282

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465

	Met	Arg	Lys	Ile	Leu	Ser	Phe	Leu	Met	Met	Cys	Ser	Leu	His	Leu	Gly
	1			5						10				15		
10	Leu	Gln	Ser	Gln	Thr	Trp	His	Gly	Asp	Pro	Asp	Ser	Val	Ala	Ala	Leu
				20					25					30		
	Pro	Ser	Ile	Gly	Ile	Gln	Glu	Ser	Ser	Cys	Thr	Arg	Ile	Thr	Phe	Glu
				35					40					45		
15	Val	Val	Phe	Pro	Gly	Phe	Tyr	Ser	Val	Glu	Lys	Arg	Glu	Gly	Asn	Gln
				50					55				60			
	Val	Phe	Gln	Arg	Ile	Ser	Met	Pro	Gly	Cys	Gly	Ser	Phe	Gly	Asn	Leu
				65					70				75			80
	Gly	Glu	Ala	Glu	Leu	Pro	Val	Leu	Lys	Lys	Met	Ile	Ala	Val	Pro	Glu
				85					90					95		
20	Phe	Ser	Thr	Ala	Asn	Val	Ala	Val	Lys	Ile	Lys	Glu	Thr	Glu	Thr	Phe
				100					105					110		
	Asp	Asn	Tyr	Asn	Ile	Tyr	Pro	Asn	Pro	Thr	Tyr	Val	Val	Glu	Glu	Leu
				115					120					125		
25	Pro	Glu	Gly	Gly	Thr	Tyr	Leu	Val	Glu	Ala	Phe	Ala	Ile	Asn	Asn	Asp
				130					135				140			
	Tyr	Tyr	Ser	Gln	Asn	Val	Ser	Leu	Pro	Ser	Thr	His	Tyr	Val	Tyr	Ser
				145					150				155			160
	Gln	Asp	Gly	Tyr	Phe	Arg	Ser	Gln	Arg	Phe	Ile	Glu	Val	Thr	Leu	Tyr
				165					170					175		
30	Pro	Phe	Arg	Tyr	Asn	Pro	Val	Arg	Gln	Glu	Ile	Leu	Phe	Ala	Lys	Lys
				180					185					190		
	Ile	Glu	Val	Thr	Ile	Thr	Phe	Asp	Asn	Pro	Gln	Pro	Pro	Leu	Gln	Lys
				195					200				205			
35	Asn	Thr	Gly	Ile	Phe	Asn	Lys	Val	Ala	Ser	Ser	Ala	Phe	Ile	Asn	Tyr
				210					215				220			
	Glu	Ala	Asp	Gly	Lys	Ser	Ala	Ile	Glu	Asn	Asp	Met	Val	Phe	Ser	Arg
				225					230				235			240
	Gly	Thr	Thr	Thr	Tyr	Ile	Ser	Gly	Asn	Val	Ala	Ser	Asn	Leu	Pro	Gln
				245					250					255		
40	Asn	Cys	Asp	Tyr	Leu	Val	Ile	Tyr	Asp	Asp	Met	Phe	Asn	Val	Asn	Gln
				260					265					270		
	Gln	Pro	His	Asp	Glu	Ile	Lys	Arg	Leu	Cys	Glu	His	Arg	Ala	Phe	Tyr
				275					280				285			
45	Asn	Gly	Phe	Asp	Val	Ala	Ala	Val	Ser	Ile	Lys	Asp	Val	Leu	Asn	Ser
				290					295				300			
	Phe	Pro	Ser	Asn	Ala	Thr	Ser	Tyr	Ile	Asn	Glu	Thr	Lys	Leu	Lys	Asn
				305					310				315			320
	Phe	Ile	Arg	Ser	Val	Tyr	Asn	Gln	Ser	Asn	Ala	Lys	Arg	Thr	Leu	Asp
				325					330					335		
50	Gly	Lys	Leu	Gly	Tyr	Val	Leu	Leu	Ile	Gly	Lys	Pro	Leu	Ser	Lys	Tyr
				340					345					350		
	Leu	Ala	Asp	Thr	Asp	Asn	Thr	Lys	Val	Pro	Thr	Ser	Phe	Ile	His	Asn
				355					360				365			
55	Val	Ser	Leu	Ile	Pro	Ser	His	Pro	Thr	Phe	Gly	Ser	Ile	Cys	Ala	Ser
				370					375				380			
	Asp	Tyr	Phe	Phe	Ser	Cys	Val	Ser	Pro	Leu	Asp	Thr	Val	Gly	Asp	Leu
				385					390				395			400
	Phe	Ile	Gly	Arg	Phe	Ser	Val	Thr	Asn	Ala	His	Glu	Leu	His	Asn	Leu
				405					410					415		
60	Ile	Glu	Lys	Thr	Ile	Asn	Lys	Glu	Ile	Ser	Tyr	Asn	Pro	Ile	Ala	His
				420					425					430		
	Lys	Asn	Ile	Leu	Tyr	Ala	Glu	Gly	Lys	Gly	Cys	Asp	Ala	Pro	Ile	Leu
				435					440				445			
65	Arg	Leu	Phe	Leu	Lys	Glu	Ile	Ala	Ser	Gly	Tyr	Thr	Val	Asn	Ser	Ile
				450					455				460			
	Leu	Lys	Ser	Asn	Gln	Val	Ser	Ala	Ile	Asp	Ser	Ile	Phe	Asp	Cys	Leu
				465					470				475			480
	Asn	Asn	Gly	Ser	His	His	Phe	Tyr	Phe	Asn	Thr	His	Gly	Met	Pro	Thr
				485					490					495		
70	Val	Trp	Gly	Ile	Gly	Gln	Gly	Leu	Asp	Val	Asn	Thr	Leu	Thr	Ala	Arg
				500					505					510		
	Leu	Asn	Asn	Thr	Ser	Ser	Gln	Gly	Leu	Cys	Thr	Ser	Leu	Ser	Cys	Ser
				515					520				525			
75	Ser	Ala	Val	Ala	Asp	Ser	Thr	Ile	Arg	Ser	Leu	Gly	Glu	Val	Leu	Thr
				530					535				540			

WO 99/29870

PCT/AU98/01023

409/ 490

Thr Tyr Ala Pro Asn Lys Gly Phe Ser Ala Phe Leu Gly Gly Ser Arg
 545 550 555 560
 Ala Thr Gln Tyr Ala Val Tyr Leu Glu Gly Pro Cys Pro Pro Ser Glu
 565 570 575
 5 Phe Tyr Glu Tyr Leu Pro Tyr Ser Leu Tyr His Asn Leu Ser Thr Val
 580 585 590
 Val Gly Glu Met Leu Leu Ser Ser Ile Ile Asn Thr Asn Ser Val Asp
 595 600 605
 10 Thr Tyr Ser Lys Phe Asn Phe Asn Leu Leu Gly Asp Pro Ala Leu Asn
 610 615 620
 Ile Met Ala His Gly Met Glu Val Ser Asn Cys Ile Thr Leu Pro Asn
 625 630 635 640
 Asn Thr Ile Ile Ser Ser Pro Ile Thr Ile Lys Asn Gly Gly Cys Leu
 645 650 655
 15 Lys Ile Pro Glu Lys Gly Val Leu His Phe Thr Asn Asn Gly Ser Ile
 660 665 670
 Gln Val Met Ser Gly Gly Thr Leu Glu Ile Gly Asn Gln Ala Lys Ile
 675 680 685
 20 Ser Gly Glu Thr Gly Ala Asn Pro Thr Phe Ile Thr Val Tyr Gly Asp
 690 695 700
 Gly Leu Ala Ile Asn Lys Gln Val Glu Ile Asp Asn Ile Asp Arg Leu
 705 710 715 720
 Asn Leu Phe Ser Thr His Ser Val Met Pro Lys Phe His Phe Asp Ser
 725 730 735
 25 Val Lys Phe Asn Ser Ala Pro Leu Tyr Thr Thr Asn Cys Ile Val Glu
 740 745 750
 Ile Ser Asn Cys Glu Phe Thr Asn Arg Ser Asp Ile Ile Ser Lys Asn
 755 760 765
 30 Cys Asp Leu Ser Val Glu Asn Ser Met Phe Ser Ser Gly Ile Thr
 770 775 780
 Val Phe Lys Pro Met Ala Thr Ser Ser Ile Thr Gly Leu Ser Thr Lys
 785 790 795 800
 Ala Lys Ile Thr Asp Asn Thr Phe Phe Ala Thr Gly Asn Phe Ala Tyr
 805 810 815
 35 His Ile Thr Asn Thr Pro Gly Leu Thr Ala Thr Ser Asn Ala Ala Ile
 820 825 830
 Lys Leu Asp Asn Ile Pro Glu Tyr Tyr Ile Ser Gly Asn Lys Ile Val
 835 840 845
 40 Asn Cys Asp Glu Ala Leu Val Leu Asn Asn Ser Gly Asn Arg Thr Asn
 850 855 860
 Arg Leu His Asn Ile Thr Arg Asn Val Ile Lys Asn Cys Arg Ile Gly
 865 870 875 880
 Ser Thr Leu Tyr Asn Ser Tyr Gly Ile Tyr Asn Arg Asn Lys Ile Ser
 885 890 895
 45 Asn Asn His Ile Gly Val Arg Leu Leu Asn Asn Ser Cys Phe Tyr Phe
 900 905 910
 Asp Asn Ala Pro Val Ile Asn Glu Glu Asp Lys Gln Thr Phe Ile Ser
 915 920 925
 50 Asn Arg Thr Trp Gln Leu Tyr Ser Ser Asn Gly Thr Phe Pro Leu Asn
 930 935 940
 Phe His Tyr Asn Ser Leu Gln Gly Gly Asp Thr Asp Thr Trp Ile Tyr
 945 950 955 960
 Asn Asp Thr Tyr Thr Asn Arg Tyr Ile Asp Val Ser Asn Asn His Trp
 965 970 975
 55 Gly Asn Asn Asp Leu Phe Asp Pro Asn Gln Val Phe Asn Thr Pro Asp
 980 985 990
 Leu Phe Ile Trp Ile Pro Phe Trp Asp Gly Leu Pro Asn Gly Arg Ser
 995 1000 1005
 60 Gly Asn Ser Ser Ala Glu Ala Val Glu Phe Gln Thr Ala Leu Asp Cys
 1010 1015 1020
 Ile Gly Asn Ser Asp Tyr Leu Ser Ala Lys Val Ala Leu Lys Met Met
 1025 1030 1035 1040
 Val Glu Thr Tyr Pro Glu Ser Asp Phe Ala Ile Ala Ala Leu Lys Glu
 1045 1050 1055
 65 Leu Phe Arg Ile Glu Lys Met Ser Gly Asn Asp Tyr Glu Gly Leu Lys
 1060 1065 1070
 Asp Tyr Phe Arg Ser Asn Pro Thr Ile Ile Ser Ser Gln Asn Leu Phe
 1075 1080 1085
 70 Pro Thr Ala Asp Phe Leu Ser Ala Arg Cys Asp Ile Val Cys Glu Asn
 1090 1095 1100
 Tyr Gln Ser Ala Ile Asp Trp Tyr Glu Asn Arg Leu Asn Ser Glu Ile
 1105 1110 1115 1120
 Ser Tyr Gln Asp Ser Val Phe Ala Val Ile Asp Leu Gly Asp Ile Tyr
 1125 1130 1135
 75 Trp Asn Met Gln Leu Asp Ser Leu Arg Gly Thr Gly Ile Asp Leu Asn

WO 99/29870

PCT/AU98/01023

412/490

Ile Tyr Asn Arg Asn Lys Ile Ser Asn Asn His Ile Gly Val Arg Leu
 885 890 895
 Leu Asn Asn Ser Cys Phe Tyr Phe Asp Asn Ala Pro Val Ile Asn Glu
 900 905 910
 5 Glu Asp Lys Gln Thr Phe Ile Ser Asn Arg Thr Trp Gln Leu Tyr Ser
 915 920 925
 Ser Asn Gly Thr Phe Pro Leu Asn Phe His Tyr Asn Ser Leu Gln Gly
 930 935 940
 10 Gly Asp Thr Asp Thr Trp Ile Tyr Asn Asp Thr Tyr Thr Asn Arg Tyr
 945 950 955 960
 Ile Asp Val Ser Asn Asn His Trp Gly Asn Asn Asp Leu Phe Asp Pro
 965 970 975
 Asn Gln Val Phe Asn Thr Pro Asp Leu Phe Ile Trp Ile Pro Phe Trp
 980 985 990
 15 Asp Gly Leu Pro Asn Gly Arg Ser Gly Asn Ser Ser Ala Glu Ala Val
 995 1000 1005
 Glu Phe Gln Thr Ala Leu Asp Cys Ile Gly Asn Ser Asp Tyr Leu Ser
 1010 1015 1020
 20 Ala Lys Val Ala Leu Lys Met Met Val Glu Thr Tyr Pro Glu Ser Asp
 1025 1030 1035 1040
 Phe Ala Ile Ala Ala Leu Lys Glu Leu Phe Arg Ile Glu Lys Met Ser
 1045 1050 1055
 Gly Asn Asp Tyr Glu Gly Leu Lys Asp Tyr Phe Arg Ser Asn Pro Thr
 1060 1065 1070
 25 Ile Ile Ser Ser Gln Asn Leu Phe Pro Thr Ala Asp Phe Leu Ser Ala
 1075 1080 1085
 Arg Cys Asp Ile Val Cys Glu Asn Tyr Gln Ser Ala Ile Asp Trp Tyr
 1090 1095 1100
 30 Glu Asn Arg Leu Asn Ser Glu Ile Ser Tyr Gln Asp Ser Val Phe Ala
 1105 1110 1115 1120
 Val Ile Asp Leu Gly Asp Ile Tyr Trp Asn Met Gln Leu Asp Ser Leu
 1125 1130 1135
 Arg Gly Thr Gly Ile Asp Leu Asn Ile Leu Ser Cys Glu Gln Arg Lys
 1140 1145 1150
 35 Ser Leu Glu Ser His Gln Asn Val Lys Asn Tyr Leu Leu Ser Thr Leu
 1155 1160 1165
 Pro Glu Ser Thr Gly Thr Leu Leu Pro Pro Leu Glu Cys Asn Lys Ser
 1170 1175 1180
 40 Ser Leu Asp Lys Ser Lys Ile Ile Ser Ile Ser Pro Asn Pro Ala Lys
 1185 1190 1195 1200
 Ala Val Val Thr Ile Ile Tyr Tyr Thr Asp Asn Pro Ser Cys Ser Val
 1205 1210 1215
 Ile Lys Ile Tyr Gly Ile Asn Gly Ala Ser Ala Asp Ile Thr Gly Leu
 1220 1225 1230
 45 Pro Lys His Leu Ser Glu Gly Tyr Tyr Ser Ile Gln Phe Asn Thr Ser
 1235 1240 1245
 Asn Phe Asp Pro Gly Phe Tyr Leu Val Thr Leu Asn Val Asp Gln Lys
 1250 1255 1260
 50 Ile Ile Asp Thr Glu Lys Leu Arg Ile Lys
 1265 1270

(2) INFORMATION FOR SEQ ID NO:467

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 925 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 60 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
- 65 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...925
- 70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:467

Met Ala Ile Met Met Lys Ser Ile Val Phe Arg Ala Phe Leu Thr Ile
 1 5 10 15
 75 Leu Leu Ser Trp Ala Ala Ile Thr Asn Pro Thr Ala Gln Glu Ile Ser
 20 25 30

WO 99/29870

PCT/AU98/01023

413/490

Gly Met Asn Ala Ser Cys Leu Ala Ala Pro Ala Gln Pro Asp Thr Ile
 35 40 45
 Leu Tyr Glu Ser Phe Glu Asn Gly Pro Val Pro Asn Gly Trp Leu Glu
 50 55 60
 5 Ile Asp Ala Asp Ala Asp Gly Ala Thr Trp Gly Ser Pro Ser Gly Ser
 65 70 75 80
 Phe Ser Val Pro Tyr Gly His Asn Gly Leu Cys Thr Tyr Ser His Ile
 85 90 95
 10 Arg Ser Gly Ile Ser Thr Ala Gly Asn Tyr Leu Ile Thr Pro Asn Ile
 100 105 110
 Glu Gly Ala Lys Arg Val Lys Tyr Trp Val Cys Asn Gln Tyr Ser Thr
 115 120 125
 Asn Pro Glu His Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala Ile
 130 135 140
 15 Glu Asp Phe Val Leu Leu Phe Asp Asp Ser Ile Thr Gly Lys Pro Thr
 145 150 155 160
 Pro Leu Val Trp Arg Arg Arg Ile Val Asp Leu Pro Glu Gly Thr Lys
 165 170 175
 20 Tyr Ile Ala Trp Arg His Tyr Lys Val Thr Asp Ser His Thr Glu Phe
 180 185 190
 Leu Lys Leu Asp Asp Val Thr Val Tyr Arg Ser Ile Glu Gly Pro Glu
 195 200 205
 Pro Ala Thr Asp Phe Thr Val Ile Asn Ile Gly Gln Asn Val Gly Arg
 210 215 220
 25 Leu Thr Trp Asn Tyr Pro Glu Asp Tyr Gln Pro Glu Gly Lys Gly Asn
 225 230 235 240
 Glu Glu Leu Gln Leu Ser Gly Tyr Asn Ile Tyr Ala Asn Gly Thr Leu
 245 250 255
 30 Leu Ala Gln Ile Lys Asp Val Ser Ile Leu Glu Tyr Val Asp Ser Thr
 260 265 270
 Tyr Ser Leu Arg Asp Asn Pro Leu Gln Val Glu Tyr Cys Val Thr Ala
 275 280 285
 Val Tyr Asp Glu Ser Ile Glu Ser Ser Thr Val Cys Gly Thr Leu His
 290 295 300
 35 Tyr Ala Thr Asp Ala Ile Leu Tyr Glu Asn Phe Glu Asn Gly Pro Val
 305 310 315 320
 Pro Asn Gly Trp Leu Val Ile Asp Ala Asp Gly Asp Gly Phe Ser Trp
 325 330 335
 40 Gly His Tyr Leu Asn Ala Tyr Asp Ala Phe Pro Gly His Asn Gly Gly
 340 345 350
 His Cys Ser Leu Ser Ala Ser Tyr Val Pro Gly Ile Gly Pro Val Thr
 355 360 365
 Pro Asp Asn Tyr Leu Ile Thr Pro Lys Val Glu Gly Ala Lys Arg Val
 370 375 380
 45 Lys Tyr Trp Val Ser Thr Gln Asp Ala Asn Trp Ala Ala Glu His Tyr
 385 390 395 400
 Ala Val Met Ala Ser Thr Thr Gly Thr Ala Val Gly Asp Phe Val Ile
 405 410 415
 50 Leu Phe Glu Glu Thr Met Thr Ala Lys Pro Thr Gly Ala Trp Tyr Glu
 420 425 430
 Arg Thr Ile Asn Leu Pro Glu Gly Thr Lys Tyr Ile Ala Trp Arg His
 435 440 445
 Tyr Asn Cys Thr Asp Ile Tyr Phe Leu Lys Leu Asp Asp Ile Thr Val
 450 455 460
 55 Phe Gly Thr Pro Ala Ser Glu Pro Glu Pro Val Thr Asp Phe Val Val
 465 470 475 480
 Ser Leu Ile Glu Asn Asn Lys Gly Arg Leu Lys Trp Asn Tyr Pro Asn
 485 490 495
 60 Gly Tyr Glu Pro Asp Lys Thr Asp Asp Lys Asp Pro Leu Gln Leu Ala
 500 505 510
 Gly Tyr Asn Ile Tyr Ala Asn Gly Ser Leu Leu Val His Ile Gln Asp
 515 520 525
 Pro Thr Val Leu Glu Tyr Ile Asp Glu Thr Tyr Ser Ser Arg Asp Asp
 530 535 540
 65 Gln Val Glu Val Glu Tyr Cys Val Thr Ala Val Tyr Asn Asp Asn Ile
 545 550 555 560
 Glu Ser Gln Ser Val Cys Asp Lys Leu Ile Tyr Asp Ser Gln Ser Asp
 565 570 575
 70 Ile Ile Leu Tyr Glu Gly Phe Glu Ala Gly Ser Ile Pro Glu Gly Trp
 580 585 590
 Leu Leu Ile Asp Ala Asp Gly Asp Asn Val Asn Trp Asp Tyr Tyr Pro
 595 600 605
 Trp Thr Met Tyr Gly His Asp Ser Glu Lys Cys Ile Ala Ser Pro Ser
 610 615 620
 75 Tyr Leu Pro Met Ile Gly Val Leu Thr Pro Asp Asn Tyr Leu Val Thr

WO 99/29870

PCT/AU98/01023

414/ 490

625 630 635 640
Pro Arg Leu Glu Gly Ala Lys Leu Val Lys Tyr Trp Val Ser Ala Gln
645 650 655
5 Asp Ala Val Tyr Ser Ala Glu His Tyr Ala Val Met Val Ser Thr Thr
660 665 670
Gly Thr Ala Val Glu Asp Phe Val Leu Leu Phe Glu Glu Thr Met Thr
675 680 685
Ala Lys Ala Asn Gly Ala Trp Tyr Glu Arg Thr Ile Thr Leu Pro Ala
690 695 700
10 Gly Thr Lys Tyr Ile Ala Trp Arg His Tyr Asp Cys Thr Asp Met Phe
705 710 715 720
Phe Leu Leu Leu Asp Asp Ile Thr Val Tyr Arg Ser Thr Glu Thr Val
725 730 735
15 Pro Glu Pro Val Thr Asp Phe Val Val Ser Leu Ile Glu Asn Asn Lys
740 745 750
Gly Arg Leu Lys Trp Asn Tyr Pro Asn Gly Tyr Glu Pro Asp Lys Thr
755 760 765
Asp Asp Lys Lys Pro Leu Gln Leu Thr Gly Tyr Asn Ile Tyr Ala Asn
770 775 780
20 Gly Ser Leu Leu Val His Ile Gln Asp Pro Thr Val Leu Glu Tyr Ile
785 790 795 800
Asp Glu Thr Tyr Ser Ser Arg Asp Gly Gln Val Glu Met Glu Tyr Cys
805 810 815
Val Thr Ala Val Tyr Asn Asp Asn Ile Glu Ser Gln Ser Val Cys Asp
820 825 830
25 Lys Leu Asn Tyr Thr Ile Thr Ser Leu Asp Asn Ile Gln Ser Asp Thr
835 840 845
Ser Leu Lys Ile Tyr Pro Asn Pro Ala Ser Tyr Val Val Arg Ile Glu
850 855 860
30 Gly Leu Ser Arg Ser Lys Ser Thr Ile Glu Leu Tyr Asn Ala Leu Gly
865 870 875 880
Ile Cys Ile Leu Arg Glu Glu Thr His Ser Glu Lys Thr Glu Ile Asp
885 890 895
35 Val Ser Arg Leu Asn Asp Gly Val Tyr Leu Ile Lys Val Val Gly Gly
900 905 910
Asn Lys Thr Thr Thr Glu Lys Val Glu Ile Lys Arg Pro
915 920 925

40 (2) INFORMATION FOR SEQ ID NO:468
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 922 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
45 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
50 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc feature
55 (B) LOCATION 1...922
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468

60 Met Met Lys Ser Ile Val Phe Arg Ala Phe Leu Thr Ile Leu Leu Ser
1 5 10 15
Trp Ala Ala Ile Thr Asn Pro Thr Ala Gln Glu Ile Ser Gly Met Asn
20 25 30
Ala Ser Cys Leu Ala Ala Pro Ala Gln Pro Asp Thr Ile Leu Tyr Glu
35 40 45
65 Ser Phe Glu Asn Gly Pro Val Pro Asn Gly Trp Leu Glu Ile Asp Ala
50 55 60
Asp Ala Asp Gly Ala Thr Trp Gly Ser Pro Ser Gly Ser Phe Ser Val
65 70 75 80
70 Pro Tyr Gly His Asn Gly Leu Cys Thr Tyr Ser His-Ile Arg Ser Gly
85 90 95
Ile Ser Thr Ala Gly Asn Tyr Leu Ile Thr Pro Asn Ile Glu Gly Ala
100 105 110
Lys Arg Val Lys Tyr Trp Val Cys Asn Gln Tyr Ser Thr Asn Pro Glu
115 120 125
75 His Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala Ile Glu Asp Phe

WO 99/29870

PCT/AU98/01023

416/ 490

Val Thr Asp Phe Val Val Ser Leu Ile Glu Asn Asn Lys Gly Arg Leu
 740 745 750
 Lys Trp Asn Tyr Pro Asn Gly Tyr Glu Pro Asp Lys Thr Asp Asp Lys
 755 760 765
 5 Lys Pro Leu Gln Leu Thr Gly Tyr Asn Ile Tyr Ala Asn Gly Ser Leu
 770 775 780
 Leu Val His Ile Gln Asp Pro Thr Val Leu Glu Tyr Ile Asp Glu Thr
 785 790 795 800
 10 Tyr Ser Ser Arg Asp Gly Gln Val Glu Met Glu Tyr Cys Val Thr Ala
 805 810 815
 Val Tyr Asn Asp Asn Ile Glu Ser Gln Ser Val Cys Asp Lys Leu Asn
 820 825 830
 Tyr Thr Ile Thr Ser Leu Asp Asn Ile Gln Ser Asp Thr Ser Leu Lys
 835 840 845
 15 Ile Tyr Pro Asn Pro Ala Ser Tyr Val Val Arg Ile Glu Gly Leu Ser
 850 855 860
 Arg Ser Lys Ser Thr Ile Glu Leu Tyr Asn Ala Leu Gly Ile Cys Ile
 865 870 875 880
 20 Leu Arg Glu Glu Thr His Ser Glu Lys Thr Glu Ile Asp Val Ser Arg
 885 890 895
 Leu Asn Asp Gly Val Tyr Leu Ile Lys Val Val Gly Gly Asn Lys Thr
 900 905 910
 Thr Thr Glu Lys Val Glu Ile Lys Arg Pro
 915 920

25 (2) INFORMATION FOR SEQ ID NO:469
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 921 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 30 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 40 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...921

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469
 45 Met Lys Ser Ile Val Phe Arg Ala Phe Leu Thr Ile Leu Leu Ser Trp
 1 5 10 15
 Ala Ala Ile Thr Asn Pro Thr Ala Gln Glu Ile Ser Gly Met Asn Ala
 20 25 30
 50 Ser Cys Leu Ala Ala Pro Ala Gln Pro Asp Thr Ile Leu Tyr Glu Ser
 35 40 45
 Phe Glu Asn Gly Pro Val Pro Asn Gly Trp Leu Glu Ile Asp Ala Asp
 50 55 60
 Ala Asp Gly Ala Thr Trp Gly Ser Pro Ser Gly Ser Phe Ser Val Pro
 65 70 75 80
 55 Tyr Gly His Asn Gly Leu Cys Thr Tyr Ser His Ile Arg Ser Gly Ile
 85 90 95
 Ser Thr Ala Gly Asn Tyr Leu Ile Thr Pro Asn Ile Glu Gly Ala Lys
 100 105 110
 60 Arg Val Lys Tyr Trp Val Cys Asn Gln Tyr Ser Thr Asn Pro Glu His
 115 120 125
 Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala Ile Glu Asp Phe Val
 130 135 140
 65 Leu Leu Phe Asp Asp Ser Ile Thr Gly Lys Pro Thr Pro Leu Val Trp
 145 150 155 160
 Arg Arg Arg Ile Val Asp Leu Pro Glu Gly Thr Lys Tyr Ile Ala Trp
 165 170 175
 Arg His Tyr Lys Val Thr Asp Ser His Thr Glu Phe Leu Lys Leu Asp
 180 185 190
 70 Asp Val Thr Val Tyr Arg Ser Ile Glu Gly Pro Glu Pro Ala Thr Asp
 195 200 205
 Phe Thr Val Ile Asn Ile Gly Gln Asn Val Gly Arg Leu Thr Trp Asn
 210 215 220
 75 Tyr Pro Glu Asp Tyr Gln Pro Glu Gly Lys Gly Asn Glu Glu Leu Gln
 225 230 235 240

WO 99/29870

PCT/AU98/01023

417 / 490

	Leu	Ser	Gly	Tyr	Asn	Ile	Tyr	Ala	Asn	Gly	Thr	Leu	Leu	Ala	Gln	Ile
					245					250					255	
	Lys	Asp	Val	Ser	Ile	Leu	Glu	Tyr	Val	Asp	Ser	Thr	Tyr	Ser	Leu	Arg
				260					265					270		
5	Asp	Asn	Pro	Leu	Gln	Val	Glu	Tyr	Cys	Val	Thr	Ala	Val	Tyr	Asp	Glu
				275				280					285			
	Ser	Ile	Glu	Ser	Ser	Thr	Val	Cys	Gly	Thr	Leu	His	Tyr	Ala	Thr	Asp
		290					295					300				
10	Ala	Ile	Leu	Tyr	Glu	Asn	Phe	Glu	Asn	Gly	Pro	Val	Pro	Asn	Gly	Trp
	305					310					315				320	
	Leu	Val	Ile	Asp	Ala	Asp	Gly	Asp	Gly	Phe	Ser	Trp	Gly	His	Tyr	Leu
				325						330					335	
	Asn	Ala	Tyr	Asp	Ala	Phe	Pro	Gly	His	Asn	Gly	Gly	His	Cys	Ser	Leu
				340					345					350		
15	Ser	Ala	Ser	Tyr	Val	Pro	Gly	Ile	Gly	Pro	Val	Thr	Pro	Asp	Asn	Tyr
		355					360						365			
	Leu	Ile	Thr	Pro	Lys	Val	Glu	Gly	Ala	Lys	Arg	Val	Lys	Tyr	Trp	Val
		370				375						380				
20	Ser	Thr	Gln	Asp	Ala	Asn	Trp	Ala	Ala	Glu	His	Tyr	Ala	Val	Met	Ala
	385					390					395				400	
	Ser	Thr	Thr	Gly	Thr	Ala	Val	Gly	Asp	Phe	Val	Ile	Leu	Phe	Glu	Glu
				405						410					415	
	Thr	Met	Thr	Ala	Lys	Pro	Thr	Gly	Ala	Trp	Tyr	Glu	Arg	Thr	Ile	Asn
				420					425					430		
25	Leu	Pro	Glu	Gly	Thr	Lys	Tyr	Ile	Ala	Trp	Arg	His	Tyr	Asn	Cys	Thr
		435						440					445			
	Asp	Ile	Tyr	Phe	Leu	Lys	Leu	Asp	Asp	Ile	Thr	Val	Phe	Gly	Thr	Pro
		450					455					460				
30	Ala	Ser	Glu	Pro	Glu	Pro	Val	Thr	Asp	Phe	Val	Val	Ser	Leu	Ile	Glu
	465					470				475					480	
	Asn	Asn	Lys	Gly	Arg	Leu	Lys	Trp	Asn	Tyr	Pro	Asn	Gly	Tyr	Glu	Pro
				485					490					495		
	Asp	Lys	Thr	Asp	Asp	Lys	Asp	Pro	Leu	Gln	Leu	Ala	Gly	Tyr	Asn	Ile
				500					505					510		
35	Tyr	Ala	Asn	Gly	Ser	Leu	Leu	Val	His	Ile	Gln	Asp	Pro	Thr	Val	Leu
		515						520						525		
	Glu	Tyr	Ile	Asp	Glu	Thr	Tyr	Ser	Ser	Arg	Asp	Asp	Gln	Val	Glu	Val
		530					535					540				
40	Glu	Tyr	Cys	Val	Thr	Ala	Val	Tyr	Asn	Asp	Asn	Ile	Glu	Ser	Gln	Ser
	545					550					555				560	
	Val	Cys	Asp	Lys	Leu	Ile	Tyr	Asp	Ser	Gln	Ser	Asp	Ile	Ile	Leu	Tyr
				565						570					575	
	Glu	Gly	Phe	Glu	Ala	Gly	Ser	Ile	Pro	Glu	Gly	Trp	Leu	Leu	Ile	Asp
				580					585					590		
45	Ala	Asp	Gly	Asp	Asn	Val	Asn	Trp	Asp	Tyr	Tyr	Pro	Trp	Thr	Met	Tyr
		595						600					605			
	Gly	His	Asp	Ser	Glu	Lys	Cys	Ile	Ala	Ser	Pro	Ser	Tyr	Leu	Pro	Met
		610					615					620				
50	Ile	Gly	Val	Leu	Thr	Pro	Asp	Asn	Tyr	Leu	Val	Thr	Pro	Arg	Leu	Glu
	625					630					635				640	
	Gly	Ala	Lys	Leu	Val	Lys	Tyr	Trp	Val	Ser	Ala	Gln	Asp	Ala	Val	Tyr
				645						650					655	
	Ser	Ala	Glu	His	Tyr	Ala	Val	Met	Val	Ser	Thr	Thr	Gly	Thr	Ala	Val
				660					665					670		
55	Glu	Asp	Phe	Val	Leu	Leu	Phe	Glu	Glu	Thr	Met	Thr	Ala	Lys	Ala	Asn
		675						680					685			
	Gly	Ala	Trp	Tyr	Glu	Arg	Thr	Ile	Thr	Leu	Pro	Ala	Gly	Thr	Lys	Tyr
		690					695					700				
60	Ile	Ala	Trp	Arg	His	Tyr	Asp	Cys	Thr	Asp	Met	Phe	Phe	Leu	Leu	Leu
	705					710				715					720	
	Asp	Asp	Ile	Thr	Val	Tyr	Arg	Ser	Thr	Glu	Thr	Val	Pro	Glu	Pro	Val
				725					730					735		
	Thr	Asp	Phe	Val	Val	Ser	Leu	Ile	Glu	Asn	Asn	Lys	Gly	Arg	Leu	Lys
				740					745					750		
65	Trp	Asn	Tyr	Pro	Asn	Gly	Tyr	Glu	Pro	Asp	Lys	Thr	Asp	Asp	Lys	Lys
		755						760					765			
	Pro	Leu	Gln	Leu	Thr	Gly	Tyr	Asn	Ile	Tyr	Ala	Asn	Gly	Ser	Leu	Leu
		770					775					780				
70	Val	His	Ile	Gln	Asp	Pro	Thr	Val	Leu	Glu	Tyr	Ile	Asp	Glu	Thr	Tyr
	785					790					795				800	
	Ser	Ser	Arg	Asp	Gly	Gln	Val	Glu	Met	Glu	Tyr	Cys	Val	Thr	Ala	Val
				805						810					815	
	Tyr	Asn	Asp	Asn	Ile	Glu	Ser	Gln	Ser	Val	Cys	Asp	Lys	Leu	Asn	Tyr
				820					825					830		
75	Thr	Ile	Thr	Ser	Leu	Asp	Asn	Ile	Gln	Ser	Asp	Thr	Ser	Leu	Lys	Ile

WO 99/29870

PCT/AU98/01023

418/490

5 Tyr Pro Asn Pro Ala Ser Tyr Val Val Arg Ile Glu Gly Leu Ser Arg
835 840 845
850 855 860
Ser Lys Ser Thr Ile Glu Leu Tyr Asn Ala Leu Gly Ile Cys Ile Leu
865 870 875 880
Arg Glu Glu Thr His Ser Glu Lys Thr Glu Ile Asp Val Ser Arg Leu
885 890 895
Asn Asp Gly Val Tyr Leu Ile Lys Val Val Gly Gly Asn Lys Thr Thr
900 910
10 Thr Glu Lys Val Glu Ile Lys Arg Pro
915 920

(2) INFORMATION FOR SEQ ID NO:470

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 593 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- 20 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
- 25 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(D) LOCATION 1...593
- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:470

Hot Asn Ser Ile Met Lys Tyr Gln Leu Tyr Thr Ala Val Ile Met Ala
1 5 10 15
35 Leu Ser Val Ser Ser Val Cys Gly Gln Thr Pro Arg Asn Thr Glu Trp
20 25 30
Lys Arg Pro Asp Thr Leu Arg Arg Glu Leu Trp Ile Val Asn Asp Gln
35 40 45
40 Thr Val Glu Met Glu His Ala Asp Pro Leu Pro Ala Tyr Lys Ala
50 55 60
Ile Glu Pro Arg Leu Lys Pro Phe Arg Pro Glu Tyr Asn Lys Arg Thr
65 70 75 80
Phe Gly Phe Val Pro Glu Val Ser Ser Ser Gly Arg Asn Asn Leu Pro
85 90 95
45 Asn Ile Leu Pro Thr Glu Gly His Met Lys His Arg Gly Tyr Leu Asn
100 105 110
Ile Gly Ile Gly His Thr Leu Asn Gln Arg Met Asp Ala Gly Tyr Arg
115 120 125
50 Leu Ile Asp Ala Glu Gln Glu Arg Leu Asn Leu Phe Leu Ser Tyr Arg
130 135 140
Gly Met Lys Ser Ala Phe Asn Thr Gly Asp Phe Asp Gly Asp Arg Lys
145 150 155 160
Asp Arg Arg Met Met Ala Gly Val Asp Tyr Glu Gln Arg Arg Pro Ser
165 170 175
55 Phe Val Leu Ala Thr Gly Leu Tyr Tyr Ser Asn His Tyr Phe Asn Asn
180 185 190
Tyr Gly Arg Gly Ala Thr Thr Asn Val Gly Ser Ile Pro Gln Leu Ser
195 200 205
60 Thr Pro Val Thr Pro Gln Met Asp Asn Gly Thr His Asn Val Arg Val
210 215 220
Tyr Leu Gly Ala Lys Asn Asp Val Ile Asp Ala Arg Ile Asp Tyr Arg
225 230 235 240
Phe Phe Arg Ser Ile Pro Tyr Leu Gly Thr Asp Pro Met Lys Ala Leu
245 250 255
65 Thr Glu His Thr Pro Glu Leu Asn Val Thr Met Ser Asn Glu Leu Ser
260 265 270
Asp Asp Ile Lys Leu Gly Val Glu Val Arg Thr Gly Gly Lys Phe Phe
275 280 285
70 Ala Lys Asn Ser Glu Met Ile Gln Thr Gly Val Leu Ser Glu Thr Asp
290 295 300
Arg Asn Leu Tyr Tyr Val Glu Gly Ala Pro Thr Ile Gly Phe Val Gly
305 310 315 320
Asp Ser Asp Asn Met Gln Trp Asn Ile Gln Ala Gly Val Gly Ile Ser
325 330 335
75 Ser His Phe Gly Ala Lys Gly Arg Leu Phe Phe Trp Pro Lys Leu Asp

WO 99/29870

PCT/AU98/01023

419/490

340 345 350
 Ala Ser Leu Ser Ile Phe Pro Ser Trp Arg Val Tyr Ala Lys Ala Phe
 355 360 365
 Gly Gly Val Ile Arg Asn Gly Leu Ala Asp Val Met Gln Glu Glu Met
 370 375 380
 5 Pro Tyr Leu Met Pro Asn Thr Ile Val Leu Pro Ser Arg Asn Ala Leu
 385 390 395 400
 Thr Ala Gln Leu Gly Val Lys Gly Asn Ile Ala Asp Val Val Arg Met
 405 410 415
 10 Glu Val Tyr Gly Asp Phe Ser Lys Leu Thr Gly Val Pro Phe Tyr Thr
 420 425 430
 Pro Thr Leu Pro Leu Tyr Asn Pro Ser Asp Leu Tyr Gln Tyr Asn Val
 435 440 445
 15 Ser Phe Leu Pro Ile Tyr Ala Asp Gly Ser Arg Trp Arg Ala Gly Gly
 450 455 460
 Lys Leu Glu Tyr Ser Tyr Arg Asp Met Leu Arg Phe Leu Val Asp Ala
 465 470 475 480
 Ser Tyr Gly Lys Trp Asn Leu Asp Gly Gly Leu Val Ala Ser Met Gln
 485 490 495
 20 Pro Asp Leu Ile Leu Lys Ala Glu Val Gly Val His Pro Ile Ala Pro
 500 505 510
 Leu Asp Val Arg Leu Arg Tyr Thr Gln Leu Asn Gly Arg Tyr Arg Tyr
 515 520 525
 25 Ser Phe Gly Ser Ala Gly Ser Glu Ala Leu Gly Ile Gly Asn Val His
 530 535 540
 Leu Leu Ser Ala Asp Val Ser Tyr Lys Leu Lys Lys Asn Leu Ser Leu
 545 550 555 560
 Tyr Leu Lys Ile Asp Asn Met Leu Ala Glu Thr Thr Glu Leu Ile Gly
 565 570 575
 30 Tyr Tyr Pro Met Gln Pro Phe His Cys Phe Ala Gly Phe Ser Trp Thr
 580 585 590
 Phe

 35 (2) INFORMATION FOR SEQ ID NO:471
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 589 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 40
 (ii) MOLECULE TYPE: protein
 45 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 50 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...589
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:471
 55 Met Lys Tyr Gln Leu Tyr Thr Ala Val Ile Met Ala Leu Ser Val Ser
 1 5 10 15
 Ser Val Cys Gly Gln Thr Pro Arg Asn Thr Glu Thr Lys Arg Pro Asp
 20 25 30
 60 Thr Leu Arg Arg Glu Leu Thr Ile Val Asn Asp Gln Thr Val Glu Met
 35 40 45
 Glu His Ala Asp Pro Leu Pro Ala Ala Tyr Lys Ala Ile Glu Pro Arg
 50 55 60
 Leu Lys Pro Phe Arg Pro Glu Tyr Asn Lys Arg Thr Phe Gly Phe Val
 65 70 75 80
 Pro Glu Val Ser Ser Ser Gly Arg Asn Asn Leu Pro Asn Ile Leu Pro
 85 90 95
 Thr Glu Gly His Met Lys His Arg Gly Tyr Leu Asn Ile Gly Ile Gly
 100 105 110
 70 His Thr Leu Asn Gln Arg Met Asp Ala Gly Tyr Arg Leu Ile Asp Ala
 115 120 125
 Glu Gln Glu Arg Leu Asn Leu Phe Leu Ser Tyr Arg Gly Met Lys Ser
 130 135 140
 Ala Phe Asn Thr Gly Asp Phe Asp Gly Asp Lys Asp Arg Arg Met
 145 150 155 160
 75 Met Ala Gly Val Asp Tyr Glu Gln Arg Arg Pro Ser Phe Val Leu Ala

WO 99/29870

PCT/AU98/01023

420/ 490

5 Thr Gly Leu Tyr Tyr Ser Asn His Tyr Phe Asn Asn Tyr Gly Arg Gly
180 185 190
Ala Thr Thr Asn Val Gly Ser Ile Pro Gln Leu Ser Thr Pro Val Thr
195 200 205
Pro Gln Met Asp Asn Gly Thr His Asn Val Arg Val Tyr Leu Gly Ala
210 215 220
Lys Asn Asp Val Ile Asp Ala Arg Ile Asp Tyr Arg Phe Phe Arg Ser
225 230 235 240
10 Ile Pro Tyr Leu Gly Thr Asp Pro Met Lys Ala Leu Thr Glu His Thr
245 250 255
Pro Glu Leu Asn Val Thr Met Ser Asn Glu Leu Ser Asp Asp Ile Lys
260 265 270
15 Leu Gly Val Glu Val Arg Thr Gly Gly Leu Phe Phe Ala Lys Asn Ser
275 280 285
Glu Met Ile Gln Thr Gly Val Leu Ser Glu Thr Asp Arg Asn Leu Tyr
290 295 300
Tyr Val Glu Gly Ala Pro Thr Ile Gly Phe Val Gly Asp Ser Asp Asn
305 310 315 320
20 Met Gln Trp Asn Ile Gln Ala Gly Val Gly Ile Ser Ser His Phe Gly
325 330 335
Ala Lys Gly Arg Leu Phe Phe Trp Pro Lys Leu Asp Ala Ser Leu Ser
340 345 350
Ile Phe Pro Ser Trp Arg Val Tyr Ala Lys Ala Phe Gly Gly Val Ile
355 360 365
25 Arg Asn Gly Leu Ala Asp Val Met Gln Glu Glu Met Pro Tyr Leu Met
370 375 380
Pro Asn Thr Ile Val Leu Pro Ser Arg Asn Ala Leu Thr Ala Gln Leu
385 390 395 400
30 Gly Val Lys Gly Asn Ile Ala Asp Val Val Arg Met Glu Val Tyr Gly
405 410 415
Asp Phe Ser Lys Leu Thr Gly Val Pro Phe Tyr Thr Pro Thr Leu Pro
420 425 430
35 Leu Tyr Asn Pro Ser Asp Leu Tyr Gln Tyr Asn Val Ser Phe Leu Pro
435 440 445
Ile Tyr Ala Asp Gly Ser Arg Trp Arg Ala Gly Gly Lys Leu Glu Tyr
450 455 460
Ser Tyr Arg Asp Met Leu Arg Phe Leu Val Asp Ala Ser Tyr Gly Lys
465 470 475 480
40 Trp Asn Leu Asp Gly Gly Leu Val Ala Ser Met Gln Pro Asp Leu Ile
485 490 495
Leu Lys Ala Glu Val Gly Val His Pro Ile Ala Pro Leu Asp Val Arg
500 505 510
45 Leu Arg Tyr Thr Gln Leu Asn Gly Arg Tyr Arg Tyr Ser Phe Gly Ser
515 520 525
Ala Gly Ser Glu Ala Leu Gly Ile Gly Asn Val His Leu Leu Ser Ala
530 535 540
Asp Val Ser Tyr Lys Leu Lys Lys Asn Leu Ser Leu Tyr Leu Lys Ile
545 550 555 560
50 Asp Asn Met Leu Ala Glu Thr Thr Glu Leu Ile Gly Tyr Tyr Pro Met
565 570 575
Gln Pro Phe His Cys Phe Ala Gly Phe Ser Trp Thr Phe
580 585

55 (2) INFORMATION FOR SEQ ID NO:472

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 346 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

65 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...346

70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:472

75 Met Met Glu Lys Cys Ile Phe Ala His Tyr Pro His Asn Leu Val Phe

WO 99/29870

PCT/AU98/01023

421/ 490

1 Met Ile Arg Lys His Phe Gly Ile Ile Leu Gly Phe Leu Ser Leu Val
20 25 30
5 Phe Ser Ala Gly Ala Gln Gln Glu Lys Gln Val Phe His Phe Leu Asn
35 40 45
Leu Pro Ala Thr Ala Gln Ala Leu Ala Ala Gly Gly Lys Ala Ile Thr
50 55 60
Ile Val Asp Asp Asn Pro Gly Leu Ala Phe Glu Asn Pro Ala Leu Leu
65 70 75 80
10 Gly Tyr Glu Ser Gly Gly Arg Ala Phe Leu Ser Tyr Leu Tyr Tyr Met
85 90 95
Ser Gly Ser His Met Gly Asn Ala Cys Tyr Ala Ser Ser Val Gly Glu
100 105 110
15 Arg Gly Met Trp Gly Val Gly Met Arg Phe Leu Asn Tyr Gly Ser Met
115 120 125
Gln Gly Tyr Asp Gln Asn Ala Ile Ala Thr Gly Ser Phe Ser Ala Ser
130 135 140
Asp Ile Ala Val Gln Gly Phe Tyr Ser His Glu Leu Ser Asn His Phe
145 150 155 160
20 Arg Gly Gly Val Ser Leu Lys Ala Leu Tyr Ser Ser Ile Glu Thr Tyr
165 170 175
Ser Ser Phe Gly Leu Gly Val Asp Val Gly Ile Ser Tyr Tyr Asp Asp
180 185 190
25 Asp Lys Gly Tyr Ser Ala Ser Ala Leu Phe Lys Asn Val Gly Ala Gln
195 200 205
Leu Lys Gly Tyr Asn Glu Glu Arg Glu Pro Leu Asp Trp Asp Phe Gln
210 215 220
Leu Gly Phe Ser Arg Ser Phe Ile Asn Ala Pro Phe Arg Leu His Ile
225 230 235 240
30 Thr Leu Phe Asn Leu Asn Pro His Tyr Phe Lys Arg Leu Val Pro Arg
245 250 255
Asp Leu Ser Lys Met Gln Lys Phe Leu Arg His Phe Ser Ile Gly Ala
260 265 270
35 Glu Phe Thr Pro Ser Glu Arg Phe Trp Val Gly Leu Gly Tyr Thr Pro
275 280 285
Gln Ile Ala Gln Asp Phe Glu Val Glu Gly Gly Asn Lys Trp Gly Gly
290 295 300
Leu Ser Ala Gly Val Gly Phe Thr Ser Gly Val Val Arg Val Gly Val
305 310 315 320
40 Ser Ala Ala Thr Tyr His Pro Ala Ala Leu Ser Phe Met Cys Ser Val
325 330 335
Gly Ile Arg Leu Asp Asp Lys Ser Ile Phe
340 345

45 (2) INFORMATION FOR SEQ ID NO:473

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 345 amino acids
(B) TYPE: amino acid
50 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
60 (B) LOCATION 1...345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473

65 Met Glu Lys Cys Ile Phe Ala His Tyr Pro His Asn Leu Val Phe Met
1 5 10 15
Ile Arg Lys His Phe Gly Ile Ile Leu Gly Phe Leu Ser Leu Val Phe
20 25 30
70 Ser Ala Gly Ala Gln Gln Glu Lys Gln Val Phe His-Phe Leu Asn Leu
35 40 45
Pro Ala Thr Ala Gln Ala Leu Ala Ala Gly Gly Lys Ala Ile Thr Ile
50 55 60
Val Asp Asp Asn Pro Gly Leu Ala Phe Glu Asn Pro Ala Leu Leu Gly
65 70 75 80
75 Tyr Glu Ser Gly Gly Arg Ala Phe Leu Ser Tyr Leu Tyr Tyr Met Ser

WO 99/29870

PCT/AU98/01023

422/490

5 Gly Ser His Met 85 Gly Asn Ala Cys Tyr 90 Ala Ser Ser Val Gly Glu Arg
100 105 110
115 120 125
130 135 140
145 150 155 160
10 Gly Tyr Asp Gln Asn Ala Ile Ala Thr Gly Ser Phe Ser Ala Ser Asp
130 135 140
145 150 155 160
11 Gly Gly Val Ser Leu Lys Ala Leu Tyr Ser Ser Ile Glu Thr Tyr Ser
165 170 175
12 Ser Phe Gly Leu Gly Val Asp Val Gly Ile Ser Tyr Tyr Asp Asp
180 185 190
15 Lys Gly Tyr Ser Ala Ser Ala Leu Phe Lys Asn Val Gly Ala Gln Leu
195 200 205
20 Lys Gly Tyr Asn Glu Glu Arg Glu Pro Leu Asp Trp Asp Phe Gln Leu
210 215 220
25 Gly Phe Ser Arg Ser Phe Ile Asn Ala Pro Phe Arg Leu His Ile Thr
225 230 235 240
30 Leu Phe Asn Leu Asn Pro His Tyr Phe Lys Arg Leu Val Pro Arg Asp
245 250 255
35 Leu Ser Lys Met Gln Lys Phe Leu Arg His Phe Ser Ile Gly Ala Glu
260 265 270
40 Phe Thr Pro Ser Glu Arg Phe Trp Val Gly Leu Gly Tyr Thr Pro Gln
275 280 285
45 Ile Ala Gln Asp Phe Glu Val Glu Gly Gly Asn Lys Trp Gly Gly Leu
290 295 300
50 Ser Ala Gly Val Gly Phe Thr Ser Gly Val Val Arg Val Gly Val Ser
305 310 315 320
55 Ala Ala Thr Tyr His Pro Ala Ala Leu Ser Phe Met Cys Ser Val Gly
325 330 335
60 Ile Arg Leu Asp Asp Lys Ser Ile Phe 340 345
65 (2) INFORMATION FOR SEQ ID NO:474
66 (i) SEQUENCE CHARACTERISTICS:
67 (A) LENGTH: 330 amino acids
68 (B) TYPE: amino acid
69 (D) TOPOLOGY: linear
70 (ii) MOLECULE TYPE: protein
71 (iii) HYPOTHETICAL: YES
72 (vi) ORIGINAL SOURCE:
73 (A) ORGANISM: Porphyromonas gingivalis
74 (ix) FEATURE:
75 (A) NAME/KEY: misc_feature
76 (B) LOCATION 1...330
77 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:474
78 Met Ile Arg Lys His Phe Gly Ile Ile Leu Gly Phe Leu Ser Leu Val
1 5 10 15
79 Phe Ser Ala Gly Ala Gln Gln Glu Lys Gln Val Phe His Phe Leu Asn
20 25 30
80 Leu Pro Ala Thr Ala Gln Ala Leu Ala Ala Gly Gly Lys Ala Ile Thr
35 40 45
81 Ile Val Asp Asp Asn Pro Gly Leu Ala Phe Glu Asn Pro Ala Leu Leu
50 55 60
82 Gly Tyr Glu Ser Gly Gly Arg Ala Phe Leu Ser Tyr Leu Tyr Tyr Met
65 70 75 80
83 Ser Gly Ser His Met Gly Asn Ala Cys Tyr Ala Ser Ser Val Gly Glu
85 90 95
84 Arg Gly Met Trp Gly Val Gly Met Arg Phe Leu Asn Tyr Gly Ser Met
100 105 110
85 Gln Gly Tyr Asp Gln Asn Ala Ile Ala Thr Gly Ser Phe Ser Ala Ser
115 120 125
86 Asp Ile Ala Val Gln Gly Phe Tyr Ser His Glu Leu Ser Asn His Phe
130 135 140
87 Arg Gly Gly Val Ser Leu Lys Ala Leu Tyr Ser Ser Ile Glu Thr Tyr
145 150 155 160
88 Ser Ser Phe Gly Leu Gly Val Asp Val Gly Ile Ser Tyr Tyr Asp Asp

WO 99/29870

PCT/AU98/01023

423/ 490

165 170 175
Asp Lys Gly Tyr Ser Ala Ser Ala Leu Phe Lys Asn Val Gly Ala Gln
180 185 190
5 Leu Lys Gly Tyr Asn Glu Glu Arg Glu Pro Leu Asp Trp Asp Phe Gln
195 200 205
Leu Gly Phe Ser Arg Ser Phe Ile Asn Ala Pro Phe Arg Leu His Ile
210 215 220
Thr Leu Phe Asn Leu Asn Pro His Tyr Phe Lys Arg Leu Val Pro Arg
225 230 235 240
10 Asp Leu Ser Lys Met Gln Lys Phe Leu Arg His Phe Ser Ile Gly Ala
245 250 255
Glu Phe Thr Pro Ser Glu Arg Phe Trp Val Gly Leu Gly Tyr Thr Pro
260 265 270
15 Gln Ile Ala Gln Asp Phe Glu Val Glu Gly Gly Asn Lys Trp Gly Gly
275 280 285
Leu Ser Ala Gly Val Gly Phe Thr Ser Gly Val Val Arg Val Gly Val
290 295 300
Ser Ala Ala Thr Tyr His Pro Ala Ala Leu Ser Phe Met Cys Ser Val
305 310 315 320
20 Gly Ile Arg Leu Asp Lys Ser Ile Phe
325 330

(2) INFORMATION FOR SEQ ID NO:475

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 324 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- 30 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
35 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...324
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:475

Met Cys Leu Glu Pro Ile Ile Ala Pro Ile Ser Ser Glu Leu Leu Glu
1 5 10 15
45 Gln Glu Leu Thr Ala Asp Arg Phe Leu Arg Met Thr Asn Lys Ala Gly
20 25 30
Asn Glu Ile Tyr Val Phe Thr Ala Glu Glu Ala Pro His Cys Met Lys
35 40 45
50 Glu Val Gly Arg Leu Arg Glu Glu Ala Phe Arg His Tyr Gly Gly Gly
50 55 60
Thr Gly Lys Ala Ile Asp Ile Asp Glu Phe Asp Thr Met Pro Gly Ser
65 70 75 80
Tyr Lys Gln Leu Ile Val Trp Asp Pro Gln Asn Lys Ala Ile Leu Gly
85 90 95
55 Gly Tyr Arg Phe Ile Tyr Gly Arg Asp Val Ala Phe Asp Thr Asp Gly
100 105 110
Lys Pro Leu Leu Ala Thr Ala Glu Met Phe Arg Phe Ser Asp Ala Phe
115 120 125
60 Leu His Asp Tyr Leu Pro Tyr Thr Val Glu Leu Gly Arg Ser Phe Val
130 135 140
Ser Leu Gln Tyr Gln Ser Thr Arg Met Gly Thr Lys Ala Ile Phe Val
145 150 155 160
Leu Asp Asn Leu Trp Asp Gly Ile Gly Ala Leu Thr Val Val Asn Pro
165 170 175
65 Glu Ala Leu Tyr Phe Tyr Gly Lys Val Thr Met Tyr Lys Asp Tyr Asp
180 185 190
Arg Arg Ala Arg Asn Leu Ile Leu Tyr Phe Leu Arg Lys His Phe Ser
195 200 205
70 Asp Pro Glu Gly Leu Val Lys Pro Ile His Pro Leu Pro Ile Glu Ile
210 215 220
Ser Ala Glu Asp Glu Ala Leu Phe Ser Ser Ser Asp Phe Asp Thr Asn
225 230 235 240
Tyr Lys Thr Leu Asn Ile Glu Val Arg Lys Leu Gly Ile Asn Ile Pro
245 250 255
75 Pro Leu Val Ser Ala Tyr Ile Ala Leu Ser Pro Glu Met Arg Val Phe

SUBSTITUTE SHEET (Rule 26) (RO/AU)

WO 99/29870

PCT/AU98/01023

424/ 490

5 Gly Thr Ala Val Asn Glu Ser Phe Gly Glu Val Glu Glu Thr Gly Ile
260 275 280 285
Phe Ile Ala Val Gly Lys Ile Leu Glu Glu Lys Lys Gln Arg His Ile
290 295 300
Glu Ser Phe Ile Leu Ser Arg Asn Glu Lys Lys Gly Leu Asp Ser Ser
305 310 315 320
Asn Gly Arg Ser

10 (2) INFORMATION FOR SEQ ID NO:476

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 547 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

25 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...547

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:476

Met Lys Thr Ile Val Arg Tyr Ser Arg Leu Pro Val Ala Leu Phe Phe
1 5 10 15
Cys Leu Leu Gly Ala Val His Leu Ser Val Glu Ala Gln Met Leu Asn
20 25 30
35 Thr Pro Phe Glu Leu Ser Asp Gln Ile Val Leu Ser Pro Thr Glu Arg
35 40 45
Gln Tyr Arg Glu Ile Cys Val Gln Thr Lys Glu Lys Arg Gly Ala Asp
50 55 60
40 Leu Phe Pro Leu Ser Asp Lys Leu Arg Asp Ser Ala Tyr Val Arg Phe
65 70 75 80
Gly Ser Ala Tyr Gly Asp Ile Ala Gly Asp Tyr Leu Pro Tyr Asn Gly
85 90 95
Asn Asn Tyr Ser Ser Leu Ser Leu Glu Ser Gly Gly Arg Ile Ser Val
100 105 110
45 Arg Asn Tyr Gly Thr Leu Gln Gly Ser Ala Ser Tyr Ser Arg Gly Met
115 120 125
His Lys Arg Ile Gly Trp Asn Ala Leu Arg Asn Ala Glu Ala Tyr Tyr
130 135 140
50 Pro Tyr Leu Val Ser Asp Ser Thr Gly Gly Asp Tyr His Phe Glu Asp
145 150 155 160
Tyr Arg Leu Ala Gly Tyr Tyr Ser Phe Arg Ala Gly Arg Leu Pro Leu
165 170 175
Gly Ile Gly Phe Ser Tyr Arg Gly Glu Val Ala Tyr Arg Leu Thr Asp
180 185 190
55 Pro Arg Thr Thr Asn Thr Thr Gly Ala Leu Glu Leu Ser Cys Ala Thr
195 200 205
Ser Leu Thr Leu Pro Arg Glu Asn Arg Leu Ser Leu Ser Ala Ala Tyr
210 215 220
60 Leu Tyr His Arg Gln His Leu Thr Gln Tyr Asn Trp Arg Pro Gly Gln
225 230 235 240
Gln Asp Lys Phe Phe Val Ser Tyr Gly Phe Gly Gln Val Asp Val Ser
245 250 255
Asn Ser Pro Ile Trp Phe Gly Ile Ser Arg Met Asn Tyr Val Asn Gly
260 265 270
65 Trp Lys Leu Ser Ser Arg Leu Asp Thr Arg Arg Gly Asp Ala Ile Gly
275 280 285
Leu Asp Tyr Ser Gly Tyr Phe Leu Asp Thr Glu Glu Arg Ser Ser Ile
290 295 300
70 Asn Leu Phe Ala Leu Leu Tyr Asn Arg Leu Arg Leu Tyr Gly Ser Trp
305 310 315 320
His Leu Ser Asp Phe Asp Phe Ser Phe Ala Asp Tyr Ala Leu Arg
325 330 335
Gln Gly Ile Glu Arg Ile Tyr Glu Asp Tyr Lys Pro Asp Asp Asn Tyr
340 345 350
75 His Ile Tyr Asp Leu Arg Ile Leu Ala Ile Arg Arg Trp Tyr Met Leu

WO 99/29870

PCT/AU98/01023

425/ 490

355 360 365
Asn Glu Phe Ser Ala Gln Ala Gln Ala Ser Tyr Arg Ile Arg Thr Asp
370 375 380
5 Arg Gly Cys Ala Leu Arg Val Ser Ala Gly Ser Asp Phe Tyr Gly Tyr
385 390 395 400
Asp Glu Thr Tyr Arg Lys His Gly His His Thr Met Ser Gly Met Leu
405 410 415
Pro Pro Phe Ala Gly Ile Ala Tyr Asp His Ala Gly Ser Lys Leu Asp
420 425 430
10 Phe Gly Leu Ser Leu Ser Ala Ala Tyr Arg Met Val Leu Thr His Ser
435 440 445
Tyr Lys Ile Arg Thr Ile Gln Lys Glu Gln Leu Asp Tyr Gln Leu Ala
450 455 460
15 Tyr Leu Pro Tyr Ala Tyr Arg Asn Arg Glu Gly Val Glu Val Arg Ser
465 470 475 480
Ser Leu Tyr Val Ser Ile Pro Met Gln Asn Thr His Arg Leu Met Thr
485 490 495
Glu Leu Arg Leu Tyr Gly Asp Leu Met Lys Arg Lys Asp Gly Ile Ala
500 505 510
20 Tyr Gly Lys Thr Pro Gly Val Ile Ser His Ile Leu Ser Asp Pro Gln
515 520 525
Ala Glu Arg Thr Ser Gly His Thr Ile Gly Ala Ile Cys Asn Ile Ser
530 535 540
25 Tyr Leu Phe
545

(2) INFORMATION FOR SEQ ID NO:477

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 750 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- 35 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
40 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...750
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:477

Met Lys Lys Leu His Met Ile Ala Ala Leu Ala Val Leu Pro Phe Cys
1 5 10 15
50 Leu Thr Ala Gln Ala Pro Val Ser Asn Ser Glu Ile Asp Ser Leu Ser
20 25 30
Asn Val Gln Leu Gln Thr Val Gln Val Val Ala Thr Arg Ala Thr Ala
35 40 45
Lys Thr Pro Val Ala Tyr Thr Asn Val Arg Lys Ala Glu Leu Ser Lys
50 55 60
55 Ser Asn Tyr Gly Arg Asp Ile Pro Tyr Leu Leu Met Leu Thr Pro Ser
65 70 75 80
Val Val Ala Thr Ser Asp Ala Gly Thr Gly Ile Gly Tyr Ser Gly Phe
85 90 95
60 Arg Val Arg Gly Thr Asp Ala Asn Arg Ile Asn Ile Thr Thr Asn Gly
100 105 110
Val Pro Leu Asn Asp Ser Glu Ser Gln Ser Val Phe Trp Val Asn Met
115 120 125
Pro Asp Phe Ala Ser Ser Ile Glu Asp Leu Gln Val Gln Arg Gly Val
130 135 140
65 Gly Thr Ser Thr Asn Gly Ala Gly Ala Phe Gly Ala Ser Val Asn Met
145 150 155 160
Arg Thr Asp Asn Leu Gly Leu Ala Pro Tyr Gly Arg Val Asp Leu Ser
165 170 175
70 Gly Gly Ser Phe Gly Thr Phe Arg Arg Ser Val Lys Leu Gly Ser Gly
180 185 190
Arg Ile Gly Arg His Trp Ala Val Asp Ala Arg Leu Ser Lys Ile Gly
195 200 205
Ser Asp Gly Tyr Val Asp Arg Gly Ser Val Asp Leu Lys Ser Tyr Phe
210 215 220
75 Ala Gln Val Gly Tyr Phe Gly Ser Asn Thr Ala Leu Arg Phe Ile Thr

WO 99/29870

PCT/AU98/01023

426/490

225 230 235 240
Phe Gly Gly Lys Glu Val Thr Gly Ile Ala Trp Asn Gly Leu Ser Lys
245 250 255
5 Glu Asp Glu Ala Lys Tyr Gly Arg Arg Tyr Asn Ser Ala Gly Leu Met
260 265 270
Tyr Val Asp Ala Gln Gly Val Pro His Tyr Tyr His Asn Thr Asp Asn
275 280 285
Tyr Glu Gln Arg His Tyr His Ala Ile Met Thr His Ser Phe Ser Pro
290 295 300
10 Ser Val Ile Leu Asn Leu Thr Ala His Tyr Thr Ala Gly Tyr Gly Tyr
305 310 315 320
Thr Asp Glu Tyr Arg Thr Gly Arg Lys Leu Lys Glu Tyr Ala Leu Gln
325 330 335
15 Pro Tyr Val Glu Asn Ser Val Thr Val Lys Lys Thr Asp Leu Ile Arg
340 345 350
Gln Lys Tyr Leu Asp Asn Asp Phe Gly Gly Leu Ile Gly Ser Leu Asn
355 360 365
Trp His Thr Gly Ala Trp Asp Leu Gln Phe Gly Ala Ser Gly Asn Ile
370 375 380
20 Tyr Lys Gly Asp His Phe Gly Arg Ile Thr Tyr Ile Lys Lys Tyr Asn
385 390 395 400
Gln Pro Leu Ala Pro Asp Phe Glu Tyr Tyr Arg Asn Arg Ala Asp Lys
405 410 415
25 Arg Glu Gly Ala Ala Phe Ala Lys Ala Asn Trp Gln Ile Thr Pro Glu
420 425 430
Leu Asn Met Tyr Ala Asp Leu Gln Tyr Arg Thr Ile Gly Tyr Thr Ile
435 440 445
Asn Gly Ile Thr Asp Glu Tyr Asp Glu Val Gln Gly Ser Met Gln His
450 455 460
30 Ile Asp Leu Asp Lys Thr Phe Arg Phe Leu Asn Pro Lys Ala Gly Leu
465 470 475 480
Thr Tyr Ser Phe Asp Ala His Thr Ala Tyr Ala Ser Val Ala Val
485 490 495
35 Ala His Arg Glu Pro Asn Arg Thr Asn Tyr Thr Glu Ala Gly Ile Gly
500 505 510
Gln Tyr Pro Thr Pro Glu Arg Leu Ile Asp Tyr Glu Leu Gly Tyr Arg
515 520 525
Tyr Ala Ser Pro Leu Leu Ser Ala Gly Val Gly Leu Tyr Tyr Met Gln
530 535 540
40 Tyr Lys Asp Gln Leu Val Leu Asp Gly Arg Leu Ser Asp Val Gly Gln
545 550 555 560
Met Leu Thr Ser Asn Val Pro Asp Ser Tyr Arg Met Gly Leu Glu Leu
565 570 575
45 Thr Leu Gly Trp Gln Ile Leu Pro Arg Leu Leu Arg Trp Asp Ala Ser
580 585 590
Phe Thr Met Ser Arg Asn Lys Ile Asp Arg Tyr Val Gln Tyr Thr Ser
595 600 605
Val Tyr Asp Ala Asp Tyr Asn Trp Leu Glu Leu Lys Glu Glu Thr Leu
610 615 620
50 Glu Ser Thr Asp Ile Ala Tyr Ser Pro Asn Val Ile Ala Gly Ser Met
625 630 635 640
Leu Thr Leu Ser His Ala Gly Phe Glu Met Ala Trp Thr Ser Arg Phe
645 650 655
55 Val Ser Lys Gln Tyr Leu Asp Asn Thr Gln Arg Ser Asp Arg Met Leu
660 665 670
Ser Ser Tyr Trp Val Asn Asp Leu Arg Leu Gly Tyr Val Leu Pro Val
675 680 685
His Phe Val Lys Arg Val Ala Leu Gly Val Gln Leu Asn Asn Leu Phe
690 695 700
60 Asn Leu Met Tyr Ala Ser Asn Ala Tyr Ile Tyr Asp Ala Gly Tyr Val
705 710 715 720
Gln Ala Ser Gly Glu Leu Ser Ala Tyr Ala Asp Leu Arg Tyr Tyr Pro
725 730 735
65 Gln Ala Gly Phe Asn Ala Leu Gly Ser Leu Thr Ile Asp Phe
740 745 750

(2) INFORMATION FOR SEQ ID NO:478

70 (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 494 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

75 (1) MOLECULE TYPE: protein

WO 99/29870

PCT/AU98/01023

427/490

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...494

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478

Met Lys Arg Arg Phe Leu Ser Leu Leu Leu Tyr Ile Leu Ser Ser
1 5 10 15
Ile Ser Leu Ser Ala Gln Arg Phe Pro Met Val Gln Gly Ile Glu Leu
20 25 30
Asp Thr Asp Ser Leu Phe Ser Leu Pro Lys Arg Pro Trp Arg Ala Ile
35 40 45
Gly Lys Thr Ile Gly Val Asn Leu Ala Val Trp Gly Phe Asp His Phe
50 55 60
Ile Met Asn Glu Asp Phe Ala Asp Ile Ser Trp Gln Thr Ile Lys Ser
65 70 75 80
Asn Phe Gln Thr Gly Phe Gly Trp Asp Asn Asp Lys Phe Val Thr Asn
85 90 95
Leu Phe Ala His Pro Tyr His Gly Ser Leu Tyr Phe Asn Ala Ala Arg
100 105 110
Ser Asn Gly Leu Ser Phe Arg His Ser Ala Pro Phe Ala Phe Phe Gly
115 120 125
Ser Leu Met Trp Glu Leu Leu Met Glu Asn Glu Pro Pro Ser Ile Asn
130 135 140
Asp Leu Cys Ala Thr Thr Ile Gly Gly Ile Ala Leu Gly Glu Met Gly
145 150 155 160
His Arg Leu Ser Asp Leu Leu Ile Asp Asn Arg Thr Thr Gly Trp Glu
165 170 175
Arg Met Gly Arg Glu Val Ala Ile Ala Leu Ile Asn Pro Met Arg Phe
180 185 190
Leu Asn Arg Leu Thr Ala Gly Glu Val Thr Ser Val Gly Ser Arg Ser
195 200 205
Gly Gln Ile Phe Gln Ser Val Pro Ile Asn Ile Val Val Asp Ala Gly
210 215 220
Phe Arg Phe Leu Ala Asp Lys Arg His Ala Arg Thr Gly Ala Thr Ala
225 230 235 240
Leu Thr Leu Asn Leu Arg Phe Asp Tyr Gly Asp Pro Phe Arg Ser Glu
245 250 255
Thr Phe Ser Pro Tyr Asp Phe Phe Gln Phe Lys Ala Gly Leu Ser Phe
260 265 270
Ser Glu Ser Gln Pro Leu Leu Ser Gln Ile Asn Leu Ile Gly Ile Leu
275 280 285
Ser Gly Cys Gln Leu Leu Ala His Glu Arg Thr Val Leu Val Gly Gly
290 295 300
Leu Phe Gln His Phe Asp Tyr Tyr Asn Ser Glu Lys Arg Ile Ser Lys
305 310 315 320
Asn Ser Glu Glu Val Leu Val Thr Pro Tyr Arg Ile Ser Gln Val Ala
325 330 335
Ala Leu Gly Gly Gly Leu Ile Phe Gln His His Gly Lys Phe Arg Arg
340 345 350
Arg Pro Leu Glu Leu Tyr Ala Glu Thr Tyr Leu Asn Val Val Pro Met
355 360 365
Gly Ala Ser Leu Ser Asp His Tyr Asn Val Asp Asn Arg Asp Tyr Asn
370 375 380
Leu Gly Ser Gly Leu Ser Gly Lys Leu Tyr Leu Gly Ala Thr Tyr Asn
385 390 395 400
Asp Leu Trp Ser Trp Leu Leu Gly Val Glu Ser Tyr Arg Leu Tyr Thr
405 410 415
Trp Ile Gly Tyr Glu Glu Pro His Gln Lys Asn Thr Asp Val Ser Ser
420 425 430
Phe Met Val Gln Gly Asp Glu Ser Lys Ala Arg Leu Leu Val Thr Ser
435 440 445
Ser Glu Phe Ala Phe His Pro Gly Pro Trp His Val Ala Ile Val Ala
450 455 460
Arg Arg Phe Ile Arg Lys Thr Ala Tyr Gln Phe Tyr Pro Asn Val Ser
465 470 475 480
Phe Asp Thr Gly Asp Ile Gln Leu Arg Val Gly Phe His Phe
485 490

(2) INFORMATION FOR SEQ ID NO:479

WO 99/29870

PCT/AU98/01023

428/ 490

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 294 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...294

(x.i) SEQUENCE DESCRIPTION: SEQ ID NO:479

20	Het	Lys	Arg	Leu	Ile	Val	Phe	Leu	Ala	Met	Gly	Gly	Leu	Leu	Phe	Thr
	1			5						10					15	
	Leu	Ala	Asn	Ala	Gln	Glu	Ala	Asn	Thr	Ala	Ser	Asp	Thr	Pro	Lys	Lys
				20						25					30	
25	Asp	Trp	Thr	Ile	Lys	Gly	Val	Thr	Gly	Leu	Asn	Ala	Ser	Gln	Thr	Ser
				35						40					45	
	Leu	Thr	Asn	Trp	Ala	Ala	Gly	Gly	Glu	Asn	Thr	Val	Ala	Gly	Asn	Leu
				50						55					60	
	Tyr	Leu	Asn	Ile	Asp	Ala	Asn	Tyr	Leu	Lys	Asp	Lys	Trp	Ser	Trp	Asp
				65						70					75	
30	Asn	Gly	Leu	Arg	Thr	Asp	Phe	Gly	Leu	Thr	Tyr	Thr	Thr	Ala	Asn	Lys
				85						90					95	
	Trp	Asn	Lys	Ser	Val	Asp	Lys	Ile	Glu	Leu	Phe	Thr	Lys	Ala	Gly	Tyr
				100						105					110	
35	Glu	Ile	Gly	Lys	His	Trp	Tyr	Gly	Ser	Ala	Leu	Phe	Thr	Phe	Leu	Ser
				115						120					125	
	Gln	Tyr	Ala	Lys	Gly	Tyr	Glu	Lys	Pro	Ser	Asp	His	Leu	Thr	Gly	Val
				130						135					140	
	Lys	His	Ile	Ser	Asn	Phe	Phe	Ala	Pro	Ala	Tyr	Leu	Thr	Leu	Gly	Ile
				145						150					155	
40	Gly	Ala	Asp	Tyr	Lys	Pro	Asn	Glu	Lys	Phe	Ser	Leu	Tyr	Leu	Ser	Pro
				165						170					175	
	Thr	Thr	Gly	Lys	Leu	Thr	Val	Val	Ala	Asp	Asp	Tyr	Leu	Ser	Ser	Leu
				180						185					190	
45	Gly	Ala	Phe	Gly	Val	Lys	Val	Gly	Glu	Lys	Thr	Met	Phe	Glu	Leu	Gly
				195						200					205	
	Ala	Leu	Val	Val	Gly	Ser	Ala	Asn	Ile	Asn	Leu	Met	Glu	Asn	Val	Asn
				210						215					220	
	Leu	Ile	Thr	Lys	Ala	Ser	Phe	Phe	Ser	Ala	Tyr	Thr	His	Asp	Phe	Gly
				225						230					235	
50	Asn	Ile	Asp	Ile	Asn	Trp	Glu	Ala	Met	Leu	Ala	Met	Lys	Ile	Asn	Lys
				245						250					255	
	Phe	Leu	Thr	Ala	Thr	Ile	Ala	Thr	Asn	Leu	Ile	Tyr	Asp	Asp	Asp	Val
				260						265					270	
55	Lys	Ile	Asn	Asp	Gly	Pro	Lys	Ile	Gln	Phe	Lys	Glu	Val	Val	Gly	Val
				275						280					285	
	Gly	Val	Ala	Tyr	Thr	Phe										
				290												

(2) INFORMATION FOR SEQ ID NO:480

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 204 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...204

WO 99/29870

PCT/AU98/01023

430/490

5 Leu Asn Asp Asn Arg Gln Ser Ser Ser Thr Thr Ala Leu Arg Glu Lys
210 215 220
Gly Asn Asn Glu Tyr Ala Tyr Asn Arg Asp Phe Phe Val Gly Ile Gly
225 230 235 240
Tyr Arg Phe

10 (2) INFORMATION FOR SEQ ID NO:482

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 207 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

20 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...207

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:482

30 Met Lys Arg Met Leu Leu Leu Val Val Leu Leu Tyr Gly Ile Ala
1 5 10 15
Gly Arg Leu Ala Ala Gln Asp Val Ile Arg Pro Trp Ser Leu Gln Val
20 25 30
Gly Ala Gly Tyr Ser Asp Thr Glu Asn Ile Pro Gly Gly Phe Thr Tyr
35 40 45
Gly Phe Tyr Leu Gly Lys Arg Met Gly Ser Phe Leu Glu Val Gly Leu
50 55 60
Ser Met Tyr Asn Ser Thr Arg Gln Thr Ala Asn Asn Ala Asp Ser Phe
65 70 75 80
Ala Ser Asn Glu Gly Asp Gly Ser Phe Gln Val Asn Met Ser Ser Pro
85 90 95
Asn Glu Lys Trp Ser Phe Phe Asp Ala Gly Ser Ala Asn Cys Tyr Met
100 105 110
Ile Val Val Gly Val Asn Pro Leu His Leu Phe Trp Gln Asn Ser Arg
115 120 125
His Asn Leu Phe Leu Ala Val Gln Ala Gly Leu Ser Asn Lys His Asn
130 135 140
Ile His Phe Ile Tyr Gly Asp Lys Gly Ala Lys Val Ser Ile Tyr Thr
145 150 155 160
Asn Ser Asn Thr Tyr Ile Gly Tyr Gly Ala Arg Val Ala Tyr Glu Tyr
50 165 170 175
Gln Ile His Lys Asn Val Gly Ala Gly Ala Ala Val Met Tyr Asp His
180 185 190
Gly Asn Lys Met Leu Thr Ala Met Ala Thr Leu Ser Thr His Phe
195 200 205

55 (2) INFORMATION FOR SEQ ID NO:483

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 951 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: protein

65 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

70 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...951

75 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:483

WO 99/29870

PCT/AU98/01023

431/490

Met Arg Val Ser Asp Leu Cys Ser Arg Leu Ser Trp Leu Leu Pro Val
1 5 10 15
Ile Leu Val Gly Leu Leu Cys Ala Thr Leu Val Ala Ala Glu Arg Pro
20 25 30
5 Met Ala Gly Ala Val Gly Leu His His Arg Arg His Ala Ala Leu Ser
35 40 45
Asp Ser Thr Ala Lys Asp Thr Val Pro Leu Ala Lys Pro Ile Pro Asp
50 55 60
10 Ser Ala Phe Arg Asp Ser Leu Pro Ala Asp Ser Thr Gly Ser Met Arg
65 70 75 80
Gln Asp Ser Val Tyr Asp Asp Glu Phe Glu Leu Glu Asp Ile Val Glu
85 90 95
Tyr Glu Ala Ala Asp Ser Ile Val Leu Leu Gly Gln Asn Arg Ala Tyr
100 105 110
15 Leu Phe Gly Lys Ser Tyr Val Ser Tyr Gln Lys Ser Arg Leu Glu Ala
115 120 125
Asn Phe Met Tyr Leu Asn Thr Asp Ser Ser Thr Val Tyr Thr Arg Tyr
130 135 140
20 Val Leu Asp Thr Ala Gly Tyr Pro Met Ala Phe Pro Val Phe Lys Asp
145 150 155 160
Gly Glu Gln Ser Phe Glu Ala Lys Asn Phe Thr Tyr Asn Phe Arg Thr
165 170 175
25 Glu Lys Gly Ile Ile Ser Gly Val Ile Thr Gln Gln Gly Glu Gly Tyr
180 185 190
Leu Thr Ala Gly Lys Thr Lys Lys Met Pro Asp Asn Ile Met Phe Met
195 200 205
Gln Gly Gly Arg Tyr Thr Thr Cys Asp Asn His Asp His Pro His Phe
210 215 220
30 Tyr Ile Asn Leu Ser Lys Ala Lys Val His Pro Glu Lys Asp Ile Val
225 230 235 240
Thr Gly Pro Val Asn Leu Val Ile Ala Asp Met Pro Leu Pro Ile Gly
245 250 255
Leu Pro Phe Gly Tyr Phe Pro Phe Ser Asn Lys Tyr Ser Ser Gly Ile
260 265 270
35 Leu Met Pro Thr Tyr Gly Glu Asp Asn Arg Tyr Gly Phe Tyr Leu Arg
275 280 285
Asn Gly Gly Tyr Tyr Phe Ala Phe Ser Asp Tyr Ile Asp Leu Ala Leu
290 295 300
40 Arg Gly Glu Ile Phe Ser Lys Gly Ser Trp Gly Ile Ser Ala Gln Ser
305 310 315 320
Lys Tyr Lys Lys Arg Tyr Lys Tyr Asn Gly Ser Phe Glu Ala Asn Tyr
325 330 335
Leu Val Ser Lys Ser Gly Asp Lys Tyr Val Pro Gly Asp Tyr Ser Lys
340 345 350
45 Thr Thr Ser Leu Asn Ile Arg Trp Thr His Ser Gln Asp Pro Lys Ala
355 360 365
Asn Pro Leu Gln Thr Leu Ser Ala Asn Val Asn Phe Ala Thr Gly Ser
370 375 380
50 Tyr Phe Gln Asn Ser Leu Asn Thr Thr Tyr Asp Val Asn Ala Arg Thr
385 390 395 400
Ala Thr Thr Arg Ser Ser Ala Val Ser Tyr Ser Arg Lys Phe Pro Gly
405 410 415
Thr Pro Phe Ser Ile Thr Gly Ser Met Asp Ile Ser Gln Asn Met Arg
420 425 430
55 Asp Thr Thr Val Ser Leu Thr Leu Pro Asn Leu Ser Ile Asn Met Ser
435 440 445
Thr Arg Tyr Pro Phe Lys Arg Lys Thr Arg Val Gly Pro Glu Arg Trp
450 455 460
60 Tyr Glu Lys Leu Ser Val Gly Tyr Ser Gly Gln Leu Arg Asn Ser Ile
465 470 475 480
Leu Thr Lys Glu Lys Asp Leu Leu Gln Ser Asn Leu Val Arg Asp Trp
485 490 495
Lys Asn Gly Met Arg His Ser Val Pro Ile Ser Leu Thr Val Pro Leu
500 505 510
65 Leu Asp Tyr Ile Asn Leu Thr Met Gly Val Asn Tyr Asn Glu Trp Trp
515 520 525
Tyr Thr Lys Gly Ile Arg Lys Ser Trp Asn Glu Asp Lys Lys Thr Phe
530 535 540
70 Leu Pro Ser Asp Thr Thr Tyr Lys Phe Arg Arg Leu Tyr Asp Tyr Ser
545 550 555 560
Leu Ser Ala Gly Leu Ser Thr Thr Leu Tyr Gly Met Phe Lys Pro Trp
565 570 575
Lys Pro Phe Ser Gly Gly Asn Leu Ile Met Ile Arg His Arg Phe
580 585 590
75 Thr Pro Thr Val Ser Phe Ser Tyr Met Pro Asp Phe Thr Lys Arg Arg

437/ 490

Ala Gly Val Pro Glu Leu Asn Asn Leu Leu Ile Gly Phe Asp Ala Asp
 1075 1080 1085
 Lys Asp Gly Gln Tyr Thr Leu Glu Phe Ala Leu Ser Asp His Phe Ala
 1090 1095 1100
 5 Lys Gly Ala Val Tyr Leu His Asp Leu Gln Ser Gly Ala Lys His Arg
 1105 1110 1115 1120
 Ile Thr Asn Ser Thr Ser Tyr Ser Phe Asp Ala Lys Arg Gly Asp Ser
 1125 1130 1135
 10 Gly Ala Arg Phe Arg Leu Ser Tyr Gly Cys Asp Glu Asn Val Asp Asp
 1140 1145 1150
 Ser His Val Val Ser Thr Asn Gly Arg Glu Ile Ile Ile Leu Asn Gln
 1155 1160 1165
 Asp Ala Leu Asp Cys Thr Val Thr Leu Phe Thr Ile Glu Gly Lys Leu
 1170 1175 1180
 15 Leu Arg Arg Leu Lys Val Leu Ala Gly His Arg Glu Val Met Lys Val
 1185 1190 1195 1200
 Gln Thr Gly Gly Ala Tyr Ile Val His Leu Gln Asn Ala Phe Thr Asn
 1205 1210 1215
 20 Asp Val His Lys Val Leu Val Glu Tyr
 1220 1225

(2) INFORMATION FOR SEQ ID NO:486

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 425 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...425
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:486

Met Glu Val Lys Lys Asn Thr Val Val Leu Arg Leu Leu Ile Trp Phe
 1 5 10 15
 45 Val Ala Ile Leu Leu Phe His Ser Ser Arg Leu Trp Gly Gln Glu Gly
 20 25 30
 Glu Gly Ser Ala Arg Tyr Arg Phe Lys Gly Phe Val Asp Thr Tyr His
 35 40 45
 Ala Val Arg Ser Ser Ser Pro Phe Asp Phe Met Ser Ser Arg Thr Arg
 50 55 60
 50 Val Arg Gly Glu Leu Glu Arg Ser Phe Gly Asn Ser Lys Val Ala Val
 65 70 75 80
 Ser Val Asn Ala Thr Tyr Asn Ala Leu Leu Lys Asp Glu Thr Gly Leu
 85 90 95
 55 Arg Leu Arg Glu Ala Phe Phe Glu His Gln Glu Glu His Trp Gly Leu
 100 105 110
 Arg Leu Gly Arg Gln Ile Val Ile Trp Gly Ala Ala Asp Gly Val Arg
 115 120 125
 Ile Thr Asp Leu Ile Ser Pro Met Asp Met Thr Glu Phe Leu Ala Gln
 130 135 140
 60 Asp Tyr Asp Asp Ile Arg Met Pro Val Asn Ala Leu Arg Phe Ser Val
 145 150 155 160
 Phe Asn Glu Ser Met Lys Val Glu Val Val Val Leu Pro Val Phe Glu
 165 170 175
 65 Gly Tyr Arg Leu Pro Val Asp Pro Arg Asn Pro Trp Asn Ile Phe Ser
 180 185 190
 Leu Ser Pro Ile Ala Gln Gly Met Asn Ile Val Trp Lys Glu Glu Ala
 195 200 205
 Gly Lys Pro Ala Phe Lys Val Ala Asn Ile Glu Tyr Gly Ala Arg Trp
 210 215 220
 70 Ser Thr Thr Leu Ser Gly Ile Asp Phe Ala Leu Ala Ala Leu His Thr
 225 230 235 240
 Trp Asn Lys Met Pro Val Ile Glu Val Gln Gly Ile Val Pro Thr Glu
 245 250 255
 75 Ile Ile Val Ser Pro Arg Tyr Tyr Arg Met Gly Phe Val Gly Gly Asp
 260 265 270

WO 99/29870

PCT/AU98/01023

438/ 490

Leu Ser Val Pro Val Gly Gln Phe Val Phe Arg Gly Glu Ala Ala Phe
275 280 285
Asn Ile Asp Lys His Phe Thr Tyr Lys Ser His Ala Glu Gln Glu Gly
290 295 300
5 Phe Gln Thr Ile Asn Trp Leu Ala Gly Ala Asp Trp Tyr Ala Pro Gly
305 310 315 320
Glu Trp Met Ile Ser Gly Gln Phe Ser Met Glu Ser Ile Phe Arg Tyr
325 330 335
10 Arg Asp Phe Ile Ser Gln Arg Gln His Ser Thr Leu Ile Thr Leu Asn
340 345 350
Val Ser Lys Lys Phe Phe Gly Ser Thr Leu Gln Leu Ser Asp Phe Thr
355 360 365
Tyr Tyr Asp Leu Thr Gly Lys Gly Trp Phe Ser Arg Phe Ala Ala Asp
370 375 380
15 Tyr Ala Leu Asn Asp Gln Ile His Leu Met Ala Gly Tyr Asp Trp Phe
385 390 395 400
Ser Ser Lys Gly Ser Gly Ile Phe Asp Arg Tyr Lys Asp Asn Ser Glu
405 410 415
20 Leu Trp Phe Lys Ala Arg Tyr Ser Phe
420 425

(2) INFORMATION FOR SEQ ID NO:487

(i) SEQUENCE CHARACTERISTICS:
25 (A) LENGTH: 404 amino acids
(B) TYPE: amino acid
(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
30 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
35 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...404

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:487

Met Ser Ser Cys Glu Val Ala Tyr Phe Ser Leu Lys Pro Ile Asp Leu
1 5 10 15
45 Gln Asn Ile Arg Glu Arg Asn His Ser Ser Asp Ile Ala Leu Ser Asn
20 25 30
Leu Leu Asp Asn Ser Asn Gln Leu Leu Ala Thr Ile Leu Ile Gly Asn
35 40 45
Asn Val Ile Asn Val Ala Ile Val Ile Leu Ser Asn Tyr Ala Ile Glu
50 55 60
Gln Thr Phe Val Phe Ser Pro Ile Ile Gly Phe Leu Ile Gln Thr
65 70 75 80
Ile Leu Leu Thr Thr Val Leu Leu Leu Gly Glu Ile Leu Pro Lys
85 90 95
55 Val Tyr Ala Arg Lys Asn Pro Leu Gln Tyr Ser Arg Phe Ser Ala Ala
100 105 110
Ala Met Ser Val Ile Tyr Lys Ile Leu Ser Pro Phe Ser Lys Leu Leu
115 120 125
Val Lys Ser Thr Gly Ile Val Thr Arg Gly Ile Ser Lys Lys Lys Tyr
130 135 140
60 Asp Met Ser Val Asp Glu Leu Ser Lys Ala Val Ala Leu Thr Thr Thr
145 150 155 160
Glu Gly Glu Pro Glu Glu Lys Glu Met Ile Asn Glu Ile Ile Lys Phe
165 170 175
65 Tyr Asn Lys Thr Ala Cys Glu Ile Met Val Pro Arg Ile Asp Ile Val
180 185 190
Asp Val Asp Leu Ser Trp Pro Phe Arg Lys Met Leu Asp Phe Val Val
195 200 205
Ser Ser Gly Tyr Ser Arg Leu Pro Val Ser Glu Gly Ser Glu Asp Asn
210 215 220
70 Ile Lys Gly Val Ile Tyr Ile Lys Asp Leu Ile Pro His Met Asp Lys
225 230 235 240
Gly Asp Glu Phe Asp Trp His Pro Leu Ile Arg Lys Ala Tyr Phe Val
245 250 255
75 Pro Glu Asn Lys Arg Ile Asp Asp Leu Leu Glu Glu Phe Arg Ala Asn
260 265 270

WO 99/29870

PCT/AU98/01023

439/ 490

Lys Val His Val Ser Ile Val Val Asp Glu Phe Gly Gly Thr Cys Gly
 275 280 285
 Leu Ile Thr Met Glu Asp Ile Leu Glu Glu Ile Val Gly Glu Ile Thr
 290 295 300
 5 Asp Glu Tyr Asp Glu Glu Leu Pro Phe Lys Val Leu Gly Asp Gly
 305 310 315 320
 Ser Tyr Leu Phe Glu Gly Lys Thr Ser Leu Ser Asp Val Arg His Tyr
 325 330 335
 10 Leu Asp Leu Pro Glu Asn Ala Phe Gly Glu Leu Gly Asp Glu Val Asp
 340 345 350
 Thr Leu Ser Gly Leu Phe Leu Glu Ile Lys Gln Glu Leu Pro His Val
 355 360 365
 Gly Asp Thr Ala Val Tyr Glu Pro Phe Arg Phe Gln Val Thr Gln Met
 370 375 380
 15 Asp Lys Arg Arg Ile Ile Glu Ile Lys Ile Phe Pro Phe Glu Arg Thr
 385 390 395 400
 Trp Glu Val Glu

 20 (2) INFORMATION FOR SEQ ID NO:488
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 260 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 25
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 30
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1...260
 35
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:488
 40 Met Lys Leu Leu Leu Tyr Leu Leu Leu Val Leu Ser Thr Leu Ser Pro
 1 5 10 15
 Met Tyr Ser Gln Met Leu Phe Ser Glu Asn Leu Thr Met Asn Ile Asp
 20 25 30
 45 Ser Thr Lys Thr Ile Gln Gly Thr Ile Leu Pro Val Leu Asp Phe Lys
 35 40 45
 Thr Glu Lys Glu Asn Val Phe Thr Phe Lys Asn Thr Ala Asn Leu Asn
 50 55 60
 Leu Leu Ile Lys His Gly Gln Val Ile Asn Leu Ile Asn Lys Leu Glu
 65 70 75 80
 50 Phe Ser Thr Tyr Gly Asn Lys Val Thr Val Ser Gly Gly Tyr Val His
 85 90 95
 Thr Glu Tyr Arg Tyr Leu Leu His His Val Phe Glu Val Tyr Pro Tyr
 100 105 110
 55 Val Glu Ser Gln Trp Ala Glu Ser Arg Gly Met Lys Tyr Lys Val Ser
 115 120 125
 Thr Gly Leu Gln Ser Arg Tyr Arg Leu Val Asn Ser Asp Asn Cys Leu
 130 135 140
 Met Phe Ala Thr Leu Gly Val Phe Phe Glu Phe Glu Lys Trp Glu Gln
 145 150 155 160
 60 Pro Ala Thr Ser Leu Phe Ala Gly Thr Tyr Ala Tyr Ser Arg Ser Ile
 165 170 175
 Lys Ser His Leu Ser Ile Ser Phe Arg His Arg Leu Gly Glu His Trp
 180 185 190
 65 Glu Phe Thr Thr Thr Ala Ile His Gln Gly Lys Pro Asp Ser Tyr Phe
 195 200 205
 Lys Lys Ala Arg Phe Gly Gly Ala Ile Asp Leu Lys Tyr His Ile Thr
 210 215 220
 Pro Thr Ile Gly Ile Arg Gly Ala Tyr Arg Ile Ile Tyr Asp Thr Ala
 225 230 235 240
 70 Pro Ile Val Pro Val Arg Lys Asp Tyr Asn Thr Val Asp Val Gly Ile
 245 250 255
 Asp Ile Ser Phe
 260
 75 (2) INFORMATION FOR SEQ ID NO:489

WO 99/29870

PCT/AU98/01023

440/ 490

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 834 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489

Met Lys Arg Ile Val Leu Ser Ser Phe Leu Phe Val Leu Ser Ile Leu
 1 5 10 15
 Ser Leu Met Ala Gln Asn Asn Thr Leu Asp Val His Ile Ser Gly Thr
 20 25 30
 Ile Lys Asp Ala Ser Ser Gly Glu Pro Val Pro Tyr Ala Thr Val Ser
 35 40 45
 Ile Arg Leu Thr Gly Ala Asp Thr Thr Gln Val Phe Arg Gln Val Thr
 50 55 60
 Asp Gly Asn Gly Tyr Phe Val Ile Gly Leu Pro Ala Ala Pro Ser Tyr
 65 70 75 80
 His Leu Thr Ala Ser Phe Val Gly Met Lys Thr His Thr Met Gln Ile
 85 90 95
 Ser Arg Gly Asn Gly Gln His Asp Ile Lys Ser Ile Asp Ile Ser Leu
 100 105 110
 Glu Ser Glu Asp Lys Gln Leu Ser Thr Val Thr Val Ser Ala Ala Arg
 115 120 125
 Pro Leu Val Lys Met Glu Ile Asp Arg Leu Ser Tyr Asn Met Lys Asp
 130 135 140
 Asp Pro Ala Ala Lys Thr Asn Asn Leu Leu Glu Met Leu Arg Asn Val
 145 150 155 160
 Pro Leu Val Thr Val Asp Gly Gln Gly Asn Ile Gln Val Lys Gly Ser
 165 170 175
 Ser Asn Phe Lys Ile His Leu Asn Gly Arg Pro Ser Thr Met Val Ser
 180 185 190
 Ser Asn Pro Lys Glu Val Phe Arg Ser Ile Pro Ala His Thr Ile Lys
 195 200 205
 Arg Val Glu Val Ile Thr Asp Pro Gly Val Lys Tyr Asp Ala Glu Gly
 210 215 220
 Thr Ser Ala Ile Leu Asp Ile Val Thr Glu Glu Gly Lys Lys Leu Glu
 225 230 235 240
 Gly Tyr Ser Gly Ser Ile Thr Ala Ser Val Ser Asn Asn Pro Thr Ala
 245 250 255
 Asn Gly Ser Ile Phe Leu Thr Ala Lys Ser Gly Lys Val Gly Leu Thr
 260 265 270
 Thr Asn Tyr Asn Tyr Tyr Gly Gly Lys Asn Lys Gly Ser Arg Tyr Phe
 275 280 285
 Thr Glu Arg Thr Thr Ser Met Leu Gln Thr Ile Glu Glu Gly Lys Gly
 290 295 300
 Gln Glu Thr Phe Gly Gly His Phe Gly Asn Ala Leu Leu Ser Phe Glu
 305 310 315 320
 Ile Asp Ser Leu Asn Leu Phe Thr Val Gly Gly Asn Val Arg Leu Trp
 325 330 335
 Glu Met Thr Thr Asp Arg Asn Ser Val Glu Lys Ser Phe Ala Gly Ser
 340 345 350
 Asn Leu Met Ser Tyr Ile Asp Arg Lys Leu Lys Thr Gln Met Asp Ala
 355 360 365
 Gly Ser Tyr Glu Leu Asn Ala Asp Tyr Gln His Ser Thr Arg Leu Pro
 370 375 380
 Gly Glu Leu Leu Thr Val Ser Tyr Arg Phe Thr His Asn Pro Asn Asn
 385 390 395 400
 Ser Glu Thr Phe Ile Asp Gln Trp Lys Arg Asp Pro Leu Asn Thr Ala
 405 410 415
 Asn Thr Ile Gln Tyr Ala Gly Gln His Ser Lys Ser Asp Ala Gly Met
 420 425 430
 Asp Glu His Thr Ala Gln Val Asp Tyr Thr Arg Pro Leu Gly Gln Ala
 435 440 445

WO 99/29870

PCT/AU98/01023

441/ 490

5 His Ser Leu Glu Ala Gly Leu Lys Tyr Ile Tyr Arg His Ala Thr Ser
 450 455 460
 Asp Pro Leu Tyr Glu Ile Arg Pro Ser Glu Asp Ala Pro Trp Gln Pro
 465 470 475 480
 Gly Ser Leu Tyr Ala Gln Asn Pro Ser Asn Gly Lys Phe Arg His Asp
 485 490 495
 Gln Tyr Ile Gly Ala Ala Tyr Ala Gly Tyr Asn Tyr Arg Lys Asp Gln
 500 505 510
 Tyr Ser Leu Gln Thr Gly Leu Arg Val Glu Ser Ser Arg Leu Lys Ala
 515 520 525
 10 Leu Phe Pro Glu Asn Ala Ala Asp Phe Ser His Asn Ser Phe Asp
 530 535 540
 Trp Val Pro Gln Leu Thr Leu Gly Tyr Thr Pro Ser Pro Met Lys Gln
 545 550 555 560
 15 Leu Lys Leu Ala Tyr Asn Phe Arg Ile Gln Arg Pro Ala Ile Gly Gln
 565 570 575
 Leu Asn Pro Tyr Arg Leu Gln Thr Asn Asp Tyr Gln Val Gln Tyr Gly
 580 585 590
 20 Asn Pro Asp Leu Lys Ser Glu Lys Arg His His Val Gly Leu Ser Tyr
 595 600 605
 Asn Gln Tyr Gly Ala Lys Val Met Leu Thr Ala Ser Leu Asp Tyr Asp
 610 615 620
 Phe Cys Asn Asn Ala Ile Gln Asn Tyr Thr Phe Ser Asp Pro Ala Asn
 625 630 635 640
 25 Pro Asn Leu Phe His Gln Thr Tyr Gly Asn Ile Gly Arg Glu His Ser
 645 650 655
 Phe Ser Leu Asn Thr Tyr Ala Met Tyr Thr Pro Ala Val Trp Val Arg
 660 665 670
 30 Ile Met Leu Asn Gly Asn Ile Asp Arg Thr Phe Gln Lys Ser Glu Ala
 675 680 685
 Leu Gly Ile Asp Val Asn Ser Trp Ser Gly Met Val Tyr Ser Gly Leu
 690 695 700
 Met Phe Thr Leu Pro Lys Asp Trp Thr Val Asn Leu Phe Gly Gly Tyr
 705 710 715 720
 35 Tyr His Gly Gly Arg Ser Tyr Gln Thr Lys Tyr Asp Gly Asn Val Phe
 725 730 735
 Asn Asn Ile Gly Ile Ala Lys Gln Leu Phe Asp Lys Lys Leu Arg Val
 740 745 750
 40 Ser Leu Ser Ala Asn Asn Ile His Ala Lys Tyr Ser Thr Trp Lys Ser
 755 760 765
 Arg Thr Ile Gly Asn Gly Phe Thr Ile Tyr Ser Glu Asn Ala Gly Ile
 770 775 780
 Gln Arg Ser Val Ser Leu Ser Leu Thr Tyr Ser Phe Gly Lys Met Asn
 785 790 795 800
 45 Thr Gln Val Arg Lys Val Glu Arg Thr Ile Val Asn Asp Asp Leu Lys
 805 810 815
 Gln Thr Ser Ser Gln Gly Gln Gln Gly Gly Gly Gln Gly Asn Pro Thr
 820 825 830
 50 Gly Asn

(2) INFORMATION FOR SEQ ID NO:490

55 (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 399 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 60 (11) MOLECULE TYPE: protein
 (111) HYPOTHETICAL: YES
 (v1) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 65 (12) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...399
 70 (21) SEQUENCE DESCRIPTION: SEQ ID NO:490

Met Arg Leu Ser Ala Ile Leu Ile Ala Leu Ile Val Met Leu Pro Ala
 1 5 10 15
 75 Val Leu Ser Gly Gln His Tyr Tyr Ser Met Ala Gly Glu Arg Leu Glu
 20 25 30

WO 99/29870

PCT/AU98/01023

442/ 490

Thr Asp Ser Ile Arg Pro Asn Glu Leu Ser Ala Ser Ile Arg Ser Ala
 35 40 45
 Leu Phe Phe Arg Asn Asn Glu Tyr Asn Ala Arg Ser Val Lys Gly Tyr
 50 55 60
 5 Thr Leu Pro Gly Ala Arg Val Ser Ala Phe Ala Ser Tyr Ser Leu Pro
 65 70 75 80
 Ala Ala His Gly Val Lys Leu Ser Leu Gly Val Ser Thr Leu Asn Tyr
 85 90 95
 10 Trp Gly Ala Ser Arg Tyr Pro Ala Gly Ile Ala Tyr Ser Asp Leu Pro
 100 105 110
 Tyr Trp Thr Asp Tyr Asn Asp Tyr Val Arg Leu Arg Ile Leu Pro Tyr
 115 120 125
 Val Gln Ala Met Leu Lys Pro Thr Ala Thr Thr Ala Leu Met Leu Gly
 130 135 140
 15 Asn Ile Ala Gly Gly Thr Ala His Gly Leu Ile Glu Pro Ile Tyr Asn
 145 150 155 160
 Pro Glu Leu Asp Leu Thr Ala Asp Pro Glu Ala Gly Val Gln Phe Arg
 165 170 175
 20 Gly Asp Trp Thr Arg Phe Arg Met Asp Val Trp Val Asn Trp Met Ser
 180 185 190
 Met Ile Phe Lys Asn Asp Asn His Gln Glu Ser Phe Val Phe Gly Leu
 195 200 205
 Ser Thr Thr Ser Lys Leu Leu Ser Gly Glu Gly Lys Trp Arg Leu Glu
 210 215 220
 25 Leu Pro Leu Gln Ala Ile Ala Thr His Arg Gly Gly Glu Tyr Asn Trp
 225 230 235 240
 Ala Gln Gln Asp Thr Val His Thr Trp Val Asn Gly Ala Val Gly Leu
 245 250 255
 30 Lys Leu Ser Tyr Arg Pro Arg Thr Asp Lys Pro Met Gln Ile Trp Gly
 260 265 270
 Ser Ala Tyr Gly Val Ala Ala Leu Ser Ser Gly Gly Tyr Phe Pro Tyr
 275 280 285
 Glu Arg Gly Trp Gly Gly Tyr Leu Ser Leu Gly Met Asp Leu Glu His
 290 295 300
 35 Phe Ala Phe Arg Thr Asp Tyr Trp Tyr Gly Arg His Tyr Val Ser Pro
 305 310 315 320
 Phe Ala Ala Pro Phe Ala Asn Ser Leu Thr Tyr Asp Lys Gln Pro Leu
 325 330 335
 40 Thr Asn Gly Trp Gly Asp Tyr Ile Arg Leu Tyr Ala Asp Tyr Ser Trp
 340 345 350
 Arg Met Ala Arg Ser Val Ser Leu Ala Val Ala Arg Val Trp Phe
 355 360 365
 Gln Pro Ser Asp Arg Phe Ala Met Ser His Ala Leu Glu Leu Thr Met
 370 375 380
 45 Arg Ile Asp Pro Lys Phe Pro Ile Ala Phe Leu Lys Gly Asn His
 385 390 395

(2) INFORMATION FOR SEQ ID NO:491

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 382 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 55 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 60 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...382
- 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:491

Met Asn Lys Ser Leu Leu Ser Leu Ala Cys Leu Ile Leu Cys Gly Met
 1 5 10 15
 70 Pro Ala Ile Ala Gln Gln Thr Gly Pro Ala Glu Arg Ser Gly Glu Pro
 20 25 30
 Ser Leu Ala Glu Arg Val Phe Gly Leu Glu Gln Lys Gln Lys Lys Leu
 35 40 45
 75 Lys Val Tyr Leu Gly Ile Gln Ser Phe Tyr Asp Gln Pro Leu Val Asp
 50 55 60

443/490

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Asp Glu Ser His Ile Gly His Phe Lys Val Gln Glu Leu Arg Met Ser
65      70      75      80
Ala His Gly Glu Leu Asn Arg His Leu Ser Phe Asp Trp Arg Gln Arg
      85      90      95
5  Leu Asn Arg Ala Ala Asp Gly Thr Ser Phe Ala Asp Asn Leu Ser Asn
      100      105      110
Ala Ile Asp Ile Ala Gly Val Asp Trp His Pro Asn Asp Lys Val Ser
      115      120      125
10 Phe Phe Phe Gly Arg Gln Tyr Ala Arg Phe Gly Gly Ile Glu Tyr Asp
      130      135      140
Met Asn Pro Val Glu Ile Tyr Gln Tyr Ser Asp Leu Val Asp Tyr Met
145      150      155      160
Thr Cys Tyr Thr Ser Gly Val Asn Phe Ala Trp Asn Phe His Pro Glu
      165      170      175
15 Gln Gln Leu Gln Gln Val Leu Asn Ala Tyr Asn Asn Arg Phe Ala
      180      185      190
Asp Arg Tyr His Val Thr Pro Asp Val Ala Thr Ala Thr Ser Tyr Pro
      195      200      205
20 Leu Leu Tyr Ser Ala Gln Trp Asn Gly Thr Leu Leu Gly Gly Ala Leu
      210      215      220
His Met Arg Tyr Ala Val Ser Met Ala His Gln Ala Gln Glu Arg Asn
225      230      235      240
Met Trp Tyr Phe Thr Ala Gly Asn Leu Phe Asn Pro Gly Lys Arg Ile
      245      250      255
25 Asn Gly Tyr Leu Asp Leu Thr Tyr Ser Ile Glu Gly Leu Asp Asp Lys
      260      265      270
Gly Ile Met Thr Ala Arg Tyr Gly Lys Gly Lys Thr Leu Thr Asp Val
      275      280      285
30 Lys Tyr Tyr Ala Leu Val Ser Lys Trp Asn Phe Arg Ile Phe Asp Gln
      290      295      300
Val Asn Leu Phe Leu Lys Gly Met Tyr Glu Asn Gly Tyr Ala Pro Ala
305      310      315      320
Gln Tyr Gly Glu Ser Ser His Thr Arg His Ser Tyr Gly Tyr Met Gly
      325      330      335
35 Gly Val Glu Tyr Tyr Pro Thr Glu Thr Asn Phe Arg Leu Phe Val Thr
      340      345      350
Tyr Ile Gly Arg His Tyr Arg Tyr Ser Ala Thr Glu Thr Glu Ser Thr
      355      360      365
40 Asn Ala Leu Arg Ala Gly Leu Ile Tyr Gln Ile Pro Phe Leu
      370      375      380

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(2) INFORMATION FOR SEQ ID NO:492

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 222 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 50 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
- 55 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...222
- 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:492

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Met Lys His Leu Phe Lys Ser Thr Leu Val Leu Leu Cys Ala Leu Ser
1      5      10      15
Phe Ser Gly Thr Tyr Thr Phe Ala Gln Glu Asn Asn Thr Glu Lys Ser
20      25      30
65 Arg Phe Asp Phe Ser Val Arg Leu Gly Gln Gly Tyr Ile Ala Gly Ser
      35      40      45
Thr Thr Asn Leu Met Tyr Gly Tyr Thr Ser Ala Asn Asp Arg Leu Leu
50      55      60
70 Ser Gly Ala Ile Tyr Leu Gly Leu Thr Pro Ser Lys Lys Glu Asn Ala
      65      70      75      80
Thr Gly Val Ala Phe Arg Phe Leu Ser Pro Ser Pro Gly Tyr Tyr Val
      85      90      95
75 Asp Ile Ser Gly Lys Glu Asn Thr Leu Asn Tyr Ala Phe Tyr Val Val
      100      105      110

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WO 99/29870

PCT/AU98/01023

444/ 490

5 Gly Ala Tyr Asn Arg Ile Ala Ile Pro Ile Arg Pro Ile Lys Asn Phe
115 120 125
Asn Phe Ile Phe Ser Thr Glu Val Gly Met Ala Trp Met Ser Arg His
130 135 140
10 Glu Gln Ile Tyr Asn Ser Thr Ser Gln Thr Trp Asp Lys Gln Arg Lys
145 150 155 160
Ser Arg Ser Gly Leu Asp Phe Gly Leu Gly Met His Leu Gln Unk His
165 170 175
15 Ile Asn Lys Thr Val Tyr Phe Met Ala Gly Trp Asp Leu Thr Ser Cys
180 185 190
10 Met Phe Gly Lys Arg Ile Asn Asp Tyr Gln Gln Lys Asp Arg Thr Phe
195 200 205
Ile Ala Leu Ile Asp Asn Ser Ile Gly Ile Gly Leu Asn Leu
210 215 220

(2) INFORMATION FOR SEQ ID NO:493

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 391 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493

35 Met Ile Ile Lys Lys Met Leu Lys Asn Lys Leu Ala Pro Leu Ala Ile
1 5 10 15
Leu Phe Leu Phe Ala Pro Lys Ala Met Lys Ala Gln Glu Gln Leu Asn
20 25 30
40 Val Val His Thr Ser Val Pro Ser Leu Asn Ile Ser Pro Asp Ala Arg
35 40 45
Ala Ala Gly Met Gly Asp Ile Gly Val Ala Thr Thr Pro Asp Ala Tyr
50 55 60
45 Ser Gln Tyr Trp Asn Pro Ser Lys Tyr Ala Phe Met Asp Thr Lys Ala
65 70 75 80
Gly Ile Ser Phe Ser Tyr Thr Pro Trp Leu Ser Lys Leu Val Asn Asp
85 90 95
Ile Ala Leu Met Gln Met Thr Gly Phe Tyr Lys Leu Gly Thr Asp Glu
100 105 110
50 Asn Gln Ala Ile Ser Ala Ser Leu Arg Tyr Phe Thr Leu Gly Lys Leu
115 120 125
Glu Thr Phe Asp Glu Leu Gly Glu Ser Met Gly Glu Ala His Pro Asn
130 135 140
55 Glu Phe Ala Val Asp Leu Gly Tyr Ser Arg Gln Leu Ser Glu Asn Phe
145 150 155 160
Ser Met Ala Val Ala Leu Arg Tyr Ile Arg Ser Asp Gln Ser Thr His
165 170 175
Asn Thr Gly Glu Asn Gln Ala Gly Asn Ala Phe Ala Ala Asp Ile Ala
180 185 190
60 Gly Tyr Leu Gln Lys Tyr Val Leu Leu Gly Asn Ala Glu Ser Leu Trp
195 200 205
Ser Leu Gly Phe Asn Val Lys Asn Ile Gly Thr Lys Ile Ser Tyr Asp
210 215 220
65 Gly Gly Val Thr Ser Phe Phe Ile Pro Thr Ser Leu Asn Leu Gly Thr
225 230 235 240
Gly Leu Leu Tyr Pro Ile Asp Asp Tyr Asn Ser Ile Asn Phe Asn Leu
245 250 255
Glu Leu Ser Lys Leu Leu Val Pro Thr Pro Pro Ile Met Asp Gln Asn
260 265 270
70 Asp Gln Ala Gly Tyr Glu Ala Ala Leu Lys Lys Tyr Gln Glu Thr Ser
275 280 285
Ser Ile Ser Gly Ile Phe Ser Ser Phe Gly Asp Ala Pro Gly Gly Leu
290 295 300
75 Lys Glu Glu Phe Arg Glu Ile Thr Trp Gly Leu Gly Ala Glu Tyr Ser
305 310 315 320

SUBSTITUTE SHEET (Rule 26) (RO/AU)

WO 99/29870

PCT/AU98/01023

445/490

5 Tyr Asp Asp Lys Phe Phe Val Arg Ala Gly Tyr Ser Tyr Leu His Pro
325 330 335
Thr Lys Gly Asn Leu Gln Tyr Phe Thr Ala Gly Ala Gly Phe Lys Met
340 345 350
5 Asn Ile Phe Arg Ile Asp Ala Ser Tyr Leu Leu Ser Thr Ile Gln Ser
355 360 365
Asn Pro Leu Asp Gln Thr Leu Arg Phe Thr Leu Ala Phe Asp Met Asp
370 375 380
10 Gly Leu Arg Asn Leu Phe His
385 390

(2) INFORMATION FOR SEQ ID NO:494

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 446 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- 20 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
- 25 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...446
- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:494

Met Lys Thr Thr Val Gln Gln Ile Ile Leu Cys Leu Ala Leu Met Met
1 5 10 15
35 Ser Gly Val Leu Gly Gly Asn Ala Gln Ser Phe Trp Glu Glu Ile Ala
20 25 30
Pro Pro Phe Ile Ser Asn Glu Pro Asn Val Lys Tyr Ile Ile Pro Asn
35 40 45
Met Gly Ile Asp Ser Lys Gly Thr Ile Tyr Val Thr Lys Arg
50 55 60
40 Ile Gln Gln Gly Ala Asn Tyr Thr Ser Glu Gln Leu Gly Met Tyr Tyr
65 70 75 80
Arg Pro Leu Gly Asp Asn Glu Gln Trp Trp Lys His Asp Pro Tyr Phe
85 90 95
45 Asp Asp Lys Ile Val Ala Asp Ile Gln Thr Asp Ala Tyr Gly Arg Val
100 105 110
Tyr Val Cys Thr Thr Ser Ser Arg Asp Gln Glu Tyr Gln Leu Tyr Ile
115 120 125
Asn Glu Gln Asn Glu Trp Arg Cys Ile Phe Lys Thr Ser Val Ser Thr
130 135 140
50 Tyr Glu His Gly Met Ala Val Phe Arg Ser Ser Thr Gly Val Thr Tyr
145 150 155 160
Ile Gly Thr Arg His His Ile Phe Ala Ser Gly Val Asn Asp Phe Glu
165 170 175
55 Phe Asn Thr Ile Tyr Glu Asp Ser Thr Pro Met Ser Cys Arg Phe Ala
180 185 190
Glu Ala Thr Asn Ser Gly Thr Ile Tyr Leu Ala Leu Met His Glu Thr
195 200 205
Thr Met Ser Thr Thr Ile Leu Thr Tyr Gln Asn Gly Glu Phe Val Asp
210 215 220
60 Ile Ser Glu Ser Glu Leu Ser Asn Ser Ile Ile Ala Ser Met Cys Ser
225 230 235 240
Asn Lys Glu Gly Asp Ile Ile Ala Leu Val Thr Ser Tyr Thr Gly Phe
245 250 255
65 Met Ser Gly Thr Leu Ala Ile Arg Lys Ala Asp Glu Gly Lys Trp Gln
260 265 270
Leu Val Gly Gly Asp Ile Gln Asn Ala Ile Val Gln Asn Ile Cys Met
275 280 285
Met Asp Asp Asn Lys Ile Ala Cys Glu Val Phe Gly Thr Pro Asn Gly
290 295 300
70 Val Asp Gly Arg Thr Arg Val Cys Val Ser Asp Ala Ser Val Phe Asp
305 310 315 320
Phe Glu Trp Tyr Glu Asp Glu Ile Tyr Gly Gly Leu Ile Phe Asp Thr
325 330 335
75 Phe Phe Tyr Ser Pro Trp Asp Lys Leu Leu Tyr Ala Lys Phe Gly Gly
340 345 350

WO 99/29870

PCT/AU98/01023

446/ 490

Ile Met Leu Arg Ser Lys Glu Ser Phe Ile Thr Ser Phe Ile Ser Pro
 355 360 365
 Thr Val Val Gln Gly Val Asp Val Tyr Thr Leu Ala Gly Lys Ile Arg
 370 375 380
 5 Ile Glu Ser Glu Thr Pro Val Ser Glu Val Leu Leu Phe Asp Leu Ala
 385 390 395 400
 Gly Arg Met Val Leu Arg Gln Thr Ile Asp Asn Lys Ile Tyr Ser Asp
 405 410 415
 10 Ile Asp Thr Asn Gly Leu Lys Arg Ser Gly Ile Tyr Val Val Ser Val
 420 425 430
 Arg Leu Ser Ser Gly Gln Val Phe Ser His Lys Val Gln Val
 435 440 445
 (2) INFORMATION FOR SEQ ID NO:495
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 308 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...308
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:495
 Met Ile Ile Arg Cys Leu Ile Arg Arg Pro Arg Thr Val Leu Phe Gly
 1 5 10 15
 Leu Ile Phe Val Val Gly Leu Phe Ser Ala Met Ala Gln Glu Lys Lys
 20 25 30
 Asp Ser Leu Ser Thr Val Gln Pro Val Pro Asn Ser Ser Met Val Glu
 35 40 45
 40 Gln Thr Pro Leu Leu Ser Ile Asp His Pro Val Leu Pro Ala Ser Phe
 50 55 60
 Gln Asn Thr Arg Thr Leu Lys Arg Phe Arg Asp Lys His Leu Ser Asp
 65 70 75 80
 45 Ala Leu Leu Asn Gly Leu Lys Pro His Arg Ser Ser Leu Gln Leu Asn
 85 90 95
 Glu Glu Leu Asn Phe Ala Ala Glu Arg Arg Asp Phe Val Ser Pro Leu
 100 105 110
 Leu Gln Thr Arg His Ala Ala Gly Val Leu Ser Trp Arg Pro Thr Asp
 115 120 125
 50 Arg Met His Phe Tyr Thr Ser Gly Asn Ile Gly Leu Gly His Asp Leu
 130 135 140
 Leu Thr Gly Val Arg Lys Asp Phe Gly Trp Asn Ala Gly Ala Asp Phe
 145 150 155 160
 55 Leu Leu Ser Gln Asn Leu Thr Ala His Val Gln Gly Gly Trp Gln Gln
 165 170 175
 Asn Phe Gly Phe Ile Pro Met Thr Ala Val Asn Gly Gln Leu Arg Trp
 180 185 190
 Gln Ala Thr Glu Arg Leu Ser Phe Thr Thr Gly Ile Asp Tyr Arg Gln
 195 200 205
 60 Val Gln Trp Asn Ala Phe Asp Asn Arg Thr Phe Ser Leu Lys Gly Ser
 210 215 220
 Ala Arg Tyr Glu Val Met Asp Asn Val Phe Val Asn Gly Phe Gly Ser
 225 230 235 240
 Tyr Pro Leu Tyr Ser Ser Thr Arg Ser Gly Leu Asn Met Ala Val Pro
 245 250 255
 65 Met His Gly Phe Gly Pro Gln Tyr Gly Gly Ser Leu Glu Leu Lys Val
 260 265 270
 Ser Glu Arg Phe Gly Phe Ala Val Gly Met Glu Arg Glu Tyr Asn Ile
 275 280 285
 70 Trp Thr Arg Arg Trp Glu Thr His Tyr Phe Ala Tyr Pro Val Phe Tyr
 290 295 300
 Gly Asp Lys Lys
 305
 (2) INFORMATION FOR SEQ ID NO:496

447/ 490

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 315 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496

1	Met	Lys	Thr	Asn	Arg	Arg	Tyr	Ala	Phe	Val	Leu	Pro	Leu	Leu	Leu
5	Thr	Gly	Leu	Leu	Ala	Trp	Gly	Gln	Asp	Ser	Ser	His	Gly	Ser	Asn
10	Ala	Phe	Ala	Thr	Asp	Ser	Ser	Ser	Arg	Glu	Leu	Pro	Thr	Glu	Gln
15	Ala	Tyr	Arg	Ile	His	Ser	Ala	Tyr	Met	Val	Gly	Gly	Gly	Ser	Ile
20	Thr	Arg	Asp	Thr	Tyr	Leu	Ser	Pro	Leu	Arg	Tyr	Gly	Gly	Trp	Thr
25	Asn	Leu	Leu	Gly	Glu	Lys	Thr	Phe	Pro	Leu	Lys	Ala	Ser	Asp	Ser
30	Trp	Met	Ile	Arg	Thr	Gly	His	Glu	Leu	Asp	Phe	Ala	Leu	Met	Asp
35	Pro	Ala	Asn	Asn	Ala	His	Phe	Tyr	Ser	Leu	Leu	Tyr	Asn	Gly	Ser
40	Ala	Ala	Leu	Tyr	Arg	Leu	Gly	Ala	Lys	His	Leu	Arg	Ala	Ala	Trp
45	Asp	Asn	Leu	Arg	Leu	Ala	Phe	Gly	Pro	Gly	Leu	Glu	Ile	Gly	Leu
50	Gly	Ile	Tyr	Ser	Thr	Arg	Asn	Gly	Asn	Asn	Pro	Ala	Thr	Leu	Lys
55	Tyr	Thr	Asn	Ala	Ile	Ala	Gln	Ala	Ser	Ile	Gly	Tyr	Tyr	Val	Pro
60	Glu	Thr	Phe	Pro	Leu	Tyr	Phe	Arg	Leu	Leu	Ser	Gln	Ile	Asn	Leu
65	Gly	Ile	Ala	Tyr	Gly	Asn	Gly	Phe	Gly	Glu	Ser	Tyr	Tyr	Glu	Asn
70	Leu	Leu	Asn	Asn	Gly	Ile	Ala	Gly	Ser	Leu	His	Phe	Thr	Tyr	Pro
75	Lys	Phe	Thr	Arg	Phe	Thr	Thr	Leu	Ile	Thr	Ala	Asp	Ile	Pro	Ile
80	Asn	Phe	Cys	Thr	Leu	Arg	Val	Gly	Tyr	Arg	Tyr	Ser	His	Leu	Gly
85	Ser	Leu	Asn	Ala	Leu	Asp	Thr	Arg	Ile	His	Ser	His	Thr	Ala	Phe
90	Gly	Phe	Val	Thr	Glu	Phe	Tyr	Arg	Phe	Arg	Gly	Arg	Lys	Ala	Met
95	Thr	Gly	Arg	Arg	Thr	Ser	Leu	Tyr	Tyr	His	Asp				

(2) INFORMATION FOR SEQ ID NO:497

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 285 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

WO 99/29870

PCT/AU98/01023

449/ 490

100 105 110
Ala Ala Arg Ser Tip Glu Arg Val Asn Glu Ala Leu Glu Lys Asp Glu
115 120 125
5 Ile Val Lys Gly Tyr Val Lys Cys Arg Thr Lys Gly Gly Met Ile Val
130 135 140
Asp Val Phe Gly Ile Glu Ala Phe Leu Pro Gly Ser Gln Ile Asp Val
145 150 155 160
Arg Pro Ile Arg Asp Tyr Asp Ala Phe Val Glu Lys Thr Met Glu Phe
165 170 175
10 Lys Ile Val Lys Ile Asn Gln Glu Tyr Lys Asn Val Val Val Ser His
180 185 190
Lys Val Leu Ile Glu Ala Glu Leu Glu Gln Gln Lys Lys Glu Ile Ile
195 200 205
15 Gly Lys Leu Glu Lys Gly Gln Val Leu Glu Gly Ile Val Lys Asn Ile
210 215 220
Thr Ser Tyr Gly Val Phe Ile Asp Leu Gly Gly Val Asp Gly Leu Ile
225 230 235 240
His Ile Thr Asp Leu Ser Trp Gly Arg Val Ala His Pro Glu Glu Ile
245 250 255
20 Val Gln Leu Asp Gln Lys Ile Asn Val Val Ile Leu Asp Phe Asp Glu
260 265 270
Asp Arg Lys Arg Ile Ala Leu Gly Leu Lys Gln Leu Met Pro His Pro
275 280 285
25 Trp Asp Ala Leu Asp Ser Glu Leu Lys Val Gly Asp Lys Val Lys Gly
290 295 300
Lys Val Val Val Met Ala Asp Tyr Gly Ala Phe Val Glu Ile Ala Gln
305 310 315 320
Gly Val Glu Gly Leu Ile His Val Ser Glu Met Ser Trp Thr Gln His
325 330 335
30 Leu Arg Ser Ala Gln Asp Phe Leu His Val Gly Asp Glu Val Glu Ala
340 345 350
Val Ile Leu Thr Leu Asp Arg Glu Glu Arg Lys Met Ser Leu Gly Leu
355 360 365
35 Lys Gln Leu Lys Pro Asp Pro Trp Ala Asp Ile Glu Thr Arg Phe Pro
370 375 380
Val Gly Ser Arg His His Ala Arg Val Arg Asn Phe Thr Asn Phe Gly
385 390 395 400
Val Phe Val Glu Ile Glu Glu Gly Val Asp Gly Leu Ile His Ile Ser
405 410 415
40 Asp Leu Ser Trp Thr Lys Lys Ile Lys His Pro Ser Glu Phe Thr Glu
420 425 430
Val Gly Ala Asp Ile Glu Val Gln Val Ile Glu Ile Asp Lys Glu Asn
435 440 445
45 Arg Arg Leu Ser Leu Gly His Lys Gln Leu Glu Glu Asn Pro Trp Asp
450 455 460
Val Phe Glu Thr Val Phe Thr Val Gly Ser Ile His Glu Gly Thr Val
465 470 475 480
Ile Glu Val Met Asp Lys Gly Ala Val Val Ser Leu Pro Tyr Gly Val
485 490 495
50 Glu Gly Phe Ala Thr Pro Lys His Met Val Lys Glu Asp Gly Ser Gln
500 505 510
Ala Val Leu Glu Glu Lys Leu Pro Phe Lys Val Ile Glu Phe Asn Lys
515 520 525
55 Asp Ala Lys Arg Ile Ile Val Ser His Ser Arg Val Phe Glu Asp Glu
530 535 540
Gln Lys Met Ala Gln Arg Glu Ala Asn Ala Glu Arg Lys Ala Glu Ala
545 550 555 560
Lys Ala Ala Gln Lys Glu Ala Ala Ala Glu Ala Asn Pro Ala Gln
565 570 575
60 Ala Val Glu Lys Ala Thr Leu Gly Asp Leu Gly Glu Leu Ala Ala Leu
580 585 590
Lys Glu Lys Leu Ser Glu Asn
595

65 (2) INFORMATION FOR SEQ ID NO:499

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 550 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

70

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

75

WO 99/29870

PCT/AU98/01023

450/ 490

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

5 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499

10 Met Gly Arg Val Thr Ala Ile Asn Lys Arg Glu Val Val Ile Asn Val
1 5 10 15
Gly Tyr Lys Ser Glu Gly Val Val Pro Ala Thr Glu Phe Arg Tyr Asn
20 25 30
15 Pro Glu Leu Lys Val Gly Asp Glu Val Glu Val Tyr Ile Glu Asn Gln
35 40 45
Glu Asp Lys Lys Gly Gln Leu Val Leu Ser His Arg Lys Gly Arg Ala
50 55 60
Ala Arg Ser Trp Glu Arg Val Asn Glu Ala Leu Glu Lys Asp Glu Ile
65 70 75 80
20 Val Lys Gly Tyr Val Lys Cys Arg Thr Lys Gly Gly Met Ile Val Asp
85 90 95
Val Phe Gly Ile Glu Ala Phe Leu Pro Gly Ser Gln Ile Asp Val Arg
100 105 110
25 Pro Ile Arg Asp Tyr Asp Ala Phe Val Glu Lys Thr Met Glu Phe Lys
115 120 125
Ile Val Lys Ile Asn Gln Glu Tyr Lys Asn Val Val Val Ser His Lys
130 135 140
Val Leu Ile Glu Ala Glu Leu Glu Gln Gln Lys Lys Glu Ile Ile Gly
145 150 155 160
30 Lys Leu Glu Lys Gly Gln Val Leu Glu Gly Ile Val Lys Asn Ile Thr
165 170 175
Ser Tyr Gly Val Phe Ile Asp Leu Gly Gly Val Asp Gly Leu Ile His
180 185 190
35 Ile Thr Asp Leu Ser Trp Gly Arg Val Ala His Pro Glu Glu Ile Val
195 200 205
Gln Leu Asp Gln Lys Ile Asn Val Val Ile Leu Asp Phe Asp Glu Asp
210 215 220
Arg Lys Arg Ile Ala Leu Gly Leu Lys Gln Leu Met Pro His Pro Trp
225 230 235 240
40 Asp Ala Leu Asp Ser Glu Leu Lys Val Gly Asp Lys Val Lys Gly Lys
245 250 255
Val Val Val Met Ala Asp Tyr Gly Ala Phe Val Glu Ile Ala Gln Gly
260 265 270
45 Val Glu Gly Leu Ile His Val Ser Glu Met Ser Trp Thr Gln His Leu
275 280 285
Arg Ser Ala Gln Asp Phe Leu His Val Gly Asp Glu Val Glu Ala Val
290 295 300
Ile Leu Thr Leu Asp Arg Glu Glu Arg Lys Met Ser Leu Gly Leu Lys
305 310 315 320
50 Gln Leu Lys Pro Asp Pro Trp Ala Asp Ile Glu Thr Arg Phe Pro Val
325 330 335
Gly Ser Arg His His Ala Arg Val Arg Asn Phe Thr Asn Phe Gly Val
340 345 350
55 Phe Val Glu Ile Glu Glu Gly Val Asp Gly Leu Ile His Ile Ser Asp
355 360 365
Leu Ser Trp Thr Lys Lys Ile Lys His Pro Ser Glu Phe Thr Glu Val
370 375 380
Gly Ala Asp Ile Glu Val Gln Val Ile Glu Ile Asp Lys Glu Asn Arg
385 390 395 400
60 Arg Leu Ser Leu Gly His Lys Gln Leu Glu Glu Asn Pro Trp Asp Val
405 410 415
Phe Glu Thr Val Phe Thr Val Gly Ser Ile His Glu Gly Thr Val Ile
420 425 430
65 Glu Val Met Asp Lys Gly Ala Val Val Ser Leu Pro Tyr Gly Val Glu
435 440 445
Gly Phe Ala Thr Pro Lys His Met Val Lys Glu Asp Gly Ser Gln Ala
450 455 460
Val Leu Glu Glu Lys Leu Pro Phe Lys Val Ile Glu Phe Asn Lys Asp
465 470 475 480
70 Ala Lys Arg Ile Ile Val Ser His Ser Arg Val Phe Glu Asp Glu Gln
485 490 495
Lys Met Ala Gln Arg Glu Ala Asn Ala Glu Arg Lys Ala Glu Ala Lys
500 505 510
75 Ala Ala Gln Lys Glu Ala Ala Ala Glu Ala Ala Asn Pro Ala Gln Ala
515 520 525

WO 99/29870

PCT/AU98/01023

454/ 490

(A) NAME/KEY: misc_feature
(B) LOCATION 1...434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503

5 Met Tyr Lys Asp Tyr Lys Gly Leu Tyr Ala Ser Leu Arg Trp Tyr Ala
1 5 10 15
Leu Ile Ile Gly Leu Leu Phe Ala Ala Asp Gly Ile Gln Ala Gln Asn
20 25 30
10 Asn Asn Phe Thr Glu Ser Pro Tyr Thr Arg Phe Gly Leu Gly Arg Asn
35 40 45
Gly Glu Arg Thr Thr Ile Ser Gly His Ser Met Gly Gly Leu Gly Val
50 55 60
15 Gly Leu Arg Gln Gly Thr Tyr Val Asn Ala Val Asn Pro Ala Ser Tyr
65 70 75 80
Ser Ala Val Asp Ser Met Thr Phe Ile Phe Asp Phe Gly Ala Ser Thr
85 90 95
Gly Ile Thr Trp Tyr Ala Glu Asn Gly Lys Lys Asp Asn Arg Lys Met
100 105 110
20 Gly Asn Ile Glu Tyr Phe Ala Met Leu Phe Pro Ile Ser Lys Ser Ile
115 120 125
Ala Met Ser Ala Gly Val Leu Pro Tyr Ser Ala Ser Gly Tyr Gln Phe
130 135 140
25 Gly Ser Val Asp Gln Val Glu Gly Gly Ser Val Gln Tyr Thr Arg Lys
145 150 155
Tyr Leu Gly Thr Gly Asn Leu Asn Asp Leu Tyr Val Gly Ile Gly Ala
160 165 170 175
Thr Pro Phe Lys Asn Phe Ser Ile Gly Ala Asn Ala Ser Ser Leu Phe
180 185 190
30 Gly Arg Phe Thr His Ser Arg Gln Val Ile Phe Ser Thr Glu Ala Pro
195 200 205
Tyr Asn Pro Val His Leu Ser Thr Leu Tyr Leu Lys Ala Ala Lys Phe
210 215 220
35 Asp Phe Gly Met Gln Tyr His Leu Leu Leu Lys Ser Asp Arg Ser Leu
225 230 235
Val Ile Gly Ala Val Tyr Ser Pro Arg Val Lys Met His Ser Glu Leu
240 245 250 255
Thr Gln Ile Lys Asn Gln Val Gln Asn Gly Val Val Val Glu Ser Glu
260 265 270
40 Thr Gln Glu Tyr Ile Lys Gly Met Asp Tyr Tyr Thr Leu Pro His Thr
275 280 285
Leu Gly Ile Gly Phe Ser Tyr Glu Lys Lys Asp Lys Leu Leu Gly
290 295 300
45 Ala Asp Val Gln Tyr Ser Lys Trp Lys Gly Glu Lys Phe Tyr Lys Ser
305 310 315 320
Asp Cys Lys Phe Gln Asp Arg Ile Arg Val Ser Leu Gly Gly Glu Ile
325 330 335
Ile Pro Asp Ile Asn Ala Val Gly Met Trp Pro Lys Val Arg Tyr Arg
340 345 350
50 Phe Gly Leu His Gly Glu Asn Ser Tyr Leu Lys Val Pro Thr Lys Gly
355 360 365
Gly Val Tyr Gln Gly Tyr His Ile Val Gly Ala Val Phe Gly Ile Gly
370 375 380
55 Ile Pro Leu Asn Asp Arg Arg Ser Phe Val Asn Val Ser Leu Glu Tyr
385 390 395 400
Asp Arg Leu Ile Pro Lys Glu Gly Met Ile Lys Glu Asn Ala Leu Lys
405 410 415
Leu Thr Phe Gly Leu Thr Phe Asn Glu Ser Trp Phe Lys Lys Leu Lys
420 425 430
60 Leu Asn

(2) INFORMATION FOR SEQ ID NO:504

65 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 926 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
70 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
75 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

456/ 490

Tyr Ser Asn Glu Phe Thr Gln Tyr Arg Ile Gly Leu Asn Leu Lys Lys
 545 550 555 560
 Ile Ala Lys Thr Trp Asp Tyr Thr Val Gly Phe Asn Val Asp Pro Asn
 565 570 575
 5 Arg Thr Val Ser Tyr Arg Ser Val Ala Gly Val Glu Gln Asp Lys Leu
 580 585 590
 Ala Phe Asn Arg Val Asn Leu Ser Pro Met Leu Arg Ile Asn Tyr Lys
 595 600 605
 10 Pro Ser Arg Thr Thr Asn Leu Arg Val Asp Tyr Arg Gly Arg Thr Thr
 610 615 620
 Gln Pro Ser Ile Asn Gln Ile Ala Pro Val Gln Asp Ile Thr Asn Pro
 625 630 635 640
 Leu Phe Val Thr Glu Gly Asn Pro Gly Leu Lys Pro Ser Tyr Ser Asn
 645 650 655
 15 Asn Val Met Ala Met Phe Ser Asp Phe Asp Ala Lys Ser Gln Arg Ala
 660 665 670
 Phe Asn Ile Val Phe Phe Gly Asn Tyr Thr Phe Asp Asp Ile Val Pro
 675 680 685
 20 Asn Thr His Tyr Asp Pro Ser Thr Gly Ile Arg Thr Thr Arg Tyr Glu
 690 695 700
 Asn Ala Ser Gly Thr Trp Gln Ala Asn Leu His Gly Thr Leu Ser Leu
 705 710 715 720
 Pro Leu Lys Asn Arg Ala Phe Ser Phe Arg Met Ser Leu Phe Asn Arg
 725 730 735
 25 Leu Ala Glu Gly Gln Ser Phe Ile Asn Asp Asp Lys Asn Lys Ala Leu
 740 745 750
 Ser Phe Arg Thr Arg Glu Arg Leu Thr Leu Thr Tyr Arg Asn Asn Trp
 755 760 765
 30 Ile Asp Thr Ser Ile Gly Gly Asn Ile Gly Phe Tyr Met Ala Asn Asn
 770 775 780
 Ser Leu Ser Gly Gln Lys Asp Ser Arg Thr Tyr Asp Phe Gly Gly Asn
 785 790 795 800
 Tyr Gln Val Ala Leu Thr Leu Pro Tyr Gly Phe Arg Ile Asp Ser Asp
 805 810 815
 35 Val Glu Tyr Asn Thr Asn Ser Gly Tyr Ser Gly Gly Phe Ser Leu Asp
 820 825 830
 Glu Trp Leu Trp Asn Ala Ser Leu Ser Tyr Ser Phe Leu Arg Asp Lys
 835 840 845
 40 Ala Gly Thr Leu Arg Val Asn Asn Gly Tyr Asp Ile Leu Gly Gln Arg Ser
 850 855 860
 Ser Ile Ser Arg Ser Ala Ser Ala Ile Asn Ile Glu Glu Ser Met Ser
 865 870 875 880
 Asn Thr Ile Gly Arg Tyr Val Met Val Asp Phe Ile Tyr Arg Phe Asn
 885 890 895
 45 Ala Phe Ser Gly Gly Gly Ser Arg Ser Asp His Gln Arg Gly Asn Met
 900 905 910
 Asn Arg Pro Gly Pro Pro Phe Gly Gly Gly Arg Arg Pro Ser
 915 920 925
 50 (2) INFORMATION FOR SEQ ID NO:505
 (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 55 (11) MOLECULE TYPE: protein
 (111) HYPOTHETICAL: YES
 (71) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 60 (12) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...400
 (121) SEQUENCE DESCRIPTION: SEQ ID NO:505
 70 Met Val Met Lys Leu Ile Lys Arg Ser Leu Leu Leu Leu Gly Ala Val
 1 5 10 15
 Leu Leu Ile Thr Leu Pro Ala Tyr Ser Gln Asn Asp Asp Ile Phe Glu
 20 25 30
 75 Asp Asp Ile Tyr Thr Ser Arg Lys Glu Ile Arg Lys Gln Asn Gln Val
 35 40 45

WO 99/29870

PCT/AU98/01023

457/490

5 Lys Asp Trp Gln Asn Gln Glu Asp Gly Tyr Gly Asp Asp Thr Glu Tyr
50 55 60
Thr Val Ala Ser Asp Arg Asp Ile Asp Ala Tyr Asn Arg Arg Asp Gly
65 70 75
10 Gln Ser Tyr Asp Gly Lys Lys Leu Ser Lys Asp Lys Lys Arg Asp Ser
85 90 95
Thr Arg Ser Ser Val Pro Gly Arg Tyr Ser Arg Arg Leu Ala Arg Phe
100 105 110
10 Tyr Lys Pro Asn Thr Ile Val Ile Ser Gly Ala Asp Asn Val Tyr Val
115 120 125
Thr Asp Asp Gly Glu Tyr Phe Val Tyr Gly Asp Glu Tyr Tyr Asp Asp
130 135 140
Ala Ser Ser Val Asn Ile Tyr Ile Asn Ser Pro Trp Cys Asp Pro Phe
145 150 155
15 Pro Tyr Thr Ser Trp Tyr Pro Ser Phe Ser Gly Trp Tyr Asn Tyr Thr
160 165 170 175
Trp Asn Tyr Pro Trp Phe Tyr Tyr Gly Ser His Ile Gly Trp Gly Gly
180 185 190
20 Tyr Tyr Pro Gly Tyr Asn Trp Tyr Trp Ser Tyr Tyr Tyr Asp Pro Phe
195 200 205
Tyr Asn Pro Tyr Gly Ile Gly Met Gly Trp Gly Tyr Pro Tyr Gly Trp
210 215 220
Gly Ser Tyr Tyr Gly Trp Gly Gly Tyr Pro Gly Val Ile His His Tyr
225 230 235 240
25 His His Tyr Pro Lys Lys Thr Tyr Ser Asn Gly Gln His Ser Gly Ala
245 250 255
Tyr Tyr Ser Tyr Gly Arg Pro Asn Arg Ile Lys Gly Gly Thr Ser Gly
260 265 270
30 Ala Lys Leu Gly Thr Gly Arg Tyr Asp Arg Ile Gln Asn Ser Ser Ser
275 280 285
Gln Lys Asn Lys Phe Gly Leu Gln Ser Asn Lys Pro Asn Asn Asn Leu
290 295 300
Gln Asn Val Lys Ser Gly Arg Thr Gly Arg Ala Asn Arg Asp Arg Asn
305 310 315 320
35 Ile Glu Thr Val Thr Pro Asn Asn Gly Gln Lys Gln Asn Arg Pro Val
325 330 335
Phe Gln Gln Asn Gln Ser Gly Asn Asp Arg Pro Thr Gly Arg Asn Ile
340 345 350
40 Arg Ser Glu Arg Gln Gly Glu Asn Asp Arg Thr Phe Ser Thr Pro
355 360 365
Ser Arg Ser Asn Ser Asn Gly Gly Phe Ser Thr Pro Ser Arg Ser Ser
370 375 380
Ser Gly Ser Met Ser Gly Gly Gly Gly Arg Ser Gly Arg Gly Arg Asn
385 390 395 400

(2) INFORMATION FOR SEQ ID NO:506

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 398 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1...398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506

65 Met Lys Leu Ile Lys Arg Ser Leu Leu Leu Leu Gly Ala Val Leu Leu
1 5 10 15
Ile Thr Leu Pro Ala Tyr Ser Gln Asn Asp Asp Ile Phe Glu Asp Asp
20 25 30
70 Ile Tyr Thr Ser Arg Lys Glu Ile Arg Lys Gln Asn Gln Val Lys Asp
35 40 45
Trp Gln Asn Gln Glu Asp Gly Tyr Gly Asp Asp Thr Glu Tyr Thr Val
50 55 60
75 Ala Ser Asp Arg Asp Ile Asp Ala Tyr Asn Arg Arg Asp Gly Gln Ser
65 70 75 80

458/490

Tyr Asp Gly Lys Lys Leu Ser Lys Asp Lys Lys Arg Asp Ser Thr Arg
 85 90 95
 Ser Ser Val Pro Gly Arg Tyr Ser Arg Arg Leu Ala Arg Phe Tyr Lys
 100 105 110
 5 Pro Asn Thr Ile Val Ile Ser Gly Ala Asp Asn Val Tyr Val Thr Asp
 115 120 125
 Asp Gly Glu Tyr Phe Val Tyr Ser Gly Asp Glu Tyr Tyr Asp Asp Ala Ser
 130 135 140
 10 Ser Val Asn Ile Tyr Ile Asn Ser Pro Trp Cys Asp Pro Phe Pro Tyr
 145 150 155 160
 Thr Ser Trp Tyr Pro Ser Phe Ser Gly Trp Tyr Asn Tyr Thr Trp Asn
 165 170 175
 Tyr Pro Trp Phe Tyr Tyr Gly Ser His Ile Gly Trp Gly Gly Tyr Tyr
 180 185 190
 15 Pro Gly Tyr Asn Trp Tyr Trp Ser Tyr Tyr Tyr Asp Pro Phe Tyr Asn
 195 200 205
 Pro Tyr Gly Ile Gly Met Gly Trp Gly Tyr Pro Tyr Gly Trp Gly Ser
 210 215 220
 20 Tyr Tyr Gly Trp Gly Gly Tyr Pro Gly Val Ile His His Tyr His His
 225 230 235 240
 Tyr Pro Lys Lys Thr Tyr Ser Asn Gly Gln His Ser Gly Ala Tyr Tyr
 245 250 255
 Ser Tyr Gly Arg Pro Asn Arg Ile Lys Gly Gly Thr Ser Gly Ala Lys
 260 265 270
 25 Leu Gly Thr Gly Arg Tyr Asp Arg Ile Gln Asn Ser Ser Ser Gln Lys
 275 280 285
 Asn Lys Phe Gly Leu Gln Ser Asn Lys Pro Asn Asn Asn Leu Gln Asn
 290 295 300
 30 Val Lys Ser Gly Arg Thr Gly Arg Ala Asn Arg Asp Arg Asn Ile Glu
 305 310 315 320
 Thr Val Thr Pro Asn Asn Gly Gln Lys Gln Asn Arg Pro Val Phe Gln
 325 330 335
 Gln Asn Gln Ser Gly Asn Asp Arg Pro Thr Gly Arg Asn Ile Arg Ser
 340 345 350
 35 Glu Arg Gln Gly Glu Asn Asn Asp Arg Thr Phe Ser Thr Pro Ser Arg
 355 360 365
 Ser Asn Ser Asn Gly Gly Phe Ser Thr Pro Ser Arg Ser Ser Ser Gly
 370 375 380
 40 Ser Met Ser Gly Gly Gly Gly Arg Ser Gly Arg Gly Arg Asn
 385 390 395

(2) INFORMATION FOR SEQ ID NO:507

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 581 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 50 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 55 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION: 1...581
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:507

Met Ile Arg Lys Leu Ile Leu Leu Leu Ala Leu Met Pro Val Ala Ser
 1 5 10 15
 Val Ala Phe Ala Val Pro Thr Asp Ser Thr Glu Ser Lys Asp Asn Arg
 20 25 30
 65 Ile Leu Thr Ser Met Gln Ser Ser Ser Leu Asn Arg Asp Asp Ala Pro
 35 40 45
 Asp Lys Trp Gln Pro Met His Ala Asn Phe Ser Ile Gln Ser Asp Met
 50 55 60
 70 Leu Leu Ser Thr Ala Gln Lys Ser Lys Asn Thr Trp Phe Gly Asn Ser
 65 70 75 80
 Tyr Ile Met Gly Ile Ile Lys Asn Asn Tyr Leu Glu Phe Gly Ala Arg
 85 90 95
 75 Phe Glu Asp Leu Tyr Lys Pro Leu Pro Gly His Glu Pro Glu Met Gly
 100 105 110

WO 99/29870

PCT/AU98/01023

459/ 490

Arg Gly Val Pro His Met Tyr Val Lys Gly Ser Tyr His Trp Ala Glu
 115 120 125
 Leu Thr Met Gly Asp Phe Tyr Asp Gln Phe Gly Ser Gly Met Val Phe
 130 135 140
 5 Arg Thr Tyr Glu Glu Arg Asn Leu Gly Ile Asp Asn Ala Val Arg Gly
 145 150 155 160
 Gly Arg Ile Val Leu Thr Pro Phe Asp Gly Val Arg Val Lys Gly Ile
 165 170 175
 10 Ala Gly Gln Gln Arg Asn Tyr Phe Asp Arg Thr Gly Lys Val Phe Asn
 180 185 190
 Ser Gly Arg Gly Tyr Leu Leu Gly Ser Asp Leu Glu Leu Asn Val Glu
 195 200 205
 Arg Trp Ser Ser Ala Met Arg Asp Asn Asp Tyr His Leu Ala Ile Gly
 210 215 220
 15 Gly Ser Phe Val Ser Lys His Glu Ala Asp Glu Asp Ile Phe Val Gly
 225 230 235 240
 Val Gly Glu Asp Arg Lys Arg Leu Asn Leu Pro Leu Asn Val Pro Ile
 245 250 255
 20 Met Gly Leu Arg Thr Asn Phe Gln Lys Gly Gly Leu Ala Leu Tyr Ala
 260 265 270
 Glu Tyr Gly Tyr Lys Tyr Asn Asp Pro Ser Ala Asp Asn Asp Tyr Ile
 275 280 285
 Tyr His Asp Gly Gln Ala Ala Leu Leu Ser Ala Ser Tyr Ser Lys Lys
 290 295 300
 25 Gly Met Ser Ile Leu Leu Gln Ala Lys Arg Cys Glu Asn Phe Ala Phe
 305 310 315 320
 Arg Ser Lys Arg Ser Ala Gln Leu Thr Pro Leu Met Ile Asn Tyr Met
 325 330 335
 30 Pro Ala Phe Thr Gln Ala His Thr Tyr Thr Leu Ala Ala Ile Tyr Pro
 340 345 350
 Tyr Ala Thr Gln Pro Gln Gly Glu Trp Ala Phe Gln Gly Glu Leu Arg
 355 360 365
 Tyr Asn Phe Ala Arg Arg Thr Ala Leu Gly Gly Arg Tyr Gly Thr Gly
 370 375 380
 35 Leu Arg Ile Asn Val Ser His Val Arg Gly Leu Asp Lys Lys Met Leu
 385 390 395 400
 Lys Glu Asn Pro Asp Glu Leu Ile Gly Thr Asp Gly Tyr Thr Val Ser
 405 410 415
 40 Phe Phe Gly Met Gly Asp Leu Tyr Tyr Ser Asp Ile Asp Val Glu Ile
 420 425 430
 Thr Lys Lys Val Ser Pro Gly Phe Asn Phe Thr Leu Thr Tyr Leu Asn
 435 440 445
 Gln Ile Tyr Asn Asn Lys Val Leu His Gly Ala Ala Gly Glu Lys Pro
 450 455 460
 45 Glu Lys Ile Tyr Ala Asn Ile Phe Val Tyr Asp Gly Lys Tyr Lys Leu
 465 470 475 480
 Ser Asn Lys Val Ala Leu Arg Thr Glu Leu Gln Tyr Leu His Thr Lys
 485 490 495
 50 Gln Asp Gln Gly Asp Trp Ile Tyr Gly Met Ala Glu Leu Ser Ile Leu
 500 505 510
 Pro Ser Leu Met Leu Ser Leu Ser Glu Gln Tyr Asn Ile Gly Glu Thr
 515 520 525
 Lys Lys His Tyr Val Met Gly Ser Val Thr Tyr Thr His Gly Ala His
 530 535 540
 55 Arg Val Ala Phe Ser Ala Gly Lys Thr Arg Ala Gly Met Asn Cys Ser
 545 550 555 560
 Gly Gly Val Cys Arg Val Val Pro Glu Thr Gln Gly Phe Tyr Leu Ser
 565 570 575
 60 Tyr Ser Thr Asn Leu
 580

(2) INFORMATION FOR SEQ ID NO:500

- 65 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 239 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 70 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 75 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

WO 99/29870

PCT/AU98/01023

460/ 490

(1x) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...239

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:508

Met	Arg	Ser	Leu	Phe	Leu	Ser	Ala	Leu	Arg	Ser	Ser	Ser	Leu	His	Gly
1				5					10					15	
Ser	Glu	Arg	Arg	Ser	Arg	Ile	Ser	Ser	Ser	Val	Val	Met	Ser	Ile	Arg
		20					25						30		
Gln	Lys	Ile	Arg	Leu	Phe	His	Leu	Ser	Val	Cys	Ala	Gln	Thr	His	Asp
		35					40					45			
His	Leu	Ile	Glu	Ile	His	Leu	Val	Cys	Ile	Glu	Phe	Gly	Ala	Ile	Asp
	50					55					60				
Thr	Asp	Glu	Phe	Arg	Leu	Ser	Ser	His	Ala	Tyr	Thr	Thr	Ser	Pro	Thr
	65				70					75				80	
His	Thr	Gly	Ala	Ile	His	His	Asn	Cys	Ile	Glu	Arg	Ser	Tyr	Gly	Arg
		85					90						95		
Tyr	Leu	Val	Thr	Phe	Gly	Gln	Glu	Arg	Asn	Glu	Leu	His	His	Ser	
		100					105						110		
Arg	Pro	Asp	Arg	Asn	Ala	Glu	Val	Tyr	Arg	Phe	Pro	Phe	Asp	Asn	Ala
		115				120						125			
Phe	His	Ser	Ile	Arg	Tyr	Glu	Ala	Phe	Arg	Pro	Ile	Arg	Pro	Ile	Val
	130					135					140				
Cys	His	Arg	Asp	His	Phe	Ile	Ala	Ile	Gly	Ser	His	Leu	Phe	Phe	Lys
	145				150					155				160	
Asp	Asn	Gln	Ile	Phe	Ser	Ser	Gly	Ser	Gln	Tyr	Asp	Asn	Tyr	Thr	Val
		165							170					175	
Ala	Cys	Phe	Val	Glu	Ser	Leu	His	Asp	Arg	Glu	Gln	Arg	Ser	His	Thr
		180						185					190		
His	Thr	Ala	Ser	Gly	Thr	Asn	His	Cys	Ala	Asp	Leu	Phe	Asp	Met	Arg
	195					200						205			
Thr	Leu	Ser	Gln	Arg	Thr	Tyr	His	Ile	Arg	Asp	Ile	Val	Ala	Asp	Phe
	210					215					220				
Glu	Phe	Gly	Gln	Phe	Leu	Gly	Arg	Phe	Ala	His	Gly	Leu	Asn	His	
	225				230					235					

(2) INFORMATION FOR SEQ ID NO:509

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 211 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

50 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...211

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:509

Met	Ser	Ile	Arg	Gln	Lys	Ile	Arg	Leu	Phe	His	Leu	Ser	Val	Cys	Ala
1				5					10					15	
Gln	Thr	His	Asp	His	Leu	Ile	Glu	Ile	His	Leu	Val	Cys	Ile	Glu	Phe
		20					25						30		
Gly	Ala	Ile	Asp	Thr	Asp	Glu	Phe	Arg	Leu	Ser	Ser	His	Ala	Tyr	Thr
		35				40						45			
Thr	Ser	Pro	Thr	His	Thr	Gly	Ala	Ile	His	His	Asn	Cys	Ile	Glu	Arg
	50					55					60				
Ser	Tyr	Gly	Arg	Tyr	Leu	Val	Thr	Phe	Gly	Gln	Glu	Arg	Asn	Glu	Leu
	65				70				75					80	
His	His	His	Ser	Arg	Pro	Asp	Arg	Asn	Ala	Glu	Val	Tyr	Arg	Phe	Pro
		85					90						95		
Phe	Asp	Asn	Ala	Phe	His	Ser	Ile	Arg	Tyr	Glu	Ala	Phe	Arg	Pro	Ile
		100					105					110			
Arg	Pro	Ile	Val	Cys	His	Asp	Asp	His	Phe	Ile	Ala	Ile	Gly	Ser	His
	115					120						125			
Leu	Phe	Phe	Lys	Asp	Asn	Gln	Ile	Phe	Ser	Ser	Gly	Ser	Gln	Tyr	Asp
	130					135					140				

WO 99/29870

PCT/AU98/01023

462/ 490

5 Leu Pro Gly Tyr Leu Tyr Thr Asp Thr Gly Phe Trp Asp Thr Phe Arg
 355 360 365
 Ala Leu Phe Pro Leu Leu Asn Leu Leu Tyr Pro Asp Glu Asn Ile Lys
 370 375 380
 10 Ile Gln Glu Gly Leu Leu Asn Val Tyr Arg Glu Ser Gly Phe Phe Pro
 385 390 395 400
 Glu Trp Ala Ser Pro Gly His Arg Asp Cys Met Ile Gly Asn Asn Ser
 405 410 415
 15 Ala Ser Val Leu Ala Asp Ala Tyr Leu Lys Gly Val Arg Val Glu Asp
 420 425 430
 Thr Arg Thr Leu Met Asn Gly Leu Leu His Ala Thr Lys Ala Val His
 435 440 445
 Pro Lys Ile Ser Ser Thr Gly Arg Lys Gly Trp Glu Trp Tyr Asn Ser
 450 455 460
 20 Leu Gly Tyr Val Pro Ala Asp Ala Gly Ile Asp Glu Ser Ala Ala Arg
 465 470 475 480
 Thr Leu Glu Tyr Ala Tyr Asn Asp Trp Cys Ile Leu Arg Leu Gly Arg
 485 490 495
 25 Thr Leu Gly Trp Asp Arg Ala Ala Leu Asp Thr Leu Ala His Arg Ser
 500 505 510
 Met Asn Tyr Arg His Leu Phe Asp Pro Glu Thr Lys Leu Met Arg Gly
 515 520 525
 Arg Asn Gln Asp Gly Ser Phe Arg Thr Pro Phe Ser Pro Phe Lys Trp
 530 535 540
 30 Gly Asp Val Phe Thr Glu Gly Asn Ala Trp His Tyr Thr Trp Ser Val
 545 550 555 560
 Phe His Asp Val Gln Gly Leu Ile Asp Leu Met Gly Gly Asp Arg Pro
 565 570 575
 35 Phe Val Ser Met Leu Asp Ser Val Phe Asn Thr Pro Pro Met Phe Asp
 580 585 590
 Glu Ser Tyr Tyr Gly Phe Val Ile His Glu Ile Arg Glu Met Gln Ile
 595 600 605
 Ala Asp Met Gly Asn Tyr Ala His Gly Asn Gln Pro Ile Gln His Met
 610 615 620
 40 Ile Tyr Leu Tyr Asn His Ala Gly His Pro Trp Lys Ala Gln Glu Arg
 625 630 635 640
 Leu Arg Glu Val Met Gly Arg Leu Tyr Arg Pro Thr Pro Asp Gly Tyr
 645 650 655
 45 Cys Gly Asp Glu Asp Asn Gly Gln Thr Ser Ala Trp Tyr Val Phe Ser
 660 665 670
 Ala Leu Gly Phe Tyr Pro Val Thr Pro Ala Thr Asp Gln Tyr Val Leu
 675 680 685
 Gly Ser Pro Ile Phe Ser Lys Val Ile Leu Ser Phe Pro Asp Gly His
 690 695 700
 50 Lys Thr Val Leu His Ala Pro Ala Asn Ser Ala Asp Thr Pro Tyr Ile
 705 710 715 720
 Arg Ser Ile Ser Val Glu Gly Lys Glu Trp Ser Cys Asn Tyr Leu Thr
 725 730 735
 55 His Glu Gln Leu Arg Ser Ser Ala Ser Ile Gln Trp Met Met Asp Thr
 740 745 750
 Lys Pro Asn Tyr Asn Arg Gly Met Lys Glu Ser Asp Arg Pro Tyr Ser
 755 760 765
 Phe Ser Thr Glu Gln Gln Arg Arg Ala Asn His Ser Asn
 770 775 780

(2) INFORMATION FOR SEQ ID NO:511

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511

463/ 490

Met Met Lys Ser Met Arg Ser Val Leu Leu Leu Leu Phe Pro Leu Ser
 1 5 10 15
 Leu Ile Thr Ala Leu Gly Cys Ser Asn Asn Lys Ala Ala Glu Ser Lys
 20 25 30
 5 Ser Val Ser Phe Asp Ser Ala Tyr Leu Glu Arg Tyr Ile Pro Leu Arg
 35 40 45
 Ala Asp Ile Asp Thr Pro Ser Leu His Val Met Ile Ser Tyr Val Tyr
 50 55 60
 10 Pro Ser Gly Asp Asp Met Leu Thr Glu Ile Phe Asn Gly Leu Leu Phe
 65 70 75 80
 Gly Asp Ser Leu Met Asp Ser Ser Ser Pro Glu Asn Ala Met Glu Gly
 85 90 95
 Tyr Ala Gln Met Leu Gly Glu Asp Tyr Arg Ser Asn Asn Ala Glu Ala
 100 105 110
 15 Asn Leu Gln Gly Leu Pro Ser Asp Leu Leu Asp Tyr Ile Tyr Lys Gln
 115 120 125
 Glu Asn Thr Ile Ala Tyr Cys Asp Thr Gly Leu Ile Ser Thr Arg Ile
 130 135 140
 20 Asn Thr Tyr Thr Tyr Glu Gly Gly Ala His Thr Glu Asn Thr Val Arg
 145 150 155 160
 Phe Ala Asn Ile Leu Arg Thr Thr Gly Lys Val Leu Glu Glu Arg Asp
 165 170 175
 Ile Phe Lys Ile Asp Tyr Ala Glu Arg Leu Ser Ala Leu Ile Ile Gly
 180 185 190
 25 Glu Leu Val His Asp Phe Gly Lys Thr Thr Pro Ala Glu Leu Asp Ala
 195 200 205
 Ile Gly Phe Phe Asn Ala Glu Glu Ile Gln Pro Asn Gly Asn Phe Met
 210 215 220
 30 Ile Asp Asp Lys Gly Leu Thr Tyr Cys Phe Asn Glu Tyr Gln Ile Ala
 225 230 235 240
 Ala Tyr Ala Arg Gly Ala Val Tyr Val Arg Leu Gly Tyr Asp Val Leu
 245 250 255
 Ala Pro Leu Leu Arg Asp Asp Ser Pro Leu Lys Arg Tyr Leu Pro
 260 265 270

(2) INFORMATION FOR SEQ ID NO:512

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512

Met Lys Ser Met Arg Ser Val Leu Leu Leu Leu Phe Pro Leu Ser Leu
 1 5 10 15
 Ile Thr Ala Leu Gly Cys Ser Asn Asn Lys Ala Ala Glu Ser Lys Ser
 20 25 30
 60 Val Ser Phe Asp Ser Ala Tyr Leu Glu Arg Tyr Ile Pro Leu Arg Ala
 35 40 45
 Asp Ile Asp Thr Pro Ser Leu His Val Met Ile Ser Tyr Val Tyr Pro
 50 55 60
 65 Ser Gly Asp Asp Met Leu Thr Glu Ile Phe Asn Gly Leu Leu Phe Gly
 65 70 75 80
 Asp Ser Leu Met Asp Ser Ser Ser Pro Glu Asn Ala Met Glu Gly Tyr
 85 90 95
 Ala Gln Met Leu Gly Glu Asp Tyr Arg Ser Asn Asn Ala Glu Ala Asn
 100 105 110
 70 Leu Gln Gly Leu Pro Ser Asp Leu Leu Asp Tyr Ile Tyr Lys Gln Glu
 115 120 125
 Asn Thr Ile Ala Tyr Cys Asp Thr Gly Leu Ile Ser Thr Arg Ile Asn
 130 135 140
 75 Thr Tyr Thr Tyr Glu Gly Gly Ala His Thr Glu Asn Thr Val Arg Phe
 145 150 155 160

WO 99/29870

PCT/AU98/01023

464/490

Ala Asn Ile Leu Arg Thr Thr Gly Lys Val Leu Glu Glu Arg Asp Ile
165 170 175
Phe Lys Ile Asp Tyr Ala Glu Arg Leu Ser Ala Leu Ile Ile Gly Gln
180 185 190
5 Leu Val His Asp Phe Gly Lys Thr Thr Pro Ala Glu Leu Asp Ala Ile
195 200 205
Gly Phe Phe Asn Ala Glu Glu Ile Gln Pro Asn Gly Asn Phe Met Ile
210 215 220
10 Asp Asp Lys Gly Leu Thr Tyr Cys Phe Asn Glu Tyr Gln Ile Ala Ala
225 230 235 240
Tyr Ala Arg Gly Ala Val Tyr Val Arg Leu Gly Tyr Asp Val Leu Ala
245 250 255
Pro Leu Leu Arg Asp Asp Ser Pro Leu Lys Arg Tyr Leu Pro
260 265 270

15 (2) INFORMATION FOR SEQ ID NO:513
(1) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 267 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(11) MOLECULE TYPE: protein
25 (12) HYPOTHETICAL: YES
(13) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
30 (14) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...267

35 (15) SEQUENCE DESCRIPTION: SEQ ID NO:513
Met Arg Ser Val Leu Leu Leu Leu Phe Pro Leu Ser Leu Ile Thr Ala
1 5 10 15
Leu Gly Cys Ser Asn Asn Lys Ala Ala Glu Ser Lys Ser Val Ser Phe
20 25 30
40 Asp Ser Ala Tyr Leu Glu Arg Tyr Ile Pro Leu Arg Ala Asp Ile Asp
35 40 45
Thr Pro Ser Leu His Val Met Ile Ser Tyr Val Tyr Pro Ser Gly Asp
50 55 60
45 Asp Met Leu Thr Glu Ile Phe Asn Gly Leu Leu Phe Gly Asp Ser Leu
65 70 75 80
Met Asp Ser Ser Ser Pro Glu Asn Ala Met Glu Gly Tyr Ala Gln Met
85 90 95
Leu Gly Glu Asp Tyr Arg Ser Asn Asn Ala Glu Ala Asn Leu Gln Gly
100 105 110
50 Leu Pro Ser Asp Leu Leu Asp Tyr Ile Tyr Lys Gln Glu Asn Thr Ile
115 120 125
Ala Tyr Cys Asp Thr Gly Leu Ile Ser Thr Arg Ile Asn Thr Tyr Thr
130 135 140
55 Tyr Glu Gly Gly Ala His Thr Glu Asn Thr Val Arg Phe Ala Asn Ile
145 150 155 160
Leu Arg Thr Thr Gly Lys Val Leu Glu Glu Arg Asp Ile Phe Lys Ile
165 170 175
Asp Tyr Ala Glu Arg Leu Ser Ala Leu Ile Ile Gly Gln Leu Val His
180 185 190
60 Asp Phe Gly Lys Thr Thr Pro Ala Glu Leu Asp Ala Ile Gly Phe Phe
195 200 205
Asn Ala Glu Glu Ile Gln Pro Asn Gly Asn Phe Met Ile Asp Asp Lys
210 215 220
65 Gly Leu Thr Tyr Cys Phe Asn Glu Tyr Gln Ile Ala Ala Tyr Ala Arg
225 230 235 240
Gly Ala Val Tyr Val Arg Leu Gly Tyr Asp Val Leu Ala Pro Leu Leu
245 250 255
Arg Asp Asp Ser Pro Leu Lys Arg Tyr Leu Pro
260 265

70 (2) INFORMATION FOR SEQ ID NO:514
(1) SEQUENCE CHARACTERISTICS:
75 (A) LENGTH: 259 amino acids
(B) TYPE: amino acid

465/ 490

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

10 (ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514

15 Met Lys Lys Thr Thr Leu Thr Gly Ser Ile Cys Ala Leu Leu Leu Phe
1 5 10 15
Leu Gly Leu Ser Ala Asn Ala Gln Ser Lys Leu Lys Ile Lys Ser Ile
20 20 25 30
Glu Ala Ala Thr Thr Phe Ser Ser Ala Thr Ala Gly Asn Gly Phe Gly
35 40 45
Gly Asn Ile Phe Gly Met Asp Met Ser Ile Arg Met Arg Val His His
50 55 60
Ser Ile Leu Pro Glu Gly Leu Asp Phe Ser Val Gly Ile His Glu Arg
25 65 70 75 80
Arg Ala His Trp Glu Ala Gly Ser Pro Lys Leu Met Tyr Thr Asn
85 90 95
Val Pro Ser Ile Ile Gly Ile Val Glu Lys Val Ile Val Phe Glu Asp
100 105 110
30 Ala Glu Asp Phe Phe Asp Lys Lys Ala Leu Gly Arg Phe Leu Ile Ser
115 120 125
Leu Gly Ile Ser Tyr Thr Lys His Leu Gly Ala Tyr Trp Gly Trp Thr
130 135 140
35 Asn Asp Ala His Ile Leu Phe Ser Pro Ile Pro Lys Ser Lys Val His
145 150 155 160
Tyr Asp Thr Tyr Thr Arg Ala Gly Ser Asp Leu Val Leu Gln Ser Glu
165 170 175
Asp Val Ala Thr Val Ser Asn Gly Phe Ser Pro Gly Ile Gly Leu Lys
180 185 190
40 Ser Ser Ile Trp Trp Lys Met Pro Ile Lys Ser Lys Tyr Asp Phe Arg
195 200 205
Leu Gly Phe Ser Leu Gly Tyr Glu Tyr Leu Asn Leu Leu Tyr Pro Tyr
210 215 220
45 Arg Asn Phe Lys Leu Asp Gly Asn Lys Pro Leu Ser Ala Leu Ser Pro
225 230 235 240
Arg Met Asn His Ile Gly His Val Gly Phe Asn Phe Thr Val Gly Leu
245 250 255
Trp Thr Asn

50 (2) INFORMATION FOR SEQ ID NO:515

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1266 amino acids

55 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

60 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

65 (ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...1266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515

70 Met Gly Lys Tyr Lys Arg Ala Lys Tyr Arg Tyr Trp Leu Phe Pro Phe
1 5 10 15
Cys Ser Asp Tyr Tyr Thr Phe Glu Gly Val Thr Phe Leu Cys Ala Ser
20 25 30
75 Asp Asp Met Thr Thr Lys Lys Pro Gln Ala Ile Leu Asp Leu Glu Lys

WO 99/29870

PCT/AU98/01023

468/490

5 1235 1240 1245
Glu Phe Lys Glu Lys Ile Leu Arg Ile Thr Lys Gln Glu Val Asn Thr
 1250 1255 1260
Asp Glu
1265

(2) INFORMATION FOR SEQ ID NO:516

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1232 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1232

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:516

Met Thr Thr Lys Lys Pro Gln Ala Ile Leu Asp Leu Glu Lys Ala Tyr
1 5 10 15
Asn Ile Glu Ile Pro Asp Leu Ser Ser Gln Glu Gly Ile Ser Trp Ser
20 25 30
Val Asn Arg Tyr Phe Lys Gln Asp Ser Ser Gly Ala Val Val Glu Leu
35 40 45
Cys Leu Arg Glu Cys Gln Ile Glu Ser Met Thr Trp Leu Ile Asp Phe
50 55 60
Pro Ala Leu Lys Lys Leu Asp Leu Ser Tyr Asn Gln Ile Ser Lys Leu
65 70 75 80
Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys Leu Arg Leu Arg Ser
85 90 95
Asn Gln Ile Arg Lys Leu Glu Gly Leu Asp Ser Leu Thr Ser Leu Thr
100 105 110
Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu
115 120 125
Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu Asp Asn Gln Ile Ser
130 135 140
Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Thr Leu Glu Leu
145 150 155 160
Ser Gly Asn Gln Ile Arg Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser
165 170 175
Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu Gly
180 185 190
Leu Glu Arg Leu Thr Ser Leu Thr Lys Leu Arg Leu Arg Ser Asn Gln
195 200 205
Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Thr Leu
210 215 220
Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu Gly Leu Glu Arg Leu
225 230 235 240
Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Ser Lys Leu
245 250 255
Glu Gly Leu Glu Arg Leu Ser Ser Leu Thr Lys Leu Arg Leu Arg Ser
260 265 270
Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr
275 280 285
Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu
290 295 300
Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu Asp Asn Gln Ile Arg
305 310 315 320
Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys Leu Arg Leu
325 330 335
Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu Asp Ser Leu Thr Ser
340 345 350
Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys Leu Glu Gly
355 360 365
Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu Asp Asn Gln
370 375 380
Ile Arg Lys Leu Glu Gly Leu Asp Gly Leu Ala Ser Leu Thr Arg Leu

WO 99/29870

PCT/AU98/01023

469/490

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WO 99/29870

PCT/AU98/01023

470/ 490

Arg Lys Lys Arg Pro Ile Gln Asp Leu Tyr Leu Ser Cys Ala Gln Ala
995 1000 1005
Asp Lys Asp Leu Thr Glu Ser His Tyr Ile His Leu Gly Thr Leu Asp
1010 1015 1020
5 Asp Glu Ser Lys Thr Thr Ala Arg Ile Ala Ala Tyr Pro Leu Lys Asn
1025 1030 1035 1040
Gly Val Ile Asp Lys Glu Arg Val Arg Glu Val Ser Thr Arg Pro Tyr
1045 1050 1055
Lys His Leu Ser Val Asn Lys Asn Leu Ala Thr Ala Lys Gln Ile Phe
1060 1065 1070
10 Ile Ser Tyr Ser Lys Glu Asp Gln Thr Glu Leu Glu Thr Cys Leu Gln
1075 1080 1085
Phe Phe Lys Pro Leu Glu Lys Asn Gly Gln Ile Glu Ile Tyr Tyr Asp
1090 1095 1100
15 Lys Leu Thr Lys Phe Glu Thr Pro Ile His Pro Glu Ile Arg Lys Arg
1105 1110 1115 1120
Ile Val Glu Ala Asp Cys Ile Ile Ala Leu Ile Ser Gln Arg Tyr Leu
1125 1130 1135
20 Ala Thr Asp Tyr Ile Leu Asp His Glu Leu Pro Val Phe Arg Glu Tyr
1140 1145 1150
Asn Lys Thr Ile Val Pro Ile Leu Ile Lys Pro Cys Thr Phe Glu Asp
1155 1160 1165
Asp Glu Phe Leu Arg Glu Lys Tyr Phe Ala Gln Lys Ala Gln Ile Ile
1170 1175 1180
25 Asn Leu Gly Lys Glu Gly Lys Thr Ile Lys Ala Tyr Asp Ser Ile Thr
1185 1190 1195 1200
Ala Ser Ala His Arg Asp Glu Asn Trp Val Ala Val Val Arg Glu Phe
1205 1210 1215
30 Lys Glu Lys Ile Leu Arg Ile Thr Lys Gln Glu Val Asn Thr Asp Glu
1220 1225 1230

(2) INFORMATION FOR SEQ ID NO:517

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- 40 (ii) MOLECULE TYPE: protein
- 45 (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1175
- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:517

Met Thr Trp Leu Ile Asp Phe Pro Ala Leu Lys Lys Leu Asp Leu Ser
1 5 10 15
55 Tyr Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu
20 25 30
Thr Lys Leu Arg Leu Arg Ser Asn Gln Ile Arg Lys Leu Glu Gly Leu
35 40 45
Asp Ser Leu Thr Ser Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile
50 55 60
60 Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr
65 70 75 80
Leu Leu Asp Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr
85 90 95
65 Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu
100 105 110
Gly Leu Glu Arg Leu Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn
115 120 125
Gln Ile Arg Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys
130 135 140
70 Leu Arg Leu Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg
145 150 155 160
Leu Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys
165 170 175
75 Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Thr Leu Glu Leu Ser
180 185 190

WO 99/29870

PCT/AU98/01023

473/ 490

5 Val Ser 35 Thr Glu Val Trp Gly 40 Met Thr His Asp Ala 45 Asn Gly Leu Pro
50 Phe Glu Ile Pro Ile Ser 55 Phe Ser Arg Phe Asn Ser Gln Gly Asp Ile
65 Ala Thr Thr Tyr Tyr Ile Ala Asn Ser Glu Ala Thr Leu Asn Glu Trp
85 Cys Asp Tyr Ala His Pro Gly Gly Ile Val Arg Val Glu Gly Arg Phe
100 Trp Lys Met Thr Tyr Asn Ile Pro Thr Tyr Asn Ala Val Cys Thr Arg
115 Ile Thr Phe Glu Asn Gln Glu Ile Glu Gly Thr Ile Val Leu Ile Pro
130 Lys Pro Lys Val Ser Leu Pro His Val Ser Glu Ser Val Pro Cys Ile
145 Arg Thr Glu Ala Gly Arg Glu Phe Ile Leu Cys Glu Glu Asp Asp Thr
165 Phe Val Ser His Asp Gly Asn Glu Val Thr Ile Gly Gly Lys Pro Phe
180 Leu Leu Asn Thr Asn Val Lys Ile Val Gly Asp Val Ser Gln Lys Tyr
195 Ala Val Gly Val Gly Glu Ile Arg Phe Leu Gln Ile Cys Ala Gln Thr
210 Val Ser Gln Gln Lys 215 220 225

(2) INFORMATION FOR SEQ ID NO:519

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 228 amino acids
(R) TYPE: amino acid
(D) TOPOLOGY: linear
- 35 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
40 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(D) LOCATION 1...228
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:519

Met Lys Lys Ala Phe Val Phe Val Leu Leu Val Cys Leu Phe Ser Ser
1 5 10 15
50 Phe Ser Ser Ser Ala Gln Thr Thr Thr Asn Ser Ser Arg Ser Tyr Phe
20 25 30
Thr Gly Arg Ile Glu Lys Val Ser Leu Asn Leu Gly Val Pro Pro Val
35 40 45
Ser Thr Glu Val Trp Gly Met Thr His Asp Ala Asn Gly Leu Pro Phe
50 55 60
55 Glu Ile Pro Ile Ser Phe Ser Arg Phe Asn Ser Gln Gly Asp Ile Ala
65 70 75 80
Thr Thr Tyr Tyr Ile Ala Asn Ser Glu Ala Thr Leu Asn Glu Trp Cys
85 90 95
60 Asp Tyr Ala His Pro Gly Gly Ile Val Arg Val Glu Gly Arg Phe Trp
100 105 110
Lys Met Thr Tyr Asn Ile Pro Thr Tyr Asn Ala Val Cys Thr Arg Ile
115 120 125
Thr Phe Glu Asn Gln Glu Ile Glu Gly Thr Ile Val Leu Ile Pro Lys
130 135 140
65 Pro Lys Val Ser Leu Pro His Val Ser Glu Ser Val Pro Cys Ile Arg
145 150 155 160
Thr Glu Ala Gly Arg Glu Phe Ile Leu Cys Glu Glu Asp Asp Thr Phe
165 170 175
70 Val Ser His Asp Gly Asn Glu Val Thr Ile Gly Gly Lys Pro Phe Leu
180 185 190
Leu Asn Thr Asn Val Lys Ile Val Gly Asp Val Ser Gln Lys Tyr Ala
195 200 205
Val Gly Val Gly Glu Ile Arg Phe Leu Gln Ile Cys Ala Gln Thr Val
210 215 220
75 Ser Gln Gln Lys

WO 99/29870

PCT/AU98/01023

474/ 490

225

(2) INFORMATION FOR SEQ ID NO:520

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 540 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

15 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...540

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:520

Met Lys Thr Lys Val Leu Arg Lys Phe Val Val Ala Ala Phe Ala Val
 1 5 10 15
 25 Ala Thr Leu Cys Pro Leu Ala Gln Ala Gln Thr Met Gly Gly Asp Asp
 20 25 30
 Val Lys Val Val Gln Tyr Asn Gln Glu Lys Leu Val Gln Thr Arg Met
 35 40 45
 30 Ser Val Ala Asp Asn Gly Trp Ile Tyr Val Met Thr His Ser Gly Tyr
 50 55 60
 Asp Thr Gly Asn Ser Asn Val Lys Ile Phe Arg Ser Lys Asp Gln Gly
 65 70 75 80
 Ala Thr Tyr Gln Lys Leu Arg Asp Trp Asp Pro Ser Asp Asp Tyr Gln
 85 90 95
 35 Phe Gln Asp Phe Asp Ile Val Val Thr Gly Lys Asn Glu Ser Asp Ile
 100 105 110
 Lys Ile Trp Ser Val Glu Leu Met Asn Lys Pro Gly Gly Tyr Lys Ser
 115 120 125
 40 Arg Val Ala Val Phe Ser Arg Asp Ala Asn Ala Gln Asn Ala Lys Leu
 130 135 140
 Val Tyr Lys Glu Asp Phe Ser Asn Val Gln Leu Tyr Asp Val Asp Ile
 145 150 155 160
 Ala Ser Asn Tyr Arg Ser Pro Ser Ser Leu Asn Asn Gly Gly Asn Pro
 165 170 175
 45 Phe Ala Leu Ala Phe Ala Tyr Thr Gly Phe Asn Asn Thr His Lys Ile
 180 185 190
 Ser Phe Val Asp Tyr Val Phe Ser Leu Asn Gly Gly Gln Asn Phe Asn
 195 200 205
 50 Lys Asn Leu Leu Phe Ser Gln Asp Gly Glu Lys Lys Ile Asp Lys Val
 210 215 220
 Asp Leu Ser Leu Gly Ser Thr Ser Glu Ser Met Gly His Asn Ala Trp
 225 230 235 240
 Pro Leu Met Gly Val Val Phe Glu Met Asn Lys Gln Gly Gly Lys Ser
 245 250 255
 55 Asp Ile Gly Phe Leu Ser Asn Phe Val Asp Asn Asp Pro Glu Phe Gln
 260 265 270
 Trp Ser Gly Pro Ile Lys Val Ser Glu Ser Asp Met Ser Phe Ser Pro
 275 280 285
 60 Lys Ile Gln Met Leu Leu Asp Glu Asp Asn Asn Thr Ile Asn Gly Glu
 290 295 300
 Ser Cys His Asn Phe Met Ile Thr Tyr Ser Asp Tyr Asp Ser Glu Tyr
 305 310 315 320
 Ser Asp Trp Asp Ile Arg Tyr Val Tyr Pro Lys Lys Ser Phe Lys Tyr
 325 330 335
 65 Glu Lys Gly Lys Thr Pro Thr Met Asp Asp Leu Val Glu Ala Phe Leu
 340 345 350
 Thr Ala Ser Tyr Gln Ser Glu Thr Asn Ser Gly Leu Gly Tyr Asp Lys
 355 360 365
 Asn Ala Asn His Tyr Leu Ile Thr Tyr Ala Lys Lys Glu Glu Asn Gly
 370 375 380
 70 Thr Asn Thr Leu Lys Tyr Arg Trp Ala Asn Tyr Asp Lys Ile His Asn
 385 390 395 400
 Lys Asp Leu Trp Ser Asp Thr Phe Thr Tyr Thr Ser Ser Ala Asn Ala
 405 410 415
 75 Leu Tyr Thr Pro Gln Val Asp Ile Asn Pro Thr Lys Gly Leu Val Cys

WO 99/29870

PCT/AU98/01023

475 / 490

5 Trp Ser Trp Val Glu Tyr Leu Pro Gly Lys Arg Ile Val Trp Ser Asp
435 440 445
Thr Gln Trp Thr His Ala Asn Gly Val Glu Asp Ile Val Met Gln Glu
450 455 460
Gly Ser Met Lys Leu Tyr Pro Asn Pro Ala Gln Glu Tyr Ala Val Ile
465 470 475 480
Ser Leu Pro Thr Ala Ala Asn Cys Lys Ala Val Val Tyr Asp Met Gln
485 490 495
10 Gly Arg Val Val Ala Glu Ala Ser Phe Ser Gly Asn Glu Tyr Arg Leu
500 505 510
Asn Val Gln His Leu Ala Lys Gly Thr Tyr Ile Leu Lys Val Val Ser
515 520 525
15 Asp Thr Glu Arg Phe Val Glu Lys Leu Ile Val Glu
530 535 540

(2) INFORMATION FOR SEQ ID NO:521

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 771 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
30 (A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...771

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:521

Met Leu Thr Ile Arg Asn Phe Leu Leu Phe Cys Cys Leu Ser Leu Ile
1 5 10 15
40 Ala Phe Ala Ala Asp Ala Gln Ser Ser Val Ser Ser Gly Arg Arg Leu
20 25 30
Thr Glu Tyr Val Asn Pro Phe Ile Gly Thr Ala Asn Tyr Gly Thr Thr
35 40 45
Asn Pro Gly Ala Val Leu Pro Asn Gly Leu Met Ser Val Thr Pro Phe
50 55 60
45 Asn Val Ser Gly Ser Thr Glu Asn Arg Phe Asp Lys Asp Ser Arg Trp
65 70 75 80
Trp Ser Ala Pro Tyr Ser Ala Asp Asn Ser Tyr Cys Ile Gly Phe Ser
85 90 95
50 His Val Asn Leu Ser Gly Val Gly Cys Pro Glu Leu Ser Gly Ile Leu
100 105 110
Leu Met Ala Thr Ser Gly Thr Phe Asp Pro Asp Tyr Cys Tyr Gly
115 120 125
Ser Ser Leu Ser Arg Glu Tyr Ala Arg Pro Gly Glu Tyr Lys Ala Val
130 135 140
55 Leu Asp Lys Tyr Gly Ile Asp Ala Ala Val Thr Val Thr Glu Arg Thr
145 150 155 160
Ala Leu Thr Glu Phe Ala Phe Pro Glu Gly Glu Gly His Ile Leu Leu
165 170 175
60 Asn Leu Gly Gln Ala Leu Ser Asn Glu Ser Gly Ala Ser Val Arg Phe
180 185 190
Leu Asn Asp Ser Thr Val Val Gly Ser Arg Leu Met Gly Thr Phe Cys
195 200 205
Tyr Asn Pro Gln Ala Val Phe Arg Gln Tyr Phe Val Leu Gln Val Ser
210 215 220
65 Arg Arg Pro Ile Ser Ala Gly Tyr Trp Lys Lys Gln Pro Pro Met Thr
225 230 235 240
Val Glu Ala Gln Trp Asp Ser Thr Ala Gly Lys Tyr Lys Gln Tyr Asp
245 250 255
70 Gly Tyr Lys Arg Glu Met Ser Gly Asp Asp Ile Gly Val Arg Phe Ser
260 265 270
Phe Asn Cys Asp Gln Gly Glu Lys Ile Tyr Val Arg Ser Ala Val Ser
275 280 285
Phe Val Ser Glu Ala Asn Ala Leu Tyr Asn Leu Glu Ala Glu Gln Glu
290 295 300
75 Glu Val Phe Lys Ser Val Gly Gly Asn Pro Ala Lys Ala Phe Ser Ala

WO 99/29870

PCT/AU98/01023

476/ 490

305 310 315 320
Ile Arg Ser Arg Ala Ile Glu Arg Trp Glu Glu Ala Leu Gly Thr Val
325 330 335
5 Glu Val Glu Gly Gly Thr Pro Asp Glu Lys Thr Ile Phe Tyr Thr Ala
340 345 350
Leu Tyr His Leu Leu Ile His Pro Asn Ile Leu Gln Asp Ala Asn Gly
355 360 365
Glu Tyr Pro Met Met Gly Ser Gly Lys Thr Gly Asn Thr Ala His Asp
370 375 380
10 Arg Tyr Thr Val Phe Ser Leu Trp Asp Thr Tyr Arg Asn Val His Pro
385 390 395 400
Leu Leu Cys Leu Leu Tyr Pro Glu Lys Gln Leu Asp Met Val Arg Thr
405 410 415
15 Leu Ile Asp Met Tyr Arg Glu Ser Gly Trp Leu Pro Arg Trp Glu Leu
420 425 430
Tyr Gly Gln Glu Thr Leu Thr Met Glu Gly Asp Pro Ser Leu Ile Val
435 440 445
Ile Asn Asp Thr Trp Gln Arg Gly Leu Arg Ala Phe Asp Thr Ala Thr
450 455 460
20 Ala Tyr Glu Ala Met Lys Lys Asn Ala Ser Ser Ala Gly Ala Thr His
465 470 475 480
Pro Ile Arg Pro Asp Asn Asp Asp Tyr Leu Thr Leu Gly Phe Val Pro
485 490 495
25 Leu Arg Glu Gln Tyr Asp Asn Ser Val Ser His Ala Leu Glu Tyr Tyr
500 505 510
Leu Ala Asp Trp Asn Leu Ser Arg Phe Ala His Ala Leu Gly His Lys
515 520 525
Glu Asp Ala Ala Leu Phe Gly Lys Arg Ser Leu Gly Tyr Arg His Tyr
530 535 540
30 Tyr Asn Lys Glu Tyr Gly Met Leu Cys Pro Leu Leu Pro Asp Gly Ser
545 550 555
Phe Leu Thr Pro Phe Asp Pro Lys Gln Gly Glu Asn Phe Glu Pro Asn
565 570 575
35 Pro Gly Phe His Glu Gly Ser Ala Tyr Asn Tyr Ala Phe Phe Val Pro
580 585 590
His Asp Ile Gln Gly Leu Ala Arg Leu Met Gly Gly Ala Lys Val Phe
595 600 605
Ser Glu Arg Leu Gln Lys Val Phe Asp Glu Gly Tyr Tyr Asp Pro Thr
610 615 620
40 Asn Glu Pro Asp Ile Ala Tyr Pro Tyr Leu Phe Ser Tyr Phe Pro Lys
625 630 635
Glu Ala Trp Arg Thr Gln Lys Leu Thr Arg Glu Leu Ile Asp Lys His
645 650 655
45 Phe Cys Asn Ala Pro Asn Gly Leu Pro Gly Asn Asp Asp Ala Gly Thr
660 665 670
Met Ser Ala Trp Leu Val Tyr Ser Met Leu Gly Phe Tyr Pro Asp Cys
675 680 685
Pro Gly Ser Pro Thr Tyr Thr Leu Thr Ser Pro Val Phe Pro Arg Val
690 695 700
50 Arg Ile Arg Leu Asn Pro Gln Tyr Tyr Pro Gln Gly Glu Leu Ile Ile
705 710 715 720
Thr Thr Asn Thr Glu Asn Gln Pro Thr Asp Ser Ile Tyr Ile His Thr
725 730 735
Val Ser Leu Gly Asn Lys Thr Leu Pro His Gly Thr Arg His Ile Ser
740 745 750
55 His Ala Asp Leu Val Arg Cys Gly His Leu Arg Tyr Glu Leu Ser Asn
755 760 765
Arg Pro Arg
770

(2) INFORMATION FOR SEQ ID NO:522

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 776 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(11) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(11) FEATURE:

WO 99/29870

PCT/AU98/01023

477/ 490

(A) NAME/KEY: misc feature
(B) LOCATION 1...776

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:522

5
Met Cys Lys Ile Arg Phe Ser Leu Leu Gln Ala Leu Val Val Cys Leu
1 5 10 15
Leu Phe Thr Ser Phe Ser Leu Gln Ala Gln Glu Glu Gly Ile Trp Asn
20 25 30
10 Thr Leu Leu Ala Ile His Lys Thr Glu Lys Ala Val Glu Thr Pro Lys
35 40 45
Lys Val Phe Ala Val Ala Asn Gly Val Leu Tyr Ser Val Gly Lys Glu
50 55 60
15 Ala Pro His Glu Ala Lys Ile Phe Asp Arg Ile Ser Gly Leu Ser Asp
65 70 75 80
Thr Ser Val Ser Ser Ile Ala Tyr Ser Glu Gln Leu Lys Ser Leu Val
85 90 95
Ile Tyr Tyr Ala Ser Gly Asn Ile Asp Ile Leu Asp Glu Ala Gly Arg
100 105 110
20 Val Thr Asn Val Pro Ala Leu Lys Asp Asn Ile Asp Leu Ile Asp Lys
115 120 125
Thr Leu Asn Arg Leu Leu Ile Val Gly Asn Arg Ala Tyr Leu Ala Gly
130 135 140
25 Gly Phe Gly Leu Ser Val Leu Asp Val Ala Glu Ala Arg Ile Pro Ala
145 150 155 160
Thr Tyr Ala Lys Gly Thr Lys Val Thr Asp Val Ala Lys Leu Asp Asn
165 170 175
Asp Arg Leu Leu Met Leu Lys Glu Gly Gln Leu Phe Ile Gly Lys Glu
180 185 190
30 Thr Asp Asn Leu Gln Asp Pro Ala Ala Trp Thr Ala Leu Ser Leu Asn
195 200 205
Leu Pro Met Gly Ser Val Thr Gly Leu Gly Ile Val Gly Glu Asp Ile
210 215 220
35 Cys Phe Leu Leu Ala Asp Gly Arg Val Tyr Val Ala Ala Asn Gln Ser
225 230 235 240
Phe Glu Pro Glu Leu Leu Leu Ser Ser Ser Ala Asp Ser Arg Leu Tyr
245 250 255
Val Thr Asp Arg Gly Leu Phe Ile Cys Ala Glu Asn Arg Ile Tyr Phe
260 265 270
40 Ile Glu Lys Gly Arg Lys Thr Thr Gln Phe Pro Ile Ala Asp Val Leu
275 280 285
Gly Val Gly Ala Met Asn Glu Ser Asn Thr Ala Tyr Ile Ala Leu Gly
290 295 300
45 Glu Glu Gly Leu Ala Ser Leu Leu Leu Ala Glu Gly Ser Thr Ala Glu
305 310 315 320
Ala Met Pro Val Ala Phe Asp Gly Pro Gly Asp Asn Asp Phe Tyr Glu
325 330 335
Met Arg Phe Ser His Gly Arg Leu Tyr Ala Ala Ser Gly Leu Trp Gly
340 345 350
50 Thr Asn Leu Met Gly His Ala Gly Met Val Lys Leu Tyr Asp Gly Asn
355 360 365
Arg Trp Thr Asn Phe Asp Lys Lys Thr Val Gln Glu Gln Leu Gly Gly
370 375 380
55 Gly Phe Ser Phe Asn Asp Ala Ile Asp Ile Ala Val Ser Asn Gly Asp
385 390 395 400
Pro Asp His Phe Phe Val Gly Thr Trp Gly Asn Gly Leu Phe Glu Phe
405 410 415
Lys Asp Gly Lys Ala Ile Ala Arg Tyr Ser Gly Asn Glu Thr Ala Ile
420 425 430
60 Ala Glu Cys Asn Pro Gly Asp Ala Arg Val Lys Ala Ile Ala Phe Asp
435 440 445
Asn Lys Gly Asn Leu Trp Gly Thr Leu Gly Ala Val Gly Lys Asn Ile
450 455 460
65 Phe Met Tyr Asp Pro Gln Ser Ser Thr Trp His Ser Phe Ser Tyr Pro
465 470 475 480
Asp Val Ala Asn Leu Ala Ser Phe Gly Asn Met Ile Ile Leu Pro Asn
485 490 495
Gly Asp Lys Trp Val Asn Ile Leu His Arg Ser Gly Gly Ser Thr Arg
500 505 510
70 Lys Gly Val Leu Ile Phe Asn Asp Arg Gly Thr Pro Glu Thr Thr Ser
515 520 525
Asp Asp Ser His Leu Tyr Val Glu Gln Phe Val Asn Arg Leu Gly Ala
530 535 540
75 Ala Ile Gly His Lys Thr Ile Tyr Ala Met Ala Val Asp His Asn Gly
545 550 555 560

478/ 490

Ser Val Trp Met Gly Ser Asp Ile Gly Ile Phe Gly Val Tyr Asn Ala
 565 570 575
 Ala Gly Val Leu Ser Ser Thr Ser Thr Pro Ile Ala Val Arg Pro Val
 580 585 590
 5 Gly Gly Glu Glu Pro Asn Leu Tyr Tyr Val Leu Asp Lys Val Thr Val
 595 600 605
 Thr Asp Ile Val Val Asp Lys Leu Asn His Lys Trp Val Ala Thr Gln
 610 615 620
 10 Gly Thr Gly Leu Tyr Leu Leu Ser Glu Asp Cys Ser Lys Ile Leu Ala
 625 630 635 640
 Gln Phe Thr Val Glu Asn Ser Pro Leu Leu Ser Asn Asn Ile Leu Ser
 645 650 655
 Leu Ala Leu Asn Asp Asp Asn Gly Leu Leu Tyr Ile Gly Thr Ala Asp
 660 665 670
 15 Gly Leu Met Thr Phe Gln Thr Gly Thr Gly Ser Gly Ser Ala Ser Glu
 675 680 685
 Leu Asp Gly Val Tyr Val Tyr Pro Asn Pro Leu Arg Pro Glu Tyr Pro
 690 695 700
 20 Asp Gly Val Thr Ile Ala Gly Leu Gln Ala Gly Cys Ser Val Lys Ile
 705 710 715 720
 Thr Asp Thr Thr Gly Arg Leu Leu Tyr Gln Thr Glu Ser Val Thr Thr
 725 730 735
 Glu Val Lys Trp Asn Ala Arg Gly Ala Asp Gly Asn Arg Val Ala Ser
 740 745 750
 25 Gly Val Tyr Ala Val Ala Val Tyr Asp Pro Val Ser Lys Lys Ser Lys
 755 760 765
 Leu Ile Arg Phe Ala Val Ile Arg
 770 775
 30 (2) INFORMATION FOR SEQ ID NO:523
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1158 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 35
 (ii) MOLECULE TYPE: protein
 40 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 45 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1...1158
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:523
 50 Met Lys Arg Ile Leu Pro Ile Val Ala Phe Leu Ser Leu Phe Leu Ala
 1 5 10 15
 Leu Ala Leu Pro Ala Lys Ala Gln Arg Ala Met Gly Lys Thr Ala Asp
 20 25 30
 55 Arg Ser Leu Met Ala Ser Gly His Trp Val Lys Ile Arg Val Asp Ala
 35 40 45
 Ser Gly Val Tyr Arg Leu Thr Asp Glu Gln Leu Arg Ala Asn Gly Phe
 50 55 60
 Ser Asp Pro Ser Lys Val Gly Val Phe Gly Tyr Gly Gly Gly Val Leu
 65 70 75 80
 60 Pro Glu Asp Leu Ser Arg Ile Thr Thr Asp Asp Leu Pro Pro Val Pro
 85 90 95
 Val Leu Arg Gln Gly Asn Ala Leu Tyr Phe Tyr Ala Val Gly Pro Val
 100 105 110
 65 Thr Trp Phe Tyr Asn Pro Ala Lys Thr Thr Met Glu His Thr Val Asn
 115 120 125
 Thr Tyr Ser Thr His Gly Tyr Tyr Phe Leu Ser Asp Ala Ala Gly Ala
 130 135 140
 Pro Leu Gln Met Ser Gln Tyr Thr Gly Gly Gly Ala Ser Ala Glu Ala
 145 150 155 160
 70 Leu Ile Asp Tyr Tyr Asp Glu Leu Met Leu His Glu Gln Glu Leu Tyr
 165 170 175
 Ser Pro Lys Glu Ser Gly Arg Asp Leu Tyr Gly Glu Ser Phe Ser Ala
 180 185 190
 75 Val Asn Thr Arg Thr Val Lys Phe Pro Leu Arg Gly Asn Thr Arg Ser
 195 200 205

WO 99/29870

PCT/AU98/01023

479/ 490

Ser Gly Glu Leu Gly Thr Val Phe Ser Tyr Ile Ala Lys Ala Arg Ser
 210 215 220
 Ala Gly Gly Gly Arg Glu Met Ser Leu Ser Ala Asn Gly Ile Leu Ile
 225 230 235 240
 5 Phe Ser Asp Pro Phe Ser Met Thr Ser Asn Glu Val Ser Asn Ser Tyr
 245 250 255
 Leu Ala Gly Lys Lys Arg Arg Leu Tyr His Ser Thr Pro Met Asn Ser
 260 265 270
 10 Leu Val Asn Glu Leu Arg Leu Asp Ala Asn Tyr Ser Met Thr Gly Asp
 275 280 285
 Ala Val Asn Leu Asp Phe Ile Glu Val Ala Thr Gln Asn Asp Leu Arg
 290 295 300
 Tyr Asp Gly Ala Pro Met His Ile Arg Arg Phe Ser Asn Leu Pro Val
 305 310 315 320
 15 Leu Gly Gly Glu Ser Cys Arg Phe Val Ile Ser Glu Val Pro Glu Ser
 325 330 335
 Leu Val Val Leu Gln Ala Asn Ser Ser Leu Thr Ala Ser Leu Val Pro
 340 345 350
 20 Val Lys Thr Val Gly Asp Lys Thr Ile Glu Phe Val Ala Pro Pro Lys
 355 360 365
 Gly Gln Asp Arg Arg Thr Ile Asn Thr Phe Tyr Ala Val Asp Leu Ser
 370 375 380
 Gln Ala Ser Ala Pro Glu Ile Leu Gly Ala Val Pro Asn Gln Asn Leu
 385 390 395 400
 25 His Gly Glu Glu Ile Pro Asp Leu Ile Ile Val Ser Thr Gln Ala Leu
 405 410 415
 Leu Leu Glu Ala Asp Arg Leu Ala Thr Tyr Arg Arg Glu Lys Asn Gly
 420 425 430
 30 Leu Lys Val Leu Val Val Leu Gln Glu Val Phe Asn Glu Phe Ser
 435 440 445
 Gly Gly Thr Pro Asp Ala Thr Ala Tyr Arg Leu Phe Ala Lys Met Phe
 450 455 460
 Tyr Asp Arg Trp Lys Ala Asn Ala Pro Val Gly Glu Thr Phe Pro Met
 465 470 475 480
 35 Gln Met Leu Leu Phe Gly Asp Gly Ala His Asp Asn Arg Lys Val Ser
 485 490 495
 Val Ala Trp Gln Lys Pro Tyr Leu Gln Gln Thr Glu Phe Leu Leu Thr
 500 505 510
 40 Phe Gln Ala Val Asn Ser Thr Asn Val Asn Ser Tyr Val Thr Asp Asp
 515 520 525
 Tyr Phe Gly Leu Leu Asp Asp Gln Pro Ala Ser Val Asn Ile Gly Trp
 530 535 540
 Arg Asn Tyr Asn Met Ala Val Gly Arg Phe Pro Val Arg Thr Pro Ala
 545 550 555 560
 45 Glu Ala Arg Ile Ala Val Asp Lys Thr Ile Arg Tyr Glu Glu Asp Arg
 565 570 575
 Glu Ser Gly Ala Trp Arg Ile Arg Ala Cys Phe Ala Ala Asp Asn Gly
 580 585 590
 50 Asp Lys His Ala Thr Glu Thr Ser Arg Leu Ile Asp Thr Val Lys Arg
 595 600 605
 Tyr Ala Pro Ala Ile Met Pro Val Arg Ala Phe Gln Asp Val Tyr Pro
 610 615 620
 His Val Ile Glu Asn Gly Leu His Ser Ile Pro Gly Ala Lys Lys Lys
 625 630 635 640
 55 Met Leu Glu Thr Leu Gln Ser Gly Ile Ile Leu Asn Tyr Ala Gly
 645 650 655
 His Gly Gly Pro Ala Gly Trp Ser Asp Glu His Leu Leu Thr Leu Asn
 660 665 670
 60 Asp Ile His Lys Phe Asn Tyr Lys His Met Pro Ile Trp Ile Thr Ala
 675 680 685
 Thr Cys Asp Phe Ala Asn Tyr Asp Ser Gln Thr Thr Ser Ala Gly Glu
 690 695 700
 Glu Val Phe Leu His Glu Lys Ser Gly Thr Pro Ile Met Phe Ser Thr
 705 710 715 720
 65 Thr Arg Val Val Tyr Asn Thr Gln Asn Glu Lys Ile Asn Gly Phe Met
 725 730 735
 Leu Arg Arg Met Phe Glu Lys Ala Lys Asp Gly Arg Tyr Arg Thr Met
 740 745 750
 70 Gly Glu Ile Ile Arg Ser Ala Lys Gln Gly Met Leu Ser Thr Val Phe
 755 760 765
 Pro Asp Ser Ile Asn Gln Leu Ser Phe Phe Leu Met Gly Asp Pro Ser
 770 775 780
 Val Arg Met Asn Leu Pro Thr His Lys Val Gln Leu Thr Ala Ile Asn
 785 790 795 800
 75 Gly Gln Asp Pro Glu Gly Gln Tyr Gly Thr Ile Met Leu Lys Ser Leu

WO 99/29870

PCT/AU98/01023

483/490

Arg Asp Tyr Thr Gly Trp Phe Ala Met Tyr Asp Thr Asn Lys Val Gly
 130 135 140
 Leu Val Asp Phe Ile Tyr Asn Arg Pro Arg Pro Asn Asp Asp Glu Phe
 145 150 155 160
 5 Pro Lys Tyr Glu Ala Gln Tyr Leu Gly Ile Glu Met Phe Gly Met Lys
 165 170 175
 Leu Lys Gln Thr Gly Gly Asn Tyr Met Thr Asp Gly Tyr Gly Ser Ala
 180 185 190
 10 Val Gln Ser His Ile Ala Tyr Thr Glu Asn Ser Ser Leu Ser Gln Ala
 195 200 205
 Gln Val Asn Gln Lys Met Lys Asp Tyr Leu Gly Ile Thr His His Asp
 210 215 220
 Val Val Gln Asp Pro Asn Gly Glu Tyr Ile Asn His Val Asp Cys Trp
 225 230 235 240
 15 Gly Lys Tyr Leu Ala Pro Asn Lys Ile Leu Ile Arg Lys Val Pro Asp
 245 250 255
 Asn His Pro Gln His Gln Ala Leu Glu Asp Met Ala Ala Tyr Phe Ala
 260 265 270
 20 Ala Gln Thr Cys Ala Trp Gly Thr Lys Tyr Glu Val Tyr Arg Ala Leu
 275 280 285
 Ala Thr Asn Glu Gln Pro Tyr Thr Asn Ser Leu Ile Leu Asn Asn Arg
 290 295 300
 Val Phe Val Pro Val Asn Gly Pro Ala Ser Val Asp Asn Asp Ala Leu
 305 310 315 320
 25 Asn Val Tyr Lys Thr Ala Met Pro Gly Tyr Glu Ile Ile Gly Val Lys
 325 330 335
 Gly Ala Ser Gly Thr Pro Trp Leu Gly Thr Asp Ala Leu His Cys Arg
 340 345 350
 30 Thr His Glu Val Ala Asp Lys Gly Tyr Leu Tyr Ile Lys His Tyr Pro
 355 360 365
 Ile Leu Gly Glu Gln Ala Gly Pro Asp Tyr Lys Ile Glu Ala Asp Val
 370 375 380
 Val Ser Cys Ala Asn Ala Thr Ile Ser Pro Val Gln Cys Tyr Tyr Arg
 385 390 395 400
 35 Ile Asn Gly Ser Gly Ser Phe Lys Ala Ala Asp Met Thr Met Glu Ser
 405 410 415
 Thr Gly His Tyr Thr Tyr Ser Phe Thr Gly Leu Asn Lys Asn Asp Lys
 420 425 430
 40 Val Glu Tyr Tyr Ile Ser Ala Ala Asp Asn Ser Gly Arg Lys Glu Thr
 435 440 445
 Tyr Pro Phe Ile Gly Glu Pro Asp Pro Phe Lys Phe Thr Cys Met Asn
 450 455 460
 Glu Thr Asn Thr Cys Thr Val Thr Gly Ala Ala Lys Ala Leu Arg Ala
 465 470 475 480
 45 Trp Phe Asn Ala Gly Arg Ser Glu Leu Ala Val Ser Val Ser Leu Asn
 485 490 495
 Ile Ala Gly Thr Tyr Arg Ile Lys Leu Tyr Asn Thr Ala Gly Glu Glu
 500 505 510
 50 Val Ala Ala Met Thr Lys Glu Leu Val Ala Gly Thr Ser Val Phe Ser
 515 520 525
 Met Asp Val Tyr Ser Gln Ala Pro Gly Thr Tyr Val Leu Val Val Glu
 530 535 540
 Gly Asn Gly Ile Arg Glu Thr Met Lys Ile Leu Lys
 545 550 555

(2) INFORMATION FOR SEQ ID NO:526

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 428 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (iv) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...428
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:526

WO 99/29870

PCT/AU98/01023

484/ 490

Met Lys Leu Ser Ser Lys Lys Ile Leu Ala Ile Ile Ala Leu Leu Thr
1 5 10 15
Met Gly His Ala Val Gln Ala Gln Phe Val Pro Ala Pro Thr Thr Gly
20 25 30
5 Ile Arg Met Ser Val Thr Thr Thr Lys Ala Val Gly Glu Lys Ile Glu
35 40 45
Leu Leu Val His Ser Ile Glu Lys Lys Gly Ile Trp Ile Asp Leu Asn
50 55 60
10 Gly Asp Ala Thr Tyr Gln Gln Gly Glu Glu Ile Thr Val Phe Asp Glu
65 70 75 80
Ala Tyr His Glu Tyr Thr Ile Gly Thr Gln Thr Leu Thr Ile Tyr Gly
85 90 95
Asn Thr Thr Arg Leu Gly Cys Arg Ser Thr Gly Ala Thr Ala Val Asp
100 105 110
15 Val Thr Lys Asn Pro Asn Leu Thr Tyr Leu Ala Cys Pro Lys Asn Asn
115 120 125
Leu Lys Ser Leu Asp Leu Thr Gln Asn Pro Lys Leu Leu Arg Val Trp
130 135 140
20 Cys Asp Ser Asn Glu Ile Glu Ser Leu Asp Leu Ser Gly Asn Pro Ala
145 150 155 160
Leu Ile Ile Leu Gly Cys Asp Arg Asn Lys Leu Thr Glu Leu Lys Thr
165 170 175
Asp Asn Asn Pro Lys Leu Ala Ser Leu Trp Cys Ser Asp Asn Asn Leu
180 185 190
25 Thr Glu Leu Glu Leu Ser Ala Asn Pro Arg Leu Asn Asp Leu Trp Cys
195 200 205
Phe Gly Asn Arg Ile Thr Lys Leu Asp Leu Ser Ala Asn Pro Leu Leu
210 215 220
30 Val Thr Leu Trp Cys Ser Asp Asn Glu Leu Ser Thr Leu Asp Leu Ser
225 230 235 240
Lys Asn Ser Asp Val Ala Tyr Leu Trp Cys Ser Ser Asn Lys Leu Thr
245 250 255
Ser Leu Asn Leu Ser Gly Val Lys Gly Leu Ser Val Leu Val Cys His
260 265 270
35 Ser Asn Gln Ile Ala Gly Glu Glu Met Thr Lys Val Val Asn Ala Leu
275 280 285
Pro Thr Leu Ser Pro Gly Ala Gly Ala Gln Ser Lys Phe Val Val Val
290 295 300
40 Asp Leu Lys Asp Thr Asp Glu Lys Asn Ile Cys Thr Val Lys Asp Val
305 310 315 320
Glu Lys Ala Lys Ser Lys Asn Trp Arg Val Phe Asp Phe Asn Gly Asp
325 330 335
Ser Asp Asn Met Leu Pro Tyr Glu Gly Ser Pro Thr Ser Asn Leu Ala
340 345 350
45 Val Asp Ala Pro Thr Val Arg Ile Tyr Pro Asn Pro Val Gly Arg Tyr
355 360 365
Ala Leu Val Glu Ile Pro Glu Ser Leu Leu Gly Gln Glu Ala Ala Leu
370 375 380
50 Tyr Asp Met Asn Gly Val Lys Val Tyr Ser Phe Ala Val Glu Ser Leu
385 390 395 400
Arg Gln Asn Ile Asp Leu Thr His Leu Pro Asp Gly Thr Tyr Phe Phe
405 410 415
Arg Leu Asp Asn Tyr Thr Thr Lys Leu Ile Lys Gln
420 425

(2) INFORMATION FOR SEQ ID NO:527

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 310 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527

WO 99/29870

PCT/AU98/01023

485/ 490

Met Arg Lys Thr Ile Ile Phe Cys Leu Leu Leu Ala Leu Phe Gly Cys
1 5 10 15
Ser Trp Ala Gln Glu Arg Val Asp Glu Lys Val Phe Ser Ala Gly Thr
20 25 30
5 Ser Ile Phe Arg Gly Ile Leu Glu Lys Val Lys Ala Pro Leu Met Tyr
35 40 45
Gly Asp Arg Glu Val Trp Gly Met Ala Arg Ala Ser Glu Asp Phe Phe
50 55 60
10 Phe Ile Leu Pro Val Thr Asp Asp Leu Thr Pro Val Leu Phe Tyr Asn
65 70 75 80
Arg Leu Thr Asn Glu Pro Cys Phe Val Ser Asp Gln Gly Ile Thr Glu
85 90 95
Tyr Phe Lys Phe Ala Gln Glu Gly Asp Tyr Ile Glu Val Glu Gly Ser
100 105 110
15 Ser Val Phe Met Ala Asn Leu Leu Tyr Tyr Arg Phe Phe Pro Thr Arg
115 120 125
Ile Thr Ser Tyr Asn Ala Pro Ile Glu Gly Val Val Ser Lys Thr Gly
130 135 140
20 Asn Pro Ala Phe Thr Ile Pro Met Leu Pro Gly Val Ser Asp Cys Ile
145 150 155 160
Glu Ile Ser Asn Asn Arg Lys Val Phe Leu Thr Asn Gln Leu Gly Val
165 170 175
Val Asn Ile Thr Asp Gly Met Glu Pro Ile Ile Ala Gly Val Ser
180 185 190
25 Ala Ser Tyr Gly Ser Ser Val Arg Val Tyr Gly His Val Ser Gln Arg
195 200 205
Trp Asp Ile Ile Gly His Cys Tyr Leu Asp Ile Tyr Pro Thr Asn Cys
210 215 220
30 Tyr Pro Leu Ser Thr Lys Pro Val Ala Gly Asp Asp Glu Val Phe Val
225 230 235 240
Lys Gln Gln Gly Arg Gln Ile Glu Ile Asp Ser Asn Ser Pro Ile Val
245 250 255
Gln Val Val Val Tyr Asp Leu Glu Gly Lys Ser Val Phe Arg Lys Arg
260 265 270
35 Met Thr Glu Asn Ala Tyr Thr Leu Ser Phe Arg Ala Pro Met Leu Gly
275 280 285
Phe Met Thr Ile Met Ile Glu Thr Gln Asn Ser Ile Ile Asn Lys Lys
290 295 300
40 Leu Asn Val Thr Gln Leu
305 310

(2) INFORMATION FOR SEQ ID NO:528

(i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 405 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
50
(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
55 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...405
60
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528

Met Lys Lys Thr Thr Ile Ile Ser Leu Ile Val Phe Gly Ala Phe Phe
1 5 10 15
65 Ala Ala Val Gly Gln Thr Lys Asp Asn Ser Ser Tyr Lys Pro Phe Ser
20 25 30
Lys Glu Asp Ile Ala Gly Gly Val Tyr Ser Leu Pro Thr Gln Asn Arg
35 40 45
Ala Gln Lys Asp Asn Ala Glu Trp Leu Leu Thr Ala Thr Val Ser Thr
50 55 60
70 Asn Gln Ser Ala Asp Thr His Phe Ile Phe Asp Glu Asn Asn Arg Tyr
65 70 75 80
Ile Ala Arg Asp Ile Lys Ala Asn Gly Val Arg Lys Ser Thr Asp Ser
85 90 95
75 Ile Tyr Tyr Asp Ala Asn Gly Arg Ile Ser His Val Asp Leu Tyr Ile
100 105 110

SUBSTITUTE SHEET (Rule 26) (RO/AU)

WO 99/29870

PCT/AU98/01023

486/490

5 Ser Phe Ser Gly Gly Glu Pro Ala Leu Asp Thr Arg Phe Lys Tyr Thr
115 120 125
Tyr Asp Asp Glu Gly Lys Met Thr Val Arg Glu Val Phe Met Leu Val
130 135 140
Met Asp Pro Asn Thr Pro Ile Ser Arg Leu Glu Tyr His Tyr Asp Ala
145 150 155 160
Gln Gly Arg Leu Thr His Trp Ile Ser Phe Ala Phe Gly Ala Glu Ser
165 170 175
10 Gln Lys Asn Thr Tyr His Tyr Asn Glu Lys Gly Leu Leu Val Ser Glu
180 185 190
Val Leu Ser Asn Ala Met Gly Thr Thr Tyr Ser Asp Thr Gly Lys Thr
195 200 205
Glu Tyr Ser Tyr Asp Asp Ala Asp Asn Met Val Lys Ala Glu Tyr Phe
210 215 220
15 Val Val Gln Gln Gly Lys Ala Trp Gln Val Leu Lys Arg Glu Glu Tyr
225 230 235 240
Thr Tyr Glu Asp Asn Ile Cys Ile Gln Tyr Leu Ala Ile Asn Gly Thr
245 250 255
20 Asp Thr Lys Val Tyr Lys Arg Asp Ile Glu Ser Asp Lys Ser Ile Ser
260 265 270
Ala Asn Val Ile Asp Ile Pro Ser Met Pro Glu Gln Thr Trp Pro Asn
275 280 285
Met Tyr Gly Phe Asn Ala Lys Arg Leu Lys Glu Thr Tyr Ser Ser Tyr
290 295 300
25 Glu Gly Asp Val Ala Thr Pro Ile Phe Asp Tyr Ile Tyr Thr Tyr Lys
305 310 315 320
Ala Leu Thr Ser Met Ala Thr Pro Ser Thr Glu Ala Gln Val Ala Val
325 330 335
30 Tyr Leu Asn Pro Ser Thr Asp Arg Leu Val Ile Leu Ala Asn Gly Ile
340 345 350
Thr His Leu Ser Met Tyr Asp Leu Gln Gly Lys Leu Ile Arg Asp Cys
355 360 365
Ala Leu Ser Gly Asp Lys Val Glu Met Gly Val Gly Ser Leu Thr Lys
370 375 380
35 Gly Thr Tyr Leu Leu Lys Val Asn Thr Asp Gln Gly Ala Phe Val Arg
385 390 395 400
Lys Val Val Ile Arg
405

40 (2) INFORMATION FOR SEQ ID NO:529
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2037 base pairs
(B) TYPE: nucleic acid
45 (C) STRANDEDNESS: double
(D) TOPOLOGY: circular
(ii) MOLECULE TYPE: DNA (genomic)
50 (iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
55 (A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...2037
60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:529

65 GTAATGGACT ACAAACTCAC TTCTCGATTG AAGCCCAAGG GCGACCAAGC GGAAGCCATT 60
CGCCAACTCG TACAGGGCAT CAACGAAGGG ATGCCGCTC AGACGCTGCT CGGCGTAACG 120
GGTTCGGGCA AACTTTTAC GTGGGCTAAC GTGGTGGGG CGGTCAATCG TCCGACCCCT 180
GTCTGTAGTC ACAACAAGAC CTTGGCAGCA CAGCTATACG GAGAGTTCAA AGCTTCTTTC 240
CCCCGAGAAT CGGTGGAGTA TTTCGTGAGC TACTACGACT ACTATCAGCC CGAGGGCCTAC 300
CTCCCCGTCA CAGACACCTA TATCGAAAAG GACATGGCCA TCAACGCGGA GATCGAAAAA 360
CTGCGATTGA GGGCCACGGC TTGCTCTCTG TCAGGGGCGA AAGATGTGCT TGTGGTCAGC 420
TCCGTATCCT GTCTCTACGG TATGGCCCAAT CCTGAAGCTT TTTCGAAAAA GGTGATCAGC 480
CTGCACACGG CACAAAGGGC AGACAGGGAT CATTTTATCC GCCTGCTGGT AGAGAGCTAC 540
TACACGAACA ATAAAGTAGA GTTCGAGAGC GGCAACTTCC GTGTCAAAGG CGACAGCGTG 600
GACATATTCC CGCCGTAGA AGGTTATGAC GGCCTGGCAT ACAGGGTGGG GTTTTGGGAT 660
GGAGAGSTCG AGCGGCTGAG TACCTTCGAT CCGCGAAGCG GACGGGAATA CGGCCTGCTG 720
75 TCGAGAGTGA AGATATATCC GGCCAATCTC TTCTGTAGCA CTAAGGAGCA GGTGGATCGG 780

WO 99/29870

PCT/AU98/01023

487 / 490

	GCAGTAGGGA	AAATCGATGT	GCATCTGGGC	GCACAGGTCG	ATT'TTCTGAA	AGAAATCGGC	840
	AAACCATATG	AAGCCAAACG	CTGTATGAG	CGGGTCACGT	ATGACTTGGG	AATGATCCGT	900
	GAGTTGGGTT	ATTGTTCCGG	TATAGAGAAC	TATTCGGGCT	ACTTOGACGG	CCGTGACGG	960
5	GGCGAACGTC	CTTCTGTCT	GTTGGATTAT	TTCCCGGAGG	ATTTCTGT	GSTCATAGAC	1020
	GAAAGCCATG	TAACGATACC	GCAGATACGT	GCCATGTACG	GAGGCGATCG	TTCGCGCAAG	1080
	GAGAACTCTG	TGGAATACGG	ATTCGCGCTG	CCTGCGGCTC	TGCAACATCG	GCCGCTTCGC	1140
	TTGACGAGT	TGGAAGCTCT	CACCCCGCGG	ACCCTTTATA	TCAGTGCCAC	CCCTGCCGAC	1200
	TATGAGCTGA	ACAGAAGCGA	AGGCGTGATC	GTCGAGCAGC	TGATCCGTCC	GACCGGACTG	1260
	CTGGATCCCA	TCATCGACGT	CAAGCCGAGG	GCAAAACCAAG	TGGACGATCT	GATGGAGGAG	1320
10	ATAGCACCGCT	GCATCGAAAA	GAAAGAGCGC	GTACTGGTAA	CGACCGTGAC	CAAACTGATG	1380
	GCAGAGGAGC	TTAGCGAATA	CCTGCTACGC	CACGSTATCA	GCACCGGCTA	CATACACAGC	1440
	GATGTGGACA	CGCTGGAGCG	TGTGCGTATC	ATGGAAGACC	TGCGCAAGGG	GGTCTACGAT	1500
	GCACTCATCG	GGGTGAATCT	GCTCCGCGAA	GGATTGSACT	TGCGGGAAGT	TTCGCTTGTG	1560
	GCTATTCTGG	ATGCGGATAA	GGAAGGATTC	CTGCGCTCGC	ATCGTTGCGT	CACCGAGACT	1620
15	GCAGGAGCTG	CCGCCCGGCA	CATTCTAGGG	CGTGTCTAT	TCTACGCGGA	CAAGATCACC	1680
	GACAGTATGC	AGCTCACCAT	GGACGAGACT	GCACGCGGAC	GCGCAAAGCA	ACTGGCTTAC	1740
	AACGAAGCGC	ACGGGATCAG	CCCCCAACAG	ATAGTGAAGA	ACAGTGCTGC	CATTGGGGGA	1800
	GAAAGCGATG	TGTGCGGCTT	GCAATCCGAT	ACAGAATCCG	GTGCGTACAT	AGAAGAGAGC	1860
	AGCATGCTGG	CTGCCGATCC	TTTGGCCGAC	TATCTGAGCA	AACCCAAAGT	GGAAGCACTC	1920
20	ATTGCTTCGA	CCAAGAAAGCA	AATGCTGGCA	GCAGCCAAAG	AGCTGGACTT	TCTGGAAGCG	1980
	GCACGACTTC	GGGACGAAGC	CGCAGGATTG	GAAAAGAAAC	TGGAGCAACT	CACAGGCC	2037
	(2) INFORMATION FOR SEQ ID NO:530						
25	(i) SEQUENCE CHARACTERISTICS:						
	(A) LENGTH: 2034 base pairs						
	(B) TYPE: nucleic acid						
30	(C) STRANDEDNESS: double						
	(D) TOPOLOGY: circular						
	(ii) MOLECULE TYPE: DNA (genomic)						
35	(iii) HYPOTHETICAL: NO						
	(iv) ANTI-SENSE: NO						
	(vi) ORIGINAL SOURCE:						
40	(A) ORGANISM: Porphyromonas gingivalis						
	(ix) FEATURE:						
	(A) NAME/KEY: misc feature						
	(B) LOCATION 1...2034						
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530						
	ATGGACTACA	AACTCACTTC	TGATTCAAG	CCACGSGGCG	ACCAGCCGGA	AGCCATTGCG	60
	CAACTCGTAC	AGGGCATCAA	CGAAGGGATG	CGGCTCAGA	CGCTGCTCGG	CGTAACGGGT	120
50	TCGGGCAAAA	CTTTACGGT	GGCTAACGTG	GTGGCGGCGG	TCAATCGTCC	GACCCCTTGT	180
	CTGAGTCACA	ACAAGACCTT	GGCAGCACAG	CTATACGGAG	AGTTCAAAGC	CTTCTTCCCC	240
	GAGAATCGCG	TGGAGTATTT	CGTCAGCTAC	TACGACTACT	ATCAGCCCGA	GGCCTACCTC	300
	CCCGTCACAG	ACACCTATAT	CGAAAAGGAC	ATGGCCATCA	ACGCGGAGAT	CGAAAAACTG	360
	CGATTGAGGG	CCACGGGCTC	GCTCCTGTCA	GGGCGGAAAG	ATGTGCTTGT	GGTCAGCTCC	420
55	GTATCCTGTC	TCTACGGTAT	GGCCAACTCT	GAAGCTTTTT	CCGAAAAGGT	GATCAGCCTG	480
	CACACGGGAC	AAAGGGCAGA	CAGGGATCAT	TTTATCCGCC	TGCTGGTAGA	GAGCTACTAC	540
	ACGAACAATA	AAGTAGAGTT	CGAGAGCGGC	AACTTCCGTG	TCAAAGGCGA	CAGCGTGGAC	600
	ATATTCCTCG	CCGTAGAAGG	TTATGACGGC	GTGGCATACA	GGGTGGAGTT	TTGGGATGGA	660
	GAGTCTGAGC	GGCTGAGTAC	CTTCGATCCG	CGAACGGGAC	GGGAATACGG	CCTGCTGTGG	720
60	GAGCTGAAGA	TATATCCGGC	CAATCTCTTC	GTGACGACTA	AGGAGCAGGT	GGATCGGGCA	780
	GTAGGGAAAA	TCATGTGGGA	TCTGGGGCGA	CAGGTCGATT	TTCTGAAAGA	AATCGGCAAA	840
	CCATATGAAG	CCAAACGCTT	GTATGAGCGG	GTACAGTATG	ACTTGGAAAT	GATCGGTGAG	900
	TTGGGTTATT	GTTCGGGTAT	AGAGAATCAT	TGCGCTACT	TGACGGGCGG	TGACGGGGGC	960
	GAACGTCCTT	TCTGTCTGTT	GGATTATTTC	CCGGAGGATT	TCCTGTTGGT	CATAGACGAA	1020
65	AGCCATGTAA	CGATACGGCA	GATACGTGCC	ATGTACGGAG	GCGATCGTTC	GCGCAAGGAG	1080
	AATCTGGTCC	AATACGGATT	CCGCCCTGCC	GCGCTCTCCG	ACAATCGGCC	GCTTCGCTTC	1140
	CACGAGTTCC	AAGCTCTCAC	CCCCCGGACC	CTTTATATCA	GTGCCACGCC	TGCCGACTAT	1200
	GAGCTGAACA	GAAGCGAAGG	CGTGATCGTC	GAGCAGCTGA	TCCGTCGGAC	CGGACTGCTG	1260
	GATCCCATCA	TGCACTCAA	GCCGACGGCA	AACCAAGTGG	ACGATCTGAT	GGAGGAGATA	1320
70	GCACGCTGCA	TGAAAAGAA	AGAGCGCGTA	CTGGTAACGA	CGCTGACCAA	ACGTATGGCA	1380
	GAGGAGCTTA	GCGAATACCT	GCTACGCCAC	GGTATCAGCA	CCGGTACAT	ACACAGCGAT	1440
	GTGGACAGCT	TGGAGCGTGT	GGGTATCATG	GAAGACCTGC	GCAAGGGGGT	CTACGATGCA	1500
	CTCATCGGGG	TGAATCTGCT	CCGCGAAGGA	TTGGACTTGC	CGGAAGTTTC	GCTTGTGGCT	1560
	ATTCTGGATG	CGGATAAGGA	AGGATTCCTG	CGCTCGCATC	GTTCTGCTAC	GCAGACTGCA	1620
75	GGACGTGCGG	CCCGGCACAT	TCATGGGCGT	GTCTATCTTT	ACGCGGACAA	GATCACCAGC	1680
	AGTATGCAAG	TCACCATGGA	CGAGACTGCA	CGCGGACGGG	CAAAGCAACT	GGCTACAAAC	1740

WO 99/29870

PCT/AU98/01023

488 / 490

GAAGCGCACG GCATCACCCC CCAACAGATA GTGAAGAACA GTGCTGCCAT TTGGGGAGAA 1800
GGCGATGTGT CGGCCTTGCA ATCCGATACA GAATCCGGTG CGTACATAGA AGAGAGCAGC 1860
ATGGTGGCTG CGGATCCTTT GGCCGACTAT CTGAGCAAAC CCAAGCTGGA AGCACTCATT 1920
GCTTCGACCA AGAAGCAAT GCTGGCAGCA GCCAAAGAGC TGGACTTTCT GGAAGCGGCA 1980
5 CGACTTCGGG ACGAAGCCGC ACGATTGGAA AAGAACTGG AGCAACTCAC AGCC 2034

(2) INFORMATION FOR SEQ ID NO:531

10

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 679 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

20

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...679

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531

Val Met Asp Tyr Lys Leu Thr Ser Arg Phe Lys Pro Thr Gly Asp Gln
1 5 10 15
30 Pro Glu Ala Ile Arg Gln Leu Val Gln Gly Ile Asn Glu Gly Met Pro
20 25 30
Ala Gln Thr Leu Leu Gly Val Thr Gly Ser Gly Lys Thr Phe Thr Val
35 40 45
Ala Asn Val Val Ala Ala Val Asn Arg Pro Thr Leu Val Leu Ser His
50 55 60
35 Asn Lys Thr Leu Ala Ala Gln Leu Tyr Gly Glu Phe Lys Ala Phe Phe
65 70 75 80
Pro Glu Asn Ala Val Glu Tyr Phe Val Ser Tyr Tyr Asp Tyr Tyr Gln
85 90 95
40 Pro Glu Ala Tyr Leu Pro Val Thr Asp Thr Tyr Ile Glu Lys Asp Met
100 105 110
Ala Ile Asn Ala Glu Ile Glu Lys Leu Arg Leu Arg Ala Thr Ala Ser
115 120 125
45 Leu Leu Ser Gly Arg Lys Asp Val Leu Val Val Ser Ser Val Ser Cys
130 135 140
Leu Tyr Gly Met Ala Asn Pro Glu Ala Phe Ser Glu Lys Val Ile Ser
145 150 155 160
Leu His Thr Gly Gln Arg Ala Asp Arg His Phe Ile Arg Leu Leu
165 170 175
50 Val Glu Ser Tyr Tyr Thr Asn Asn Lys Val Glu Phe Glu Ser Gly Asn
180 185 190
Phe Arg Val Lys Gly Asp Ser Val Asp Ile Phe Pro Ala Val Glu Gly
195 200 205
55 Tyr Asp Gly Val Ala Tyr Arg Val Glu Phe Trp Asp Gly Glu Val Glu
210 215 220
Arg Leu Ser Thr Phe Asp Pro Arg Thr Gly Arg Glu Tyr Gly Leu Leu
225 230 235 240
Ser Glu Leu Lys Ile Tyr Pro Ala Asn Leu Phe Val Thr Thr Lys Glu
245 250 255
60 Gln Val Asp Arg Ala Val Gly Lys Ile Asp Val Asp Leu Gly Ala Gln
260 265 270
Val Asp Phe Leu Lys Glu Ile Gly Lys Pro Tyr Glu Ala Lys Arg Leu
275 280 285
65 Tyr Glu Arg Val Thr Tyr Asp Leu Glu Met Ile Arg Glu Leu Gly Tyr
290 295 300
Cys Ser Gly Ile Glu Asn Tyr Ser Arg Tyr Phe Asp Gly Arg Asp Ala
305 310 315 320
Gly Glu Arg Pro Phe Cys Leu Leu Asp Tyr Phe Pro Glu Asp Phe Leu
325 330 335
70 Leu Val Ile Asp Glu Ser His Val Thr Ile Pro Gln Ile Arg Ala Met
340 345 350
Tyr Gly Gly Asp Arg Ser Arg Lys Glu Asn Leu Val Glu Tyr Gly Phe
355 360 365
75 Arg Leu Pro Ala Ala Leu Asp Asn Arg Pro Leu Arg Phe Asp Glu Phe
370 375 380

WO 99/29870

PCT/AU98/01023

490/490

	Leu	Ser	Gly	Arg	Lys	Asp	Val	Leu	Val	Val	Ser	Ser	Val	Ser	Cys	Leu
	130						135					140				
	Tyr	Gly	Met	Ala	Asn	Pro	Glu	Ala	Phe	Ser	Glu	Lys	Val	Ile	Ser	Leu
	145					150					155					160
5	His	Thr	Gly	Gln	Arg	Ala	Asp	Arg	Asp	His	Phe	Ile	Arg	Leu	Leu	Val
				165						170					175	
	Glu	Ser	Tyr	Tyr	Thr	Asn	Asn	Lys	Val	Glu	Phe	Glu	Ser	Gly	Asn	Phe
				180					185					190		
10	Arg	Val	Lys	Gly	Asp	Ser	Val	Asp	Ile	Phe	Pro	Ala	Val	Glu	Gly	Tyr
		195						200					205			
	Asp	Gly	Val	Ala	Tyr	Arg	Val	Glu	Phe	Trp	Asp	Gly	Glu	Val	Glu	Arg
	210						215					220				
15	Leu	Ser	Thr	Phe	Asp	Pro	Arg	Thr	Gly	Arg	Glu	Tyr	Gly	Leu	Leu	Ser
	225					230					235					240
	Glu	Leu	Lys	Ile	Tyr	Pro	Ala	Asn	Leu	Phe	Val	Thr	Thr	Lys	Glu	Gln
				245						250					255	
	Val	Asp	Arg	Ala	Val	Gly	Lys	Ile	Asp	Val	Asp	Leu	Gly	Ala	Gln	Val
				260					265					270		
20	Asp	Phe	Leu	Lys	Glu	Ile	Gly	Lys	Pro	Tyr	Glu	Ala	Lys	Arg	Leu	Tyr
		275						280					285			
	Glu	Arg	Val	Thr	Tyr	Asp	Leu	Glu	Met	Ile	Arg	Glu	Leu	Gly	Tyr	Cys
	290						295					300				
25	Ser	Gly	Ile	Glu	Asn	Tyr	Ser	Arg	Tyr	Phe	Asp	Gly	Arg	Asp	Ala	Gly
	305					310					315					320
	Glu	Arg	Pro	Phe	Cys	Leu	Leu	Asp	Tyr	Phe	Pro	Glu	Asp	Phe	Leu	Leu
					325					330					335	
	Val	Ile	Asp	Glu	Ser	His	Val	Thr	Ile	Pro	Gln	Ile	Arg	Ala	Met	Tyr
				340					345					350		
30	Gly	Gly	Asp	Arg	Ser	Arg	Lys	Glu	Asn	Leu	Val	Glu	Tyr	Gly	Phe	Arg
			355					360					365			
	Leu	Pro	Ala	Ala	Leu	Asp	Asn	Arg	Pro	Leu	Arg	Phe	Asp	Glu	Phe	Glu
		370					375						380			
	Ala	Leu	Thr	Pro	Arg	Thr	Leu	Tyr	Ile	Ser	Ala	Thr	Pro	Ala	Asp	Tyr
	385						390					395				400
35	Glu	Leu	Asn	Arg	Ser	Glu	Gly	Val	Ile	Val	Glu	Gln	Leu	Ile	Arg	Pro
				405						410					415	
	Thr	Gly	Leu	Leu	Asp	Pro	Ile	Ile	Asp	Val	Lys	Pro	Thr	Ala	Asn	Gln
				420					425					430		
40	Val	Asp	Asp	Leu	Met	Glu	Glu	Ile	Ala	Arg	Cys	Ile	Glu	Lys	Lys	Glu
		435						440					445			
	Arg	Val	Leu	Val	Thr	Thr	Leu	Thr	Lys	Arg	Met	Ala	Glu	Glu	Leu	Ser
		450					455					460				
	Glu	Tyr	Leu	Leu	Arg	His	Gly	Ile	Ser	Thr	Gly	Tyr	Ile	His	Ser	Asp
	465					470					475					480
45	Val	Asp	Thr	Leu	Glu	Arg	Val	Arg	Ile	Met	Glu	Asp	Leu	Arg	Lys	Gly
				485						490					495	
	Val	Tyr	Asp	Ala	Leu	Ile	Gly	Val	Asn	Leu	Leu	Arg	Glu	Gly	Leu	Asp
				500					505					510		
50	Leu	Pro	Glu	Val	Ser	Leu	Val	Ala	Ile	Leu	Asp	Ala	Asp	Lys	Glu	Gly
		515						520					525			
	Phe	Leu	Arg	Ser	His	Arg	Ser	Leu	Thr	Gln	Thr	Ala	Gly	Arg	Ala	Ala
		530					535					540				
	Arg	His	Ile	His	Gly	Arg	Val	Ile	Phe	Tyr	Ala	Asp	Lys	Ile	Thr	Asp
	545					550					555					560
55	Ser	Met	Gln	Leu	Thr	Met	Asp	Glu	Thr	Ala	Arg	Arg	Arg	Ala	Lys	Gln
				565						570					575	
	Leu	Ala	Tyr	Asn	Glu	Ala	His	Gly	Ile	Thr	Pro	Gln	Gln	Ile	Val	Lys
				580					585					590		
60	Asn	Ser	Ala	Ala	Ile	Trp	Gly	Glu	Gly	Asp	Val	Ser	Ala	Leu	Gln	Ser
			595					600					605			
	Asp	Thr	Glu	Ser	Gly	Ala	Tyr	Ile	Glu	Glu	Ser	Ser	Met	Val	Ala	Ala
		610					615						620			
	Asp	Pro	Leu	Ala	Asp	Tyr	Leu	Ser	Lys	Pro	Lys	Leu	Glu	Ala	Leu	Ile
	625					630						635				640
65	Ala	Ser	Thr	Lys	Lys	Gln	Met	Leu	Ala	Ala	Ala	Lys	Glu	Leu	Asp	Phe
				645						650					655	
	Leu	Glu	Ala	Ala	Arg	Leu	Arg	Asp	Glu	Ala	Ala	Arg	Leu	Glu	Lys	Lys
				660					665					670		
70	Leu	Glu	Gln	Leu	Thr	Ala										
				675												

INTERNATIONAL SEARCH REPORT

International application No.
PCT/AU 98/01023

A. CLASSIFICATION OF SUBJECT MATTER		
Int Cl ⁶ : C12N 15/31; C07K 14/195; A61K 38/00, 38/16, 39/00		
According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED		
Minimum documentation searched (classification system followed by classification symbols) See Electronic Database box below		
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched See Electronic Database box below		
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)		
Medline	porphyromonas gingivalis, bacterial proteins, peptides, bacterial vaccines	
CA	porphyromonas gingivalis, genes microbial, antigens	
WPAT	porphoryomonas or porphyromonas gingivalis, C07K 07, 014/195: C12N 15/31 + *Seq IDS 265, 528, 340, 341	
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	Derwent abstract 95-3513214/45 WO 95/26404 (MEITO SANGYO KK) 5 October 1995.	all
A	Derwent abstract 95-147309/19 WO 95/09181 (KYOWA HAKKO KOGYO KK) 6 April 1995.	all
<input type="checkbox"/> Further documents are listed in the continuation of Box C <input checked="" type="checkbox"/> See patent family annex		
<p>* Special categories of cited documents:</p> <p>"A" document defining the general state of the art which is not considered to be of particular relevance</p> <p>"E" earlier application or patent but published on or after the international filing date</p> <p>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</p> <p>"O" document referring to an oral disclosure, use, exhibition or other means</p> <p>"P" document published prior to the international filing date but later than the priority date claimed</p> <p>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</p> <p>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone</p> <p>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art</p> <p>"&" document member of the same patent family</p>		
Date of the actual completion of the international search 11 January 1999		Date of mailing of the international search report 28 JAN 1999
Name and mailing address of the ISA/AU AUSTRALIAN PATENT OFFICE PO BOX 200 WODEN ACT 2606 AUSTRALIA Facsimile No.: (02) 6285 3929		Authorized officer PHILIPPA WYRDEMAN Telephone No.: (02) 6283 2554

INTERNATIONAL SEARCH REPORT

International application No.

PCT/AU 98/01023

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☒ Claims Nos.: 1 to 34 in part
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

The claims are directed to a very large number of polypeptides and nucleotides such that it is economically unfeasible to perform a full and comprehensive search on all the claimed sequences.

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6 4(a)

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No.
PCT/AU 98/01023

This Annex lists the known "A" publication level patent family members relating to the patent documents cited in the above-mentioned international search report. The Australian Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

Patent Document Cited in Search Report				Patent Family Member	
WO	95/26404	EP	753577		
WO	95/09181	EP	726276	JP	7097395